

GenCore version 5.1.4 p5_4578
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OM protein - protein search, using sw model

Run on: April 1, 2003, 11:34:54 ; Search time 75 Seconds
(without alignments)
920.318 Million cell updates/sec

Title: US-09-668-314C-2

Perfect score: 518
Sequence: 1 MGALAPALLPLLAQWLRA.....RPDPPEVNDSSLVRRHWK 518

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

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- 2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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- 22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	518	100.0	518 19	AAW61362 Aspartic proteinase
2	518	100.0	518 20	AAW41714 Human PRO852 prote
3	518	100.0	518 20	AAW22329 Human CSP56, aspar
4	518	100.0	518 20	AAW13799 Human aspartyl pro
5	518	100.0	518 21	AAW43270 Human PRO852 (UNQ4
6	518	100.0	518 21	AAW88424 Human aspartyl pro
7	518	100.0	518 22	AAE10628 Human aspartyl pro
8	518	100.0	518 22	AAE10656 Human Asp 1 protei
9	518	100.0	518 22	AAU29059 Human PRO polypept
10	518	100.0	518 22	AAE06858 Human aspartyl pro

11	518	100.0	518 22	AAU06602 Human Aspartyl pro
12	518	100.0	518 22	AAU07201 Human aspartyl pro
13	518	100.0	518 22	AAE02580 Human aspartyl pro
14	518	100.0	518 22	AAE02608 Human Aspartyl pro
15	518	100.0	518 23	ABW78589 Human Asp-1 protei
16	518	100.0	518 23	ABW78617 Human Asp-1delatM
17	518	100.0	518 23	ABW06531 Human aspartyl pro
18	518	100.0	518 23	ABW07453 Human BACE2 amino
19	481	92.9	481 22	AAW75592 Human colon cancer
20	469	90.5	475 22	AAE10657 Secreted recombin
21	469	90.5	475 22	AAE02609 Human secreted asp
22	469	90.5	475 23	ABW78618 Secreted recombin
23	439	84.7	439 23	ABW90365 Human polypeptide
24	423	81.7	423 22	AAE04796 Human aspartyl pro
25	407	78.6	413 22	AAE10658 Acid-processed hu-
26	407	78.6	413 22	AAE02610 Human acid-process
27	407	78.6	413 23	ABW78619 Asp-1delatM(his)6
28	344	66.4	355 22	AAW93925 Human protein sequ
29	285	55.0	423 22	ABW84479 Human membrane or
30	59	11.4	514 22	AAW84204 Amino acid sequenc
31	50	9.7	50 22	AAW18665 Peptide #5099 enco
32	32	8.5	44 22	ABW32242 Peptide #4893 enco
33	33	8.5	44 22	ABW37490 Peptide #4996 enco
34	34	8.5	44 22	ABW2791 Protein #4790 enco
35	35	8.5	44 22	AAW70610 Human bone marrow
36	36	8.5	44 22	AAW18450 Peptide #4884 enco
37	37	8.5	44 22	AAW30925 Peptide #4662 enco
38	38	8.5	44 22	AAW06046 Peptide #4728 enco
39	39	8.5	44 23	ABW40288 Human peptide enco
40	40	8.5	44 23	ABW11020 Human ORF protein
41	41	8.5	44 22	AAE10665 Human aspartyl pro
42	42	8.5	44 22	AAU06618 Human Aspartyl pro
43	43	8.5	44 22	AAW18450 Amino acid sequenc
44	44	8.5	44 22	AAE10644 Human aspartyl pro
45	45	8.5	44 22	AAE06874 Human aspartyl pro
46	46	8.5	44 22	AAU07217 Human C-terminal A
47	47	8.5	44 22	AAE02596 Human Asp1 peptide
48	48	8.5	44 22	ABW78605 Human BACE2 C-term
49	49	8.5	44 22	ABW07455 Human protein sequ
50	50	8.5	44 22	AAW25497 Novel human enzyme
51	51	8.5	44 22	AAU23633 Novel human enzyme
52	52	8.5	44 22	AAU23068 Novel human enzyme
53	53	8.5	44 22	AAW07369 Amino acid sequenc
54	54	8.5	44 22	AAE02593 Human Asp2 amino a
55	55	8.5	44 22	AAW88437 Human polypeptide,
56	56	8.5	44 22	AAW93866 Human Asp 2 (b) pro
57	57	8.5	44 22	AAE10641 Human Asp2 (b) deli
58	58	8.5	44 22	AAE06871 Human Asp2 (b) deli
59	59	8.5	44 22	AAU07214 Human Asp2 (b) deli
60	60	8.5	44 22	AAE02593 Human aspartyl pro
61	61	8.5	44 22	AAE02593 Human aspartyl pro
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67	67	8.5	44 22	AAE02593 Human aspartyl pro
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79	79	8.5	44 22	AAE02593 Human aspartyl pro
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82	82	8.5	44 22	AAE02593 Human aspartyl pro
83	83	8.5	44 22	AAE02593 Human aspartyl pro

84	12	2.3	446	22	AAE06868	T7-Human-pro-Asp2(157	8	1.5	8	22	AAE10659	Human Aspartyl pro
85	12	2.3	446	22	AAU06612	Human T7-Human-pro	158	8	1.5	8	23	AAE02611	Human Aspartyl pro
86	12	2.3	446	22	AAU07211	T7-Human aspartyl	159	8	1.5	8	22	ABB78620	Human Asp-1 subser
87	12	2.3	446	22	AAE02590	T7-Human-pro-Asp-2	160	8	1.5	105	21	AAE45058	Arabidopsis thalia
88	12	2.3	446	21	ABB78599	Modified human asp	161	8	1.5	131	22	AAU23632	Novel human enzyme
89	12	2.3	453	21	AAE88438	Human-Asp2(a) pro	162	8	1.5	177	16	AAE80012	Human LBP(1-197)
90	12	2.3	453	22	AAE10642	Human-Asp2(a) delc	163	8	1.5	205	19	AAW98673	H. pylori GHPD 530
91	12	2.3	453	22	AAE06872	Human-pro-Asp 2(a)	164	8	1.5	224	17	AAW16833	Recombinant endoto
92	12	2.3	453	22	AAU06616	Human aspartyl pro	165	8	1.5	239	22	ABG09608	Novel human diago
93	12	2.3	453	22	AAU07215	Human aspartyl pro	166	8	1.5	262	22	AAW41741	Human polypeptide
94	12	2.3	453	22	AAE02594	Human-Asp-2(a) delc	167	8	1.5	285	21	AAE12962	Arabidopsis thalia
95	12	2.3	453	23	ABB78603	Human Asp-2(a) delc	168	8	1.5	287	23	ABB91441	Heticidially activ
96	12	2.3	456	21	AAE07897	Active enzyme port	169	8	1.5	297	22	AAE78949	C. glutamicum SRT
97	12	2.3	459	21	AAE88432	T7-caspase-human-p	170	8	1.5	307	21	AAE12861	Arabidopsis thalia
98	12	2.3	459	21	AAE88439	Modified human asp	171	8	1.5	313	22	ABG09606	Novel human diago
99	12	2.3	459	22	AAE10639	T7-Caspase-human-p	172	8	1.5	335	22	ABG18051	Novel human diago
100	12	2.3	459	22	AAE10643	Human-Asp 2(a) pro	173	8	1.5	341	20	AAE32039	Bovine pregnancy a
101	12	2.3	459	22	AAE06869	T7-Caspase-Human-p	174	8	1.5	356	22	AAW79898	Human protein SBQ
102	12	2.3	459	22	AAE06873	Human-Asp2(a) delc	175	8	1.5	358	22	AAU41391	Propionibacterium
103	12	2.3	459	22	AAU06613	Human T7-Caspase-H	176	8	1.5	380	20	AAE32041	Bovine pregnancy a
104	12	2.3	459	22	AAU06617	Human-pro-Asp 2(a)	177	8	1.5	446	17	AAW16810	Recombinant endoto
105	12	2.3	459	22	AAU07212	T7-caspase-human a	178	8	1.5	457	17	AAW16811	Recombinant endoto
106	12	2.3	459	22	AAU07216	Human aspartyl pro	179	8	1.5	458	22	AAE89932	C glutamicum prote
107	12	2.3	459	22	AAE02591	T7-Caspase-human-p	180	8	1.5	465	16	AAE76242	Recombinant LBP.
108	12	2.3	459	22	AAE02595	Human-Asp-2(a) delc	181	8	1.5	472	22	AAE39955	Recombinant LBP.
109	12	2.3	459	22	ABB78600	T7-caspase-human-p	182	8	1.5	473	22	ABB71149	Drosophila melanog
110	12	2.3	459	23	ABB78604	Human Asp-2(a) delc	183	8	1.5	475	23	ABB91454	Heticidially activ
111	12	2.3	460	21	AAE07898	Amino acid sequenc	184	8	1.5	477	14	AAE41660	Human gram-negativ
112	12	2.3	476	21	AAE88426	Human aspartyl pro	185	8	1.5	477	15	AAE53459	Human lipopolysacc
113	12	2.3	476	21	AAE10630	Human aspartyl pro	186	8	1.5	479	17	AAW16795	Recombinant endoto
114	12	2.3	476	22	AAE06860	Human aspartyl pro	187	8	1.5	479	17	AAW16799	Recombinant endoto
115	12	2.3	476	22	AAE06909	Murine aspartyl pr	188	8	1.5	479	17	AAW16808	Recombinant endoto
116	12	2.3	476	22	AAU06604	Human Aspartyl pro	189	8	1.5	479	17	AAW05242	Recombinant endoto
117	12	2.3	476	22	AAU07203	Human aspartyl pro	190	8	1.5	480	17	AAW16821	Recombinant endoto
118	12	2.3	476	22	AAE02582	Human aspartyl pro	191	8	1.5	480	17	AAW16822	Recombinant endoto
119	12	2.3	476	22	AAE02619	Murine aspartyl pr	192	8	1.5	481	14	AAE34140	LBP-beta. Synthet
120	12	2.3	476	23	ABB78591	Human Asp-2(b) pro	193	8	1.5	481	15	AAE62501	LBP amino terminal
121	12	2.3	476	23	ABB06410	Human aspartyl pro	194	8	1.5	481	16	AAE80994	Lipopolysaccharide
122	12	2.3	476	23	ABB06120	Human NS protein s	195	8	1.5	481	16	AAE81246	Recombinant lipopo
123	12	2.3	488	22	AAE66572	Human memapsin 2.	196	8	1.5	481	16	AAE880014	Human LBP. Homo s
124	12	2.3	488	22	AAE61334	Memapsin 2 protein	197	8	1.5	481	16	AAE68922	Lipopolysaccharide
125	12	2.3	488	22	AAU99488	Human memapsin 2.	198	8	1.5	481	16	AAE68000	rlBP. Homo sapien
126	12	2.3	501	19	AAE59807	Amino acid sequenc	199	8	1.5	481	16	AAE76601	Recombinant human
127	12	2.3	501	21	AAE94767	Human beta-secret	200	8	1.5	481	17	AAE16829	Recombinant endoto
128	12	2.3	501	21	AAE94768	Murine beta-secret	201	8	1.5	481	17	AAE16830	Recombinant endoto
129	12	2.3	501	21	AAE94769	Rat beta-secretase	202	8	1.5	481	17	AAE16831	Recombinant endoto
130	12	2.3	501	21	AAE07896	Amino acid sequenc	203	8	1.5	481	17	AAE16836	Recombinant endoto
131	12	2.3	501	21	AAE88425	Human aspartyl pro	204	8	1.5	481	17	AAE16837	Recombinant endoto
132	12	2.3	501	21	AAE88427	Murine aspartyl pr	205	8	1.5	481	17	AAE16838	Recombinant endoto
133	12	2.3	501	22	AAE10629	Human aspartyl pr	206	8	1.5	481	17	AAE16839	Recombinant endoto
134	12	2.3	501	22	AAE10631	Murine aspartyl pr	207	8	1.5	481	17	AAE16840	Recombinant endoto
135	12	2.3	501	22	AAE06859	Human aspartyl pro	208	8	1.5	481	17	AAE19010	Recombinant endoto
136	12	2.3	501	22	AAE06861	Murine aspartyl pr	209	8	1.5	481	17	AAE19011	Recombinant endoto
137	12	2.3	501	22	AAU06603	Human Aspartyl pro	210	8	1.5	481	17	AAE16809	Recombinant endoto
138	12	2.3	501	22	AAU06605	Mouse Aspartyl pro	211	8	1.5	481	17	AAE16807	Recombinant endoto
139	12	2.3	501	22	AAU07202	Human aspartyl pro	212	8	1.5	481	17	AAE16806	Recombinant endoto
140	12	2.3	501	22	AAU07204	Mouse aspartyl pro	213	8	1.5	481	17	AAE05851	Recombinant lipopo
141	12	2.3	501	22	AAE84948	Mouse aspartic sec	214	8	1.5	481	19	AAE77093	Lipopolysaccharide
142	12	2.3	501	22	AAE02581	Human aspartyl pro	215	8	1.5	481	19	AAE63305	Lipopolysaccharide
143	12	2.3	501	22	AAE02583	Murine aspartyl pr	216	8	1.5	481	19	AAE40139	Human recombinant
144	12	2.3	501	23	ABB78590	Human Asp-2(a) pro	217	8	1.5	481	19	AAE40812	Human lipopolysacc
145	12	2.3	501	23	ABB78592	Mouse Asp-2(a) pro	218	8	1.5	481	20	AAE78356	Human lipopolysacc
146	12	2.3	501	23	ABB06409	Human aspartyl pro	219	8	1.5	481	21	AAE16137	Lipopolysaccharide
147	12	2.3	503	22	AAE66573	Human pro-memapsin	220	8	1.5	481	21	AAE57190	Human lipopolysacc
148	12	2.3	503	22	AAE61335	T7 promoter and ve	221	8	1.5	481	22	AAE77902	Human lipopolysacc
149	12	2.3	503	23	AAU99489	Pro-memapsin 2 enc	222	8	1.5	481	22	AAU09006	Human lipopolysacc
150	12	2.3	509	23	AAE52697	FLAG-tagged human	223	8	1.5	481	22	AAE66059	Human secreted pro
151	12	2.3	509	19	AAE59808	Partial amino acid	224	8	1.5	481	22	AAE68151	Human Recombinant
152	12	2.3	969	23	ABG09611	Novel human diago	225	8	1.5	481	22	AAE52307	rlBP protein. Uni.
153	9	1.7	45	23	AAU78524	N termini of 15KD	226	8	1.5	482	17	AAE16819	Recombinant endoto
154	9	1.7	269	22	ABG18048	Novel human diago	227	8	1.5	482	17	AAE16820	Recombinant endoto
155	9	1.7	322	22	AAE04797	Human aspartyl pro	228	8	1.5	504	23	AAE4277	Human endometrial
156	9	1.7	351	20	AAE35918	Extended human sec	229	8	1.5	548	22	AAE98365	Escherichia coli p

230	8	1.5	592	22	ABR62801	Drosophila melanog	303	7	1.4	145	22	ABR50641	Human secreted pro
231	8	1.5	592	22	ABR67339	Drosophila melanog	304	7	1.4	145	23	ABP34658	Human ORF3631 prot
232	8	1.5	692	22	ACG93225	C glutamicum prote	305	7	1.4	146	22	ABG24335	Novel human diagno
233	8	1.5	1246	23	AAU84295	Human endometrial	306	7	1.4	146	22	ABR59178	Drosophila melanog
234	8	1.5	1247	23	AAO17366	Human endometrial	307	7	1.4	146	22	AAU23445	Novel human enzyme
235	8	1.5	1247	23	ABR90742	Human tumour Endoc	308	7	1.4	147	22	ABG22859	Novel human diagno
236	7	1.4	9	21	AAH19593	Human CASB616 epit	309	7	1.4	160	17	AAW01000	Apoptosis-regulati
237	7	1.4	10	21	AAH19598	Human CASB616 epit	310	7	1.4	160	20	AAW05436	Human BIK protein
238	7	1.4	14	14	AAH32965	Mastoparan analogu	311	7	1.4	160	20	AAW94326	Human B1p4 protei
239	7	1.4	14	14	AAH32968	Mastoparan analogu	312	7	1.4	161	20	AAV38638	Neisseria meningit
240	7	1.4	14	14	AAH32960	Mastoparan analogu	313	7	1.4	161	20	AAV38640	Neisseria gonorrhoe
241	7	1.4	23	22	AAH35158	Human transmembran	314	7	1.4	166	23	ABP01194	Human ORFX protein
242	7	1.4	25	22	ABR42277	Peptide #9783 enco	315	7	1.4	168	18	AAW55521	H. pylori ORF 12ge
243	7	1.4	25	22	AAH63163	Human brain expres	316	7	1.4	168	18	AAW20521	Helicobacter pylor
244	7	1.4	25	22	AAW75977	Human bone marrow	317	7	1.4	168	18	AAW24680	H. pylori cell env
245	7	1.4	25	22	AAH36085	Peptide #10122 enc	318	7	1.4	168	22	ABR52931	Escherichia coli p
246	7	1.4	28	22	AAH02657	Human gene 2 enco	319	7	1.4	168	22	ABR52965	Escherichia coli p
247	7	1.4	30	22	AAH85337	Human oaf protein	320	7	1.4	170	23	AAH02050	Hepatitis C virus
248	7	1.4	34	21	AAH12350	Fragment of human	321	7	1.4	170	23	ABR47867	Listeria monocytog
249	7	1.4	34	21	AAH12350	Fragment of human	322	7	1.4	171	22	AAU51854	Propionibacterium
250	7	1.4	43	19	AAH51187	Human secreted pro	323	7	1.4	171	22	AAU51854	Human secreted pro
251	7	1.4	43	19	AAH51187	Human secreted pro	324	7	1.4	175	22	AAH89195	Peptide #3609 enco
252	7	1.4	47	22	AAU31051	Novel human secret	325	7	1.4	175	22	AAH29668	Peptide #3705 enco
253	7	1.4	61	19	AAH75196	Human secreted pro	326	7	1.4	175	22	AAH40930	Human polypeptide
254	7	1.4	61	22	AAU42241	Propionibacterium	327	7	1.4	175	22	AAH40930	Human polypeptide
255	7	1.4	68	22	AAU20237	Human novel endocr	328	7	1.4	175	22	AAH40930	Peptide #3552 enco
256	7	1.4	69	23	ABP03389	Human ORFX protein	329	7	1.4	175	23	ABP41517	Human colon cancer
257	7	1.4	71	21	AAH00466	Human secreted pro	330	7	1.4	180	22	AAH09655	Human ovarian anti
258	7	1.4	72	22	AAH83333	Human immune/haema	331	7	1.4	185	19	AAH98220	Human polypeptide
259	7	1.4	76	22	AAH48836	Propionibacterium	332	7	1.4	187	22	AAH23494	H. pylori GHPD 234
260	7	1.4	79	21	AAH56889	Arabidopsis thalia	333	7	1.4	192	16	AAH69640	Human EST encoded
261	7	1.4	86	22	AAH51186	Human secreted pro	334	7	1.4	192	16	AAH69658	Hepatitis C virus
262	7	1.4	88	22	AAO33578	Human polypeptide	335	7	1.4	192	16	AAH69656	Hepatitis C virus
263	7	1.4	90	22	AAU47158	Propionibacterium	336	7	1.4	192	16	AAH69644	Hepatitis C virus
264	7	1.4	91	22	ABR44259	Peptide #11765 enc	337	7	1.4	192	17	AAH89527	Hepatitis C virus
265	7	1.4	91	22	ABR27130	Protein #9129 enco	338	7	1.4	192	17	AAH89529	Hepatitis C virus
266	7	1.4	91	22	AAH65297	Human brain expres	339	7	1.4	192	17	AAH89511	Hepatitis C virus
267	7	1.4	91	22	AAH21888	Peptide #8322 enco	340	7	1.4	192	17	AAH89515	Hepatitis C virus
268	7	1.4	91	22	AAH38214	Peptide #12251 enco	341	7	1.4	193	22	AAH16973	Human novel secret
269	7	1.4	94	23	ABR78860	Tumour necrosis fa	342	7	1.4	194	21	AAH53465	Human colon cancer
270	7	1.4	95	22	AAH00047	Plastidic trioseph	343	7	1.4	206	21	AAH91339	Group B Streptococ
271	7	1.4	105	23	ABP02682	Human ORFX protei	344	7	1.4	208	16	AAH77167	Arabidopsis condens
272	7	1.4	106	22	AAH02654	Human gene 2 enco	345	7	1.4	209	21	AAH04117	Arabidopsis thalia
273	7	1.4	109	22	ABG11071	Novel human diagno	346	7	1.4	209	21	AAH1858	Arabidopsis thalia
274	7	1.4	109	22	ABG32787	Novel human diagno	347	7	1.4	209	21	AAH54004	Arabidopsis thalia
275	7	1.4	112	22	ABR67791	Drosophila melanog	348	7	1.4	210	18	AAH11261	Streptococcus pneu
276	7	1.4	115	18	AAH55383	H. pylori ORF hp4p	349	7	1.4	217	22	AAH40476	Human polypeptide
277	7	1.4	115	18	AAH21006	H. pylori cell env	350	7	1.4	219	21	AAH58938	Arabidopsis thalia
278	7	1.4	115	21	AAH58939	Arabidopsis thalia	351	7	1.4	222	19	AAH72187	HSV-2 strain SBS C
279	7	1.4	115	22	AAH88647	Human immune/haema	352	7	1.4	222	19	AAH72187	HSV-2 strain SBS C
280	7	1.4	117	23	ABP3337	Human ORF2310 prot	353	7	1.4	222	19	AAH72040	HSV-2 strain SBS C
281	7	1.4	119	23	ABR54744	Lactococcus lactis	354	7	1.4	231	22	AAH75438	Human colon cancer
282	7	1.4	120	21	AAH03247	Human secreted pro	355	7	1.4	231	22	AAH75087	Human secreted pro
283	7	1.4	121	20	AAH12208	Human 5' EST secre	356	7	1.4	232	23	ABR90294	Human polypeptide
284	7	1.4	123	22	AAO13332	Human polypeptide	357	7	1.4	233	22	AAH61608	Human protein HP03
285	7	1.4	126	19	AAH77364	Human Tumour Suppr	358	7	1.4	234	16	AAH82605	Eph transmembrane
286	7	1.4	126	22	AAH39144	Human polypeptide	359	7	1.4	235	20	AAH35512	Chlamydia pneumoni
287	7	1.4	126	22	AAH93017	Human protein sequ	360	7	1.4	238	16	AAH71481	Human hek-L protei
288	7	1.4	130	22	AAH01648	Human polypeptide	361	7	1.4	241	20	AAH71435	Amino acid sequenc
289	7	1.4	139	22	AAH99857	Human excretory re	362	7	1.4	245	22	AAH38690	Human polypeptide
290	7	1.4	139	22	AAH42672	Human kidney relat	363	7	1.4	253	22	AAH10135	Streptomyces novus
291	7	1.4	140	20	AAH06823	P. methanolic	364	7	1.4	255	22	AAH63235	Human breast cancer
292	7	1.4	140	20	AAH93839	P. methanolic	365	7	1.4	261	22	AAH40710	Propionibacterium
293	7	1.4	140	20	AAH93840	S. cerevisiae prot	366	7	1.4	262	21	AAH58184	lung cancer associ
294	7	1.4	140	21	AAH19018	Amino acid sequenc	367	7	1.4	265	23	ABR72331	Rat protein isolat
295	7	1.4	140	21	AAH1057	P. methanolic	368	7	1.4	267	22	ABR64636	Drosophila melanog
296	7	1.4	140	22	AAH05416	Pichia methanolic	369	7	1.4	268	22	AAH69751	Escherichia coli e
297	7	1.4	140	22	AAH67567	Amino acid sequenc	370	7	1.4	269	22	ABG07213	Novel human diagno
298	7	1.4	140	22	AAH61993	P. methanolic	371	7	1.4	272	22	AAH49513	Propionibacterium
299	7	1.4	140	22	AAH72372	Pichia methanolic	372	7	1.4	273	22	AAH85336	Human oaf protein
300	7	1.4	140	22	AAH92227	P. methanolic	373	7	1.4	273	22	AAH03825	Human gene 8 enco
301	7	1.4	140	22	AAH01974	Protein derived fr	374	7	1.4	273	22	AAH03851	Human gene 8 enco
302	7	1.4	145	23	ABG08183	Novel human diagno	375	7	1.4	273	23	ABG64540	Human albumin fusi

376	7	1.4	273	23	ABG64541	Human albumin fusi	449	7	1.4	456	21	AAV71062	Human membrane tra
377	7	1.4	273	23	AAU81188	Novel secreted pro	450	7	1.4	456	22	AAW78336	Human protein sequ
378	7	1.4	276	23	AAE14745	Human triacylglyce	451	7	1.4	460	22	AAE94655	Human protein sequ
379	7	1.4	279	21	AAE08981	Human secreted pro	452	7	1.4	465	22	ABE66239	Drosophila melanog
380	7	1.4	280	22	AAE69194	Human secreted pro	453	7	1.4	470	22	AAE66083	Murine TANGO 202.
381	7	1.4	280	22	AAE14743	Human triacylglyce	454	7	1.4	477	22	ABE61772	Drosophila melanog
382	7	1.4	289	21	AAE04116	Arabidopsis thalia	455	7	1.4	477	22	ABE67670	Amino acid sequenc
383	7	1.4	289	21	AAE11857	Arabidopsis thalia	456	7	1.4	477	22	ABE61908	Herbicideally activ
384	7	1.4	289	21	AAE54003	Arabidopsis thalia	457	7	1.4	489	22	ABE11767	Human membrane tra
385	7	1.4	289	23	AAU77494	Human lipid metabo	458	7	1.4	489	22	AAW79320	Human protein sequ
386	7	1.4	290	21	AAV74500	Neisseria gonorrhe	459	7	1.4	490	21	AAV75584	Neisseria meningit
387	7	1.4	290	21	AAV74501	Neisseria meningit	460	7	1.4	490	21	AAV75585	Neisseria meningit
388	7	1.4	290	21	AAV74502	Neisseria meningit	461	7	1.4	491	22	AAE81101	Mycobacterium tube
389	7	1.4	290	22	AAU61105	Propionibacterium	462	7	1.4	494	15	AAE62825	Human steroid-21-h
390	7	1.4	292	22	ABE65598	Drosophila melanog	463	7	1.4	506	21	AAE17818	Arabidopsis thalia
391	7	1.4	295	22	AAE72119	Human olfactory re	464	7	1.4	508	21	AAE11635	Arabidopsis thalia
392	7	1.4	298	14	AAE36678	Ethylene-induced a	465	7	1.4	513	21	AAE45529	Arabidopsis thalia
393	7	1.4	298	22	ABE64796	Drosophila melanog	466	7	1.4	517	21	AAE32390	Herpesvirus enty
394	7	1.4	306	22	AAE98408	Escherichia coli p	467	7	1.4	517	23	AAE23294	Human nectin-1alp
395	7	1.4	313	22	ABE64037	Drosophila coli p	468	7	1.4	522	21	AAE17817	Arabidopsis thalia
396	7	1.4	320	15	AAE62044	Leptospira melano	469	7	1.4	525	23	ABE28514	Streptococcus poly
397	7	1.4	320	18	AAE14278	Leptospira OmpL1	470	7	1.4	529	21	AAE51569	Arabidopsis thalia
398	7	1.4	323	21	AAE12341	Fragment of human	471	7	1.4	529	23	ABE93699	Herbicideally activ
399	7	1.4	326	22	ABE6589	Human pepsin. Hom	472	7	1.4	537	22	ABE61550	Drosophila melanog
400	7	1.4	326	22	AAE61351	Pepsin protein. H	473	7	1.4	537	22	ABE67157	Drosophila melanog
401	7	1.4	327	22	AAE00099	Plastidic trioseph	474	7	1.4	550	18	AAE23282	Brevibacterium lac
402	7	1.4	330	20	AAE05383	Mouse GCR9 protein	475	7	1.4	550	18	AAE06584	Brevibacterium lac
403	7	1.4	330	21	AAE94269	Mouse 7-transmembr	476	7	1.4	550	19	AAE68149	Brevibacterium lac
404	7	1.4	330	22	ABE28764	Streptococcus poly	477	7	1.4	550	19	AAE69551	Brevibacterium lac
405	7	1.4	330	22	ABE15392	Novel human dieno	478	7	1.4	550	19	AAE47398	B. lactofermentum
406	7	1.4	346	23	ABE54038	Lactococcus lactis	479	7	1.4	550	22	AAE93196	C. glutamicum prote
407	7	1.4	354	17	AAE14463	Yeast glycoprotein	480	7	1.4	559	22	AAE34910	Enterococcus faeca
408	7	1.4	359	22	ABE24341	Novel human dieno	481	7	1.4	589	12	AAE10681	Polyhydroxybutyric
409	7	1.4	359	22	ABE90878	Herbicideally activ	482	7	1.4	589	14	AAE32190	Sequence encoded b
410	7	1.4	363	18	AAE24256	Ammonifex histidin	483	7	1.4	589	22	AAE10892	Alcaligenes eutrop
411	7	1.4	366	23	AAU91299	Human protein NOV6	484	7	1.4	590	19	AAE85912	S. pneumoniae deri
412	7	1.4	368	22	ABE29719	Novel human dieno	485	7	1.4	590	22	AAU42564	Propionibacterium
413	7	1.4	369	22	ABE01477	Novel human dieno	486	7	1.4	601	22	AAE10894	Rhodoceterium spae
414	7	1.4	373	21	AAE04115	Arabidopsis thalia	487	7	1.4	604	15	AAE51267	Sequence of human
415	7	1.4	373	21	AAE11856	Arabidopsis thalia	488	7	1.4	604	15	AAE56660	Cyclooxigenase-2.
416	7	1.4	373	21	AAE54002	Arabidopsis thalia	489	7	1.4	604	16	AAE72228	Human cyclooxigena
417	7	1.4	379	23	AAU72876	Human aspartyl pro	490	7	1.4	604	18	AAE12698	Human prostraglandi
418	7	1.4	380	20	AAE32036	Bovine pregnancy a	491	7	1.4	604	22	AAE72199	Human prostraglandi
419	7	1.4	380	20	AAE32048	Bovine pregnancy a	492	7	1.4	604	23	ABE07244	Human cyclooxigena
420	7	1.4	387	20	AAE32052	Bovine pregnancy a	493	7	1.4	604	23	ABE07247	Guinea pig cycloo
421	7	1.4	388	20	AAE32058	Cat pregnancy asso	494	7	1.4	604	23	ABE07248	Rabbit cyclooxygen
422	7	1.4	388	22	AAU27708	Human full-length	495	7	1.4	604	23	ABE07249	Horse cyclooxigena
423	7	1.4	392	20	AAE32057	Bovine pregnancy a	496	7	1.4	604	23	ABE07250	Sheep cyclooxigena
424	7	1.4	392	22	AAE63550	Putative P. abysssi	497	7	1.4	613	22	AAU04887	Micromonospora eve
425	7	1.4	395	23	AAE14744	Human triacylglyce	498	7	1.4	621	20	AAE21549	Porcine heparin-bl
426	7	1.4	397	18	AAE31628	Aspergillus oryzae	499	7	1.4	622	22	ABE58015	Porcine heparin-bl
427	7	1.4	397	23	AAE17308	Human lysosomal ac	500	7	1.4	622	22	ABE67236	Drosophila melanog
428	7	1.4	399	22	AAE67513	Amino acid sequenc	501	7	1.4	634	20	AAE21548	Human heparin-bind
429	7	1.4	399	23	AAU77496	Human lipid metabo	502	7	1.4	638	18	AAE32098	Miniature swine re
430	7	1.4	407	16	AAE80749	Canine cholecystok	503	7	1.4	638	22	AAE70633	Porcine endogenous
431	7	1.4	407	17	AAE92291	Canine cholecystok	504	7	1.4	638	22	AAE70634	Porcine endogenous
432	7	1.4	409	17	AAE88460	Canine cholecystok	505	7	1.4	638	22	AAE73287	Retoviral protein
433	7	1.4	409	15	AAE48060	Sequence of protea	506	7	1.4	638	22	AAE35114	PERV-C env protein
434	7	1.4	410	13	AAE28030	Pichia pastoris pr	507	7	1.4	652	22	AAU42709	Propionibacterium
435	7	1.4	417	23	AAE49396	Human zinc finger	508	7	1.4	655	22	ABE66839	Novel human dieno
436	7	1.4	420	21	ABE80665	Candida boidinii p	509	7	1.4	657	23	AAU11356	Human DNA cyto
437	7	1.4	428	20	AAE09000	E. coli suza prote	510	7	1.4	659	22	AAU04957	Human interleukin
438	7	1.4	433	21	AAE30824	Arabidopsis thalia	511	7	1.4	667	22	AAE35117	PERV-1-15 env prot
439	7	1.4	433	21	AAE31636	Arabidopsis thalia	512	7	1.4	667	23	AAU83601	Human PEO protein.
440	7	1.4	436	23	ABE29086	Streptococcus poly	513	7	1.4	668	22	AAE36888	Portuguese Water d
441	7	1.4	445	16	AAE80750	Canine cholecystok	514	7	1.4	672	16	AAE71325	Poly-beta-hydroxya
442	7	1.4	445	17	AAE92292	Canine cholecystok	515	7	1.4	674	22	AAE94461	Human protein sequ
443	7	1.4	445	17	AAE88461	Canine cholecystok	516	7	1.4	674	22	AAE94461	Human protein sequ
444	7	1.4	449	19	AAE57043	Human aspartic pro	517	7	1.4	674	23	ABE66691	Human novel polype
445	7	1.4	450	21	AAE57041	Plasmodium vivax p	518	7	1.4	677	22	ABE61957	Drosophila melanog
446	7	1.4	451	22	AAE6063	Murine protein: SE	519	7	1.4	690	5	AAE40306	Sequence encoded b
447	7	1.4	453	14	AAE1675	Canine gastrin rec	520	7	1.4	692	22	ABE23281	Novel human dieno
448	7	1.4	453	22	AAE66628	Canine gastrin rec	521	7	1.4	702	23	ABE28373	Streptococcus poly

522	7	1.4	702	23	AAH47575	Drosophila cell cy	595	6	1.2	12	22	AAH50475	Bacterial A1a pep
523	7	1.4	704	21	AAH55891	E. coli proliferat	596	6	1.2	12	23	AAH52423	Putative protease
524	7	1.4	704	22	AAU34770	E. coli cellular p	597	6	1.2	14	22	AAH55906	Vascular dementia-
525	7	1.4	704	22	AAU38372	Salmonella typhi c	598	6	1.2	14	22	AAH72296	ADAMTS-R1 immunog
526	7	1.4	715	23	AAH53379	Lactococcus lactis	599	6	1.2	14	23	AAJ00604	B lymphocyte stimu
527	7	1.4	723	22	AAH39467	Human polypeptide	600	6	1.2	14	23	AAH33465	B lymphocyte Stimu
528	7	1.4	726	22	AAH66716	Human transcriptio	601	6	1.2	15	22	AAH78131	Human actin 49 pep
529	7	1.4	730	22	AAH41253	Human polypeptide	602	6	1.2	15	22	AAH98299	Human ribosomal ph
530	7	1.4	731	23	AAH47466	Human triacylglyce	603	6	1.2	15	22	AAH66721	Cytochrome b559 10
531	7	1.4	760	23	AAH20507	Streptococcus muta	604	6	1.2	15	23	AAH81892	Transcriptional el
532	7	1.4	760	23	AAH20592	Streptococcus muta	605	6	1.2	16	22	AAH99379	Vaccine related MH
533	7	1.4	773	23	AAH57374	Mouse ischaemic co	606	6	1.2	18	23	AAH78513	Human and mouse BA
534	7	1.4	775	21	AAH67250	Mouse protein tyro	607	6	1.2	19	18	AAH22374	S. pneumoniae HSP7
535	7	1.4	775	21	AAH67251	Mutant mouse ptp-p	608	6	1.2	19	22	AAH72292	ADAMTS-7 immunogen
536	7	1.4	784	23	AAH47322	Listeria monocytog	609	6	1.2	19	23	AAH23897	PIR-A1 receptor pe
537	7	1.4	802	17	AAH90848	Glibberellin (GAI)	610	6	1.2	20	9	AAH2056	Pep-13 comprising
538	7	1.4	802	23	AAH92819	Herbically activ	611	6	1.2	20	12	AAH10788	S-antigen polypept
539	7	1.4	862	22	AAH90202	C glutamincum prote	612	6	1.2	21	18	AAH10215	Endoglycoceramidas
540	7	1.4	863	22	AAH63583	Drosophila melanog	613	6	1.2	21	19	AAH48387	Synthetic don-1 po
541	7	1.4	868	22	AAH24427	Novel human diagno	614	6	1.2	22	19	AAH59850	Amino acid sequenc
542	7	1.4	880	23	AAH27173	Streptococcus poly	615	6	1.2	22	22	AAH72346	Mammalian T8 signa
543	7	1.4	896	22	AAH28532	Novel human diagno	616	6	1.2	22	23	AAH10579	Membrane attachmen
544	7	1.4	902	22	AAH60606	Drosophila melanog	617	6	1.2	23	22	AAH60685	PT101A 1031-encode
545	7	1.4	925	22	AAH53591	Novel human diagno	618	6	1.2	23	23	AAH49118	Cationic amphipath
546	7	1.4	933	23	AAH28348	Streptococcus poly	619	6	1.2	24	15	AAH47014	Cathepsin E positl
547	7	1.4	942	21	AAH25536	Eucalyptus grandis	620	6	1.2	24	22	AAH99380	Vaccine related MH
548	7	1.4	981	23	AAH78727	Human calyptrenin-	621	6	1.2	25	18	AAH35870	Leader sequence fo
549	7	1.4	987	21	AAH19590	Human CASB616. HO	622	6	1.2	25	19	AAH59838	Ramy1A signal pept
550	7	1.4	993	20	AAH49897	Rat TAO2 kinase.	623	6	1.2	25	23	AAH77596	Human cancer assoc
551	7	1.4	993	20	AAH66086	Drosophila melanog	624	6	1.2	26	21	AAH84367	Amino acid sequenc
552	7	1.4	994	18	AAH87018	Receptor tyrosine	625	6	1.2	26	22	AAH76928	Human colon cancer
553	7	1.4	994	18	AAH26366	Mouse Nrk tyrosine	626	6	1.2	26	23	AAH24389	Human prokineticin
554	7	1.4	994	22	AAU01907	Murine neural kina	627	6	1.2	27	21	AAH88094	Preproinsulin secr
555	7	1.4	1055	21	AAH19591	Human CASB616. HO	628	6	1.2	27	21	AAH43836	Secretory signal s
556	7	1.4	1062	21	AAH40294	Human ORFX ORF58 p	629	6	1.2	27	22	AAH94075	Human reproductive
557	7	1.4	1127	22	AAH95541	Human protein sequ	630	6	1.2	27	22	AAH45954	Transdominant elfe
558	7	1.4	1133	22	AAH28516	Novel human diagno	631	6	1.2	27	22	AAH35084	Preproinsulin secr
559	7	1.4	1191	22	AAH60219	Human protein SEQ	632	6	1.2	27	23	AAH49941	Human D40 associat
560	7	1.4	1193	22	AAH81808	Novel human diagno	633	6	1.2	27	23	AAH49962	Human D40 associat
561	7	1.4	1235	21	AAH41663	Human ORFX ORF1427	634	6	1.2	27	23	AAH76403	Preproinsulin secr
562	7	1.4	1379	22	AAH57823	Drosophila melanog	635	6	1.2	30	23	AAH49997	Human D40 associat
563	7	1.4	1429	20	AAH93941	Human brx protein.	636	6	1.2	31	21	AAH15670	Alpha V beta 3 rec
564	7	1.4	1429	22	AAH50537	Novel human diagno	637	6	1.2	31	21	AAH49997	Human 5' EST relat
565	7	1.4	1520	22	AAH90690	C glutamincum prote	638	6	1.2	31	22	AAH77180	Human 5' EST relat
566	7	1.4	1822	15	AAH55273	Beta subunit of in	639	6	1.2	31	23	AAH18959	Rice alpha-amylase
567	7	1.4	1873	23	AAH14708	Human beta4 integr	640	6	1.2	32	18	AAH20205	H. pylori secreted
568	7	1.4	1873	23	AAH14714	Human beta4 integr	641	6	1.2	32	20	AAH11389	Human 5' EST secre
569	7	1.4	1875	22	AAH68089	Amino acid sequenc	642	6	1.2	32	21	AAH86536	Human gene 77-enco
570	7	1.4	2042	22	AAH59689	Drosophila melanog	643	6	1.2	32	22	AAH42768	Peptide #10274 enc
571	7	1.4	2047	22	AAH99541	Human CLASP-7 prot	644	6	1.2	32	22	AAH26061	Protein #8060 enco
572	7	1.4	2047	23	AAH61707	Human cadherin-lik	645	6	1.2	32	22	AAH63659	Human brain expres
573	7	1.4	2404	20	AAH30640	HIV-1-NC7 envelope	646	6	1.2	32	22	AAH76473	Human bone marrow
574	6	1.2	8	22	AAH14602	HIV A03 super moti	647	6	1.2	32	22	AAH20905	Peptide #7339 enco
575	6	1.2	8	22	AAH16775	HIV B07 super moti	648	6	1.2	32	22	AAH36581	Peptide #10618 enc
576	6	1.2	8	22	AAH18951	HIV B62 super moti	649	6	1.2	32	23	AAH45734	Human polypeptide
577	6	1.2	8	22	AAH20976	HIV A03 motif nef	650	6	1.2	33	22	AAH07615	Human polypeptide
578	6	1.2	8	22	AAH23037	HIV A11 motif nef	651	6	1.2	33	22	AAH60686	Plasmid T101A 1031
579	6	1.2	8	23	AAH06440	Beta-secretase rel	652	6	1.2	33	22	AAH60688	PT101ADP-encoded r
580	6	1.2	8	23	AAH07465	Theodroma cacao as	653	6	1.2	34	20	AAH92216	Analogue of parath
581	6	1.2	9	22	AAH11718	HIV A01 super moti	654	6	1.2	34	20	AAH03951	Human secreted pep
582	6	1.2	9	22	AAH15783	HIV A24 super moti	655	6	1.2	34	21	AAH37357	Human novel foetal
583	6	1.2	9	22	AAH17991	HIV B58 super moti	656	6	1.2	34	21	AAH20673	Human novel foetal
584	6	1.2	9	22	AAH20919	HIV A03 motif nef	657	6	1.2	35	21	AAH56638	Arabidopsis thalia
585	6	1.2	10	22	AAH13056	HIV A02 super moti	658	6	1.2	35	22	AAH30124	Peptide #2775 enco
586	6	1.2	10	22	AAH15796	HIV A02 super moti	659	6	1.2	35	22	AAH35296	Peptide #2802 enco
587	6	1.2	10	22	AAH16792	HIV B07 super moti	660	6	1.2	35	22	AAH39561	Peptide #7067 enco
588	6	1.2	10	22	AAH23034	HIV A14 motif nef	661	6	1.2	35	22	AAH20738	Protein #2377 enco
589	6	1.2	10	22	AAH24173	HIV A24 motif nef	662	6	1.2	35	22	AAH24282	Human brain expres
590	6	1.2	11	21	AAH76394	Fragment of human	663	6	1.2	35	22	AAH56125	Human brain expres
591	6	1.2	11	22	AAH13083	HIV A02 super moti	664	6	1.2	35	22	AAH60260	Human bone marrow
592	6	1.2	11	22	AAH15818	HIV A24 super moti	665	6	1.2	35	22	AAH68497	Human bone marrow
593	6	1.2	11	22	AAH17992	HIV B58 super moti	666	6	1.2	35	22	AAH72887	Peptide #2377 enco
594	6	1.2	12	21	AAH09319	Hepatitis GB virus	667	6	1.2	35	22	AAH16303	

668	6	1.2	35	22	AAI19767	Peptide #6201 enco	741	6	1.2	48	22	AAO07651	Human polypeptide
669	6	1.2	35	22	AAI28796	Peptide #2833 enco	742	6	1.2	48	23	ABG44108	Human peptide enco
670	6	1.2	35	22	AAI33118	Peptide #7155 enco	743	6	1.2	49	21	AAI56387	Arabidopsis thalia
671	6	1.2	35	22	AAI04039	Peptide #2721 enco	744	6	1.2	49	22	ABB29630	Peptide #2281 enco
672	6	1.2	35	23	ABB80917	Human sprouty-4 or	745	6	1.2	49	22	ABB34808	Peptide #2314 enco
673	6	1.2	35	23	ABB38078	Human peptide enco	746	6	1.2	49	22	ABB50577	Human secreted pro
674	6	1.2	35	23	ABG42721	Human peptide enco	747	6	1.2	49	22	ABB52024	Protein #2223 enco
675	6	1.2	36	16	AAI75130	PLAP glycosyl-phos	748	6	1.2	49	22	ABB5610	Human brain expres
676	6	1.2	36	20	AAI49764	Compact structure	749	6	1.2	49	22	AAI67995	Human bone marrow
677	6	1.2	36	20	AAI11642	Human 5' EST seque	750	6	1.2	49	22	AAI01940	Human polypeptide
678	6	1.2	36	21	AAI88082	Lamp-1 lysosomal t	751	6	1.2	49	22	AAI03342	Human polypeptide
679	6	1.2	36	21	AAI43825	Lysosomal membrane	752	6	1.2	49	22	AAI15811	Peptide #2345 enco
680	6	1.2	36	21	AAI56348	Streptococcus pyog	753	6	1.2	49	22	AAI28321	Peptide #2358 enco
681	6	1.2	36	22	ABB03311	Human musculoskele	754	6	1.2	49	22	AAI03549	Peptide #2231 enco
682	6	1.2	36	22	AAI45941	Transdominant effe	755	6	1.2	49	23	ABG37527	Human peptide enco
683	6	1.2	36	22	AAI35073	Lamp-1 lysosomal m	756	6	1.2	50	19	AAI35017	Peptide used in po
684	6	1.2	36	23	AAI76179	Lysosome associate	757	6	1.2	50	20	AAI29804	Human GABA B recep
685	6	1.2	37	21	AAI56637	Arabidopsis thalia	758	6	1.2	50	22	AAI40556	Propionibacterium
686	6	1.2	38	13	AAI20962	Sequence of human	759	6	1.2	50	22	AAU43237	Propionibacterium
687	6	1.2	38	18	AAI27479	Preproinsulin lead	760	6	1.2	51	22	AAU57744	Propionibacterium
688	6	1.2	38	18	AAI27480	Preproinsulin lead	761	6	1.2	51	19	AAI71570	Hepatocyte nuclear
689	6	1.2	38	18	AAI27481	Preproinsulin lead	762	6	1.2	51	21	AAI41435	Human 5' EST relat
690	6	1.2	38	18	AAI27482	Preproinsulin lead	763	6	1.2	51	22	AAI41435	Propionibacterium
691	6	1.2	38	20	AAI48503	Human breast tumou	764	6	1.2	51	22	AAI66756	Human immune/haema
692	6	1.2	38	20	ABBI4697	Peptide #9203 enco	765	6	1.2	51	22	AAO07411	Human polypeptide
693	6	1.2	38	22	ABBI25470	Protein #7469 enco	766	6	1.2	51	22	AAI37342	Chaperone cpn60 pr
694	6	1.2	38	22	AAI62570	Human brain expres	767	6	1.2	51	22	AAI77229	Human colon cancer
695	6	1.2	38	22	AAI75381	Human bone marrow	768	6	1.2	52	20	AAI11651	Human 5' EST seque
696	6	1.2	38	22	AAI20580	Peptide #7014 enco	769	6	1.2	52	22	AAI48976	Propionibacterium
697	6	1.2	38	22	AAI35493	Peptide #9530 enco	770	6	1.2	52	22	AAI66713	Human immune/haema
698	6	1.2	38	22	AAI60745	Human secreted pro	771	6	1.2	52	22	AAO03436	Human polypeptide
699	6	1.2	38	23	ABG44975	Human peptide enco	772	6	1.2	52	23	ABP26180	Streptococcus poly
700	6	1.2	38	23	AAI47896	Zinc finger protei	773	6	1.2	52	23	ABP26181	Streptococcus poly
701	6	1.2	40	10	AAI90808	N-terminal sequenc	774	6	1.2	53	21	AAI35397	Human colon cancer
702	6	1.2	40	22	AAI60689	Plasmid RED1-enco	775	6	1.2	53	21	AAI35398	Human colon cancer
703	6	1.2	41	22	AAI68296	Human bone marrow	776	6	1.2	53	21	AAI35399	Human colon cancer
704	6	1.2	41	22	ABG37843	Human peptide enco	777	6	1.2	53	21	AAI35425	Lung cancer associ
705	6	1.2	42	18	AAI34597	C-terminal "signal	778	6	1.2	53	22	AAI41231	Propionibacterium
706	6	1.2	42	20	AAI02721	Human secreted pro	779	6	1.2	53	22	AAI41231	Human immune/haema
707	6	1.2	42	23	AAI50531	Anchor peptide seq	780	6	1.2	53	22	AAI6781	Human colon cancer
708	6	1.2	43	19	AAI74930	Human secreted pro	781	6	1.2	53	22	AAI7781	Human colon cancer
709	6	1.2	43	19	AAI71247	Human gene 5-enco	782	6	1.2	53	23	ABP42223	Human ovarian anti
710	6	1.2	43	22	AAI71277	Human gene 5-enco	783	6	1.2	53	23	ABP42819	Human ovarian anti
711	6	1.2	43	22	AAE01241	Human gene 10 enco	784	6	1.2	53	23	ABP02592	Human ORFX protein
712	6	1.2	43	22	AAE01278	Human gene 10 enco	785	6	1.2	54	20	AAI78192	Human secreted pro
713	6	1.2	43	23	ABG63470	Human albumin fusi	786	6	1.2	54	21	AAI51724	Human secreted pro
714	6	1.2	43	23	ABG63471	Human albumin fusi	787	6	1.2	54	22	AAI50698	Propionibacterium
715	6	1.2	43	23	ABG63702	Human albumin fusi	788	6	1.2	54	22	AAI65073	Propionibacterium
716	6	1.2	43	23	ABG63703	Human albumin fusi	789	6	1.2	54	22	ABBI0379	Human musculoskele
717	6	1.2	44	21	AAI64715	Human 5' EST relat	790	6	1.2	55	16	AAI80193	Internal portion o
718	6	1.2	44	22	ABG16321	Novel human diagno	791	6	1.2	55	19	AAI79444	Staphylococcus aur
719	6	1.2	44	23	AAI78527	N terminus of 11kd	792	6	1.2	55	21	AAI35778	Rat CARP peptide f
720	6	1.2	45	19	AAI79315	Staphylococcus aur	793	6	1.2	55	21	AAI35782	Murine CARP peptid
721	6	1.2	45	20	AAI41440	Fragment of human	794	6	1.2	55	21	AAI02879	Human secreted pro
722	6	1.2	45	22	AAI87000	Human immune/haema	795	6	1.2	55	22	ABG60250	Human ovarian anti
723	6	1.2	45	22	AAI013181	Human polypeptide	796	6	1.2	55	22	AAI63757	Propionibacterium
724	6	1.2	46	22	AAI38062	Fragment of human	797	6	1.2	55	22	AAI64206	Propionibacterium
725	6	1.2	46	21	AAI48490	Arabidopsis thalia	798	6	1.2	55	22	ABBI39033	Peptide #6539 enco
726	6	1.2	46	22	ABBI4398	Peptide #8904 enco	799	6	1.2	55	22	ABBI4396	Peptide #7902 enco
727	6	1.2	46	22	ABBI4268	Human brain expres	800	6	1.2	55	22	ABBI23977	Peptide #5976 enco
728	6	1.2	46	22	AAI62267	Human bone marrow	801	6	1.2	55	22	ABBI24768	Protein #6767 enco
729	6	1.2	46	22	AAI86213	Human immune/haema	802	6	1.2	55	22	AAI94384	Human brain expres
730	6	1.2	46	22	AAI35190	Peptide #9227 enco	803	6	1.2	55	22	AAI59687	Human brain expres
731	6	1.2	47	13	AAI20963	Sequence of human	804	6	1.2	55	22	AAI61204	Human brain expres
732	6	1.2	47	19	AAI59847	Anchoring sequence	805	6	1.2	55	22	AAI72263	Human bone marrow
733	6	1.2	47	22	ABBI1222	Peptide #3873 enco	806	6	1.2	55	22	AAI73923	Human bone marrow
734	6	1.2	47	22	ABBI36429	Peptide #3935 enco	807	6	1.2	55	22	AAI19522	Peptide #5956 enco
735	6	1.2	47	22	AAI57187	Human brain expres	808	6	1.2	55	22	AAI20159	Peptide #6593 enco
736	6	1.2	47	22	AAI69592	Human bone marrow	809	6	1.2	55	22	AAI32522	Peptide #6559 enco
737	6	1.2	47	22	AAI29928	Peptide #3773 enco	810	6	1.2	55	22	AAI34102	Peptide #8139 enco
738	6	1.2	47	22	AAI05091	Peptide #3773 enco	811	6	1.2	55	22	AAI80584	Human secreted pro
739	6	1.2	47	22	ABG39213	Human placental al	812	6	1.2	55	23	ABG61721	Novel ovarian rela
740	6	1.2	47	23	AAI0577	Human placental al	813	6	1.2	55	23	ABG65465	Human albumin fusi

814	6	1.2	55	23	ABG42078	Human peptide enco	887	6	1.2	66	22	AAW03819	Peptide #2501 enco
815	6	1.2	55	23	ABG43811	Human peptide enco	888	6	1.2	66	23	ABG37807	Human peptide enco
816	6	1.2	56	21	AAAG01468	Human secreted pro	889	6	1.2	67	22	ABB67943	Drosophila melanog
817	6	1.2	56	22	AAU47306	Proionibacterium	890	6	1.2	67	22	ABG27225	Novel human diagno
818	6	1.2	56	22	AAU20338	Human novel endocr	891	6	1.2	67	22	ABB30615	Peptide #3265 enco
819	6	1.2	56	22	AAW85195	Human immune/haema	892	6	1.2	67	22	ABB35779	Peptide #3285 enco
820	6	1.2	56	22	AAW60781	Scorpion letuotrope	893	6	1.2	67	22	ABB17373	Human nervous syst
821	6	1.2	57	21	ABP34242	Human ORF3215 prot	894	6	1.2	67	22	ABB21202	Human protein #3201 enco
822	6	1.2	57	21	ABB32846	Eucalyptus grandis	895	6	1.2	67	22	AAW56587	Human brain expres
823	6	1.2	57	22	ABBA2299	Peptide #9805 enco	896	6	1.2	67	22	AAW68968	Human bone marrow
824	6	1.2	57	22	ABR25802	Protein #7801 enco	897	6	1.2	67	22	AAW16795	Peptide #3229 enco
825	6	1.2	57	22	AAW63185	Human brain expres	898	6	1.2	67	22	AAW29277	Peptide #3141 enco
826	6	1.2	57	22	AAW75999	Human bone marrow	899	6	1.2	67	22	AAW04513	Peptide #3195 enco
827	6	1.2	57	22	AAW23573	Human EST encoded	900	6	1.2	67	23	ABG38553	Human peptide enco
828	6	1.2	57	22	AAW6107	Peptide #10144 enc	901	6	1.2	67	23	ABP03159	Human ORFX protein
829	6	1.2	57	23	ABG45406	Human peptide enco	902	6	1.2	67	23	ABBA49594	Listeria monocytog
830	6	1.2	57	23	ABP02519	Human ORFX protein	903	6	1.2	68	21	AAW84596	Fragment of human
831	6	1.2	58	20	AAW59754	Human normal ovari	904	6	1.2	68	22	ABB31892	Peptide #4543 enco
832	6	1.2	58	22	AAU47118	Proionibacterium	905	6	1.2	68	22	ABB37130	Peptide #4636 enco
833	6	1.2	58	22	AAU18640	Human lung antigen	906	6	1.2	68	22	ABB22441	Peptide #4440 enco
834	6	1.2	58	23	ABP31864	Human glycoprotein	907	6	1.2	68	22	AAW80954	Human haematologic
835	6	1.2	59	13	AAW27732	Salp20.5R. Vaccin	908	6	1.2	68	22	AAW57849	Human brain expres
836	6	1.2	59	14	AAW43264	RCAL1 N-terminal.	909	6	1.2	68	22	AAW70267	Human bone marrow
837	6	1.2	59	22	AAU20680	Human novel foetal	910	6	1.2	68	22	AAW18095	Peptide #4529 enco
838	6	1.2	59	22	AAW94522	Human reproductiv	911	6	1.2	68	22	AAW23699	Human EST encoded
839	6	1.2	59	22	AAW67918	Human immune/haema	912	6	1.2	68	22	AAW30650	Peptide #4641 enco
840	6	1.2	59	23	ABP42252	Human ovarian anti	913	6	1.2	68	22	AAW05730	Peptide #4412 enco
841	6	1.2	59	23	ABP02996	Human ORFX protein	914	6	1.2	68	23	ABG39911	Human peptide enco
842	6	1.2	59	23	AAW80947	Caubacter crescec	915	6	1.2	68	23	ABP03696	Human ORFX protein
843	6	1.2	60	19	AAW98556	H. pylori GHP. 167	916	6	1.2	68	23	ABP07588	Human ORFX protein
844	6	1.2	60	22	AAU54616	Proionibacterium	917	6	1.2	68	23	ABP09809	Human ORFX protein
845	6	1.2	60	22	AAU62553	Proionibacterium	918	6	1.2	68	23	ABB54500	Laccococcus lactis
846	6	1.2	60	22	AAW87965	Human immune/haema	919	6	1.2	69	21	AAW17411	Arabidopsis thalia
847	6	1.2	60	22	AAW07148	Human polypeptide	920	6	1.2	69	22	AAW99898	Human excretory re
848	6	1.2	60	22	AAW69147	M. catarrhalis str	921	6	1.2	69	22	AAW43697	Human bladder anti
849	6	1.2	61	21	AAW20221	Arabidopsis thalia	922	6	1.2	69	22	ABP00667	Human ORFX protein
850	6	1.2	61	21	AAW00525	Human secreted pro	923	6	1.2	70	21	AAW53966	Human colon cancer
851	6	1.2	61	21	AAW03465	Human secreted pro	924	6	1.2	70	21	AAW18531	Zea mays protein f
852	6	1.2	61	22	AAU56087	Proionibacterium	925	6	1.2	70	22	ABG18828	Novel human diagno
853	6	1.2	61	22	AAW010476	Human polypeptide	926	6	1.2	70	22	AAW24095	Human EST encoded
854	6	1.2	61	23	ABP33124	Human ORF2097 prot	927	6	1.2	70	23	ABP42243	Human ovarian anti
855	6	1.2	62	21	AAW37069	Arabidopsis thalia	928	6	1.2	71	19	AAW60973	Streptococcus pneu
856	6	1.2	62	21	AAW86274	Human secreted pro	929	6	1.2	71	21	AAW25363	Arabidopsis thalia
857	6	1.2	62	21	ABG01887	Novel human diagno	930	6	1.2	71	22	AAU45743	Proionibacterium
858	6	1.2	62	22	AAW63837	Human prostate can	931	6	1.2	71	22	AAW64516	Proionibacterium
859	6	1.2	62	23	ABP09488	Human ORFX protein	932	6	1.2	71	22	AAW91322	Human immune/haema
860	6	1.2	63	20	AAW29800	Human GABA B recep	933	6	1.2	72	13	AAW25119	Non-A, Non-B Hepat
861	6	1.2	63	20	AAW29801	Human GABA B recep	934	6	1.2	72	21	AAW20172	Arabidopsis thalia
862	6	1.2	63	20	AAW29802	Human GABA B recep	935	6	1.2	72	22	AAW62168	Proionibacterium
863	6	1.2	63	20	AAW29803	Human GABA B recep	936	6	1.2	72	22	AAU02065	Synthetic human ta
864	6	1.2	63	22	AAU42008	Proionibacterium	937	6	1.2	72	23	ABP05481	Human ORFX protein
865	6	1.2	63	22	AAU50416	Proionibacterium	938	6	1.2	73	17	AAW04202	Peptide encoded by
866	6	1.2	63	22	AAU57838	Proionibacterium	939	6	1.2	73	17	AAW04190	Peptide encoded by
867	6	1.2	63	22	AAU59994	Proionibacterium	940	6	1.2	73	17	AAW04199	Peptide encoded by
868	6	1.2	63	22	AAW012008	Human polypeptide	941	6	1.2	73	21	AAW34462	Human secreted pro
869	6	1.2	64	21	AAW39473	Human secreted pro	942	6	1.2	73	21	AAW343580	Arabidopsis thalia
870	6	1.2	64	21	AAW38199	Human secreted pro	943	6	1.2	73	22	AAW45304	Proionibacterium
871	6	1.2	64	22	AAU47819	Proionibacterium	944	6	1.2	73	22	ABG03752	Novel human diagno
872	6	1.2	64	22	AAW07361	Human polypeptide	945	6	1.2	73	22	ABG03752	Novel human diagno
873	6	1.2	64	22	AAW60687	Proionibacterium	946	6	1.2	73	23	ABP33587	Human protease-11k
874	6	1.2	65	21	AAW45293	Sequence #7 homolo	947	6	1.2	73	23	ABP05087	Human ORFX protein
875	6	1.2	65	21	AAW45294	Protein fragment #	948	6	1.2	74	22	AAW53361	Proionibacterium
876	6	1.2	65	21	AAW45294	Human secreted pro	949	6	1.2	74	22	AAW83188	Human immune/haema
877	6	1.2	65	21	ABP04162	Human ORFX protein	950	6	1.2	74	22	AAW07082	Human polypeptide
878	6	1.2	65	20	AAW74034	Human prostate tum	951	6	1.2	74	22	AAW35777	Rat CART peptide f
879	6	1.2	66	21	AAW42112	Human ORFX ORF1876	952	6	1.2	75	21	AAW35781	Murine CART peptid
880	6	1.2	66	21	AAW32863	Zea mays protein f	953	6	1.2	75	21	AAW08492	Amino acid sequenc
881	6	1.2	66	22	AAW32901	Peptide #2552 enco	954	6	1.2	75	22	AAW99788	Human excretory re
882	6	1.2	66	22	AAW30496	Protein #2495 enco	955	6	1.2	75	22	AAW67855	Murine leukemia vi
883	6	1.2	66	22	AAW55895	Human brain expres	956	6	1.2	75	22	AAW08074	Human polypeptide
884	6	1.2	66	22	AAW68269	Human bone marrow	957	6	1.2	75	22	AAW42603	Human kidney relat
885	6	1.2	66	22	AAW16091	Peptide #2525 enco	958	6	1.2	76	21	AAW12275	Zea mays protein f
886	6	1.2	66	22	AAW28582	Peptide #2619 enco	959	6	1.2	76	22	AAW67129	Proionibacterium

960	6	1.2	76	22	ABG05836	Novel human diagno
961	6	1.2	76	23	ABP03498	Human OREF protein
962	6	1.2	77	19	AAW44726	Amino acid sequenc
963	6	1.2	77	22	AAW90374	Human immune/haema
964	6	1.2	77	22	AAO10251	Human polypeptide
965	6	1.2	77	23	ABP02872	Human OREF protein
966	6	1.2	78	21	AAW98260	H. pylori GHP0 144
967	6	1.2	78	19	AAW98260	Pinus radiata tran
968	6	1.2	79	22	AAW04846	Human SGP003 parti
969	6	1.2	79	23	ABP00842	Human OREF protein
970	6	1.2	79	23	ABP05175	Human OREF protein
971	6	1.2	80	21	AAW42338	Human OREF ORF2102
972	6	1.2	80	22	ABG00065	Novel human diagno
973	6	1.2	80	22	ABG11887	Novel human diagno
974	6	1.2	80	22	ABG17171	Novel human diagno
975	6	1.2	80	22	AAW20323	Human novel endocr
976	6	1.2	80	22	AAW85491	Human immune/haema
977	6	1.2	80	23	ABP43203	Human ovarian anti
978	6	1.2	80	23	ABP08150	Human OREF protein
979	6	1.2	81	22	AAO03474	Human polypeptide
980	6	1.2	81	22	AAO06868	Human polypeptide
981	6	1.2	82	18	AAW28194	Amino acid sequenc
982	6	1.2	82	19	AAW21011	Human glial fibril
983	6	1.2	82	20	AAW35995	Extended human sec
984	6	1.2	82	20	AAW88606	Secreted protein e
985	6	1.2	82	21	AAW12159	Hydrophobic domain
986	6	1.2	82	21	AAW28196	Human artemin neur
987	6	1.2	82	22	ABW31944	Peptide #4595 enco
988	6	1.2	82	22	ABW37183	Peptide #4689 enco
989	6	1.2	82	22	ABW50373	Human secreted pro
990	6	1.2	82	22	ABW22487	Protein #4486 enco
991	6	1.2	82	22	AAW57895	Human brain expres
992	6	1.2	82	22	AAW70313	Human bone marrow
993	6	1.2	82	22	AAW18151	Peptide #4585 enco
994	6	1.2	82	22	AAW25544	Human protein sequ
995	6	1.2	82	22	AAW30654	Peptide #4691 enco
996	6	1.2	82	23	ABG39957	Human peptide enco
997	6	1.2	83	20	AAW78170	Human secreted pro
998	6	1.2	83	22	AAW4883	Propionibacterium
999	6	1.2	83	22	ABG28088	Novel human diagno
1000	6	1.2	83	22	ABG28088	Novel human diagno

ALIGNMENTS

RESULT 1

AAW61362 ID AAW61362 standard; Protein; 518 AA.

AAW61362;

25-SEP-1998 (first entry)

Aspartic proteinase ASP1.

ASP1; Aspartic proteinase; Alzheimer's disease; cancer; melanoma.

Homo sapiens.

EP848062-A2.

17-JUN-1998.

01-DEC-1997; 97BP-0309648.

14-DEC-1996; 96GB-0026022.

(SMIK) SMITHKLINE BEECHAM CORP.
(SMIK) SMITHKLINE BEECHAM PLC.

Chapman CG, Evans JR, Powell DJ, Southan C;

DR WPI; 1998-314477/28.
DR N-FSDB; AAV27962.
XX New isolated polynucleotide encodes Aspartic protease polypeptide -
PT used to diagnosis, treat and vaccinate against Alzheimer's disease,
PT cancer and melanoma
XX Claim 11; Page 7; 19pp; English.

CC The human ASP1 protein is structurally related to other proteins of the
CC Aspartic proteinase family. ASP 1 polypeptides and polynucleotides can
CC be used to diagnosis, treat and vaccinate against Alzheimer's disease,
CC cancer and melanoma.
XX

Sequence 518 AA;

Query Match 100.0%; Score 518; DB 19; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy	1	MGALRALLLPLAQLLRAAPELAPAPFTLPLRVAATNRVVAFTPGPTPARHADGL	60
Db	1	MGALRALLLPLAQLLRAAPELAPAPFTLPLRVAATNRVVAFTPGPTPARHADGL	60
Oy	61	ALALEPALASPAGANFLAWVDNLQDGRGYLEMLIGTPPQQLIVDTGSSNFAVAG	120
Db	61	ALALEPALASPAGANFLAWVDNLQDGRGYLEMLIGTPPQQLIVDTGSSNFAVAG	120
Oy	121	TPHGYIDYFPTERSSTYRSKGFVYKYTGSGTGVGEBLVITIPGFTSELVNATI	180
Db	121	TPHGYIDYFPTERSSTYRSKGFVYKYTGSGTGVGEBLVITIPGFTSELVNATI	180
Oy	181	FESENFPLPGIKMNGILGLAYATLAKPSSLETFFDSLVTQANIPNFSMQCAGLPVA	240
Db	181	FESENFPLPGIKMNGILGLAYATLAKPSSLETFFDSLVTQANIPNFSMQCAGLPVA	240
Oy	241	GSGTNGSGVLVGIPELSLYKGDWYTPIKEWYQIEILKIEIGQSILNDCREYNADKA	300
Db	241	GSGTNGSGVLVGIPELSLYKGDWYTPIKEWYQIEILKIEIGQSILNDCREYNADKA	300
Oy	301	IVDSGTTILRLPQKVPFVAVAVARASLIPFSNGFMTGSLACWTSEFPMSYFPKISI	360
Db	301	IVDSGTTILRLPQKVPFVAVAVARASLIPFSNGFMTGSLACWTSEFPMSYFPKISI	360
Oy	361	YLRDENSRSFRITILPOLYIQPMGAGLNEYCYRFGISPESTNALVIGATVMEGFYIFD	420
Db	361	YLRDENSRSFRITILPOLYIQPMGAGLNEYCYRFGISPESTNALVIGATVMEGFYIFD	420
Oy	421	RAQKRVGFAASPCAEIAAGAVSEISGPFSTEDVANSVCVPAQSLSEPIIMIVSYALMSVCG	480
Db	421	RAQKRVGFAASPCAEIAAGAVSEISGPFSTEDVANSVCVPAQSLSEPIIMIVSYALMSVCG	480
Oy	481	ALLVLYLVLLLPFCQRRPRDPEVNDSESLVHRMK	518
Db	481	ALLVLYLVLLLPFCQRRPRDPEVNDSESLVHRMK	518

RESULT 2

AAW41714 ID AAW41714 standard; Protein; 518 AA.

AAW41714;

07-DEC-1999 (first entry)

Human PRO852 protein sequence.

Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
probe; blood coagulation disorder; cancer; cellular adhesion disorder;
secreted protein; transmembrane protein.

Homo sapiens.

QY 301 IVDGTTLLRLPQKVFDAVVAVARASLIPEFSDGFWTGSQACWNTSETPMWYFPKISI 360
 DB 301 IVDGTTLLRLPQKVFDAVVAVARASLIPEFSDGFWTGSQACWNTSETPMWYFPKISI 360
 QY 361 YLRDENSRSFRITITLPQLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYI 420
 DB 361 YLRDENSRSFRITITLPQLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYI 420
 QY 421 RAOKRVGFPAASPCAEIAGAASEISGPFSTEDVASCNCPAOSLSEPLIMVSYALMSVCG 480
 DB 421 RAOKRVGFPAASPCAEIAGAASEISGPFSTEDVASCNCPAOSLSEPLIMVSYALMSVCG 480
 QY 481 AILVLIVLILLPFRCORRPRDPEVNDSSLVHRMK 518
 DB 481 AILVLIVLILLPFRCORRPRDPEVNDSSLVHRMK 518

RESULT 3
 ID AAY22239
 AAY22239 standard; Protein; 518 AA.
 AC AAY22239;
 XX 20-SEP-1999 (first entry)
 DT 20-SEP-1999 (first entry)
 DE Human CSP56, aspartyl-type protease, protein sequence.
 XX Metastatic marker protein; human; cancer metastasis; breast cancer;
 KM colon cancer; diagnosis; therapy; tumour; metastatic potential;
 KM CSP56; aspartyl-type protease.
 XX Homo sapiens.
 OS
 XX MO9934004-A2.
 PN 08-JUL-1999.
 PD 08-JUL-1999.
 XX 24-DEC-1998; 98WO-US27608.
 PF 24-DEC-1998; 98WO-US27608.
 PR 31-DEC-1997; 97US-0070112.
 XX (CHIR) CHIRON CORP.
 PA
 XX Gliese K, Xin H;
 PI
 XX WPI: 1999-430248/36.
 DR N-PSDB; AAX84708.
 XX New polynucleotides associated with cancer metastasis
 PT
 XX Claim 4; Page 78-80; 80pp; English.
 PS
 XX This sequence represents a polypeptide of the invention, and is
 CC an aspartyl-type protease, designated CSP56. The polynucleotides (PNS) of
 CC the invention encode metastatic marker protein variants. The PNS and
 CC polypeptides can be used as markers for cancer metastasis. The products
 CC can be used for identifying metastatic tissue or metastatic potential of
 CC a tissue, e.g. breast or colon tissue. They can also be used for
 CC screening test compounds for the ability to suppress the metastatic
 CC potential of a tumour. The products can be used for developing products
 CC for the therapy of cancers, particularly breast or colon cancer.
 XX
 XX Sequence 518 AA;
 SQ

Query Match 100.0%; Score 518; DB 20; Length 518;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALRAAILLPILAOWLRAAPELAPAPFTPLRVAATNRVAPRPGTPEAERHADDGL 60
 DB 1 MGALRAAILLPILAOWLRAAPELAPAPFTPLRVAATNRVAPRPGTPEAERHADDGL 60
 QY 61 ALALEPALASPAGANFLAMVDNLQDSSGRGYLEMLIGTPQKQILVDTGSSNFAVAG 120

DB 61 ALALEPALASPAGANFLAMVDNLQDSSGRGYLEMLIGTPQKQILVDTGSSNFAVAG 120
 QY 121 TPHSYIDTPYPTERSSTYRSKGFDTVTKYTOGSWTCGVGEDLVITPKGFNTSFLVNIATI 180
 DB 121 TPHSYIDTPYPTERSSTYRSKGFDTVTKYTOGSWTCGVGEDLVITPKGFNTSFLVNIATI 180
 QY 181 FESENFELPGIKWNGILGLAVATLAKPSSLETFEDSLVTOANI PNVSQMCGAGLPVA 240
 DB 181 FESENFELPGIKWNGILGLAVATLAKPSSLETFEDSLVTOANI PNVSQMCGAGLPVA 240
 QY 241 GSGTNGSGLVIGIEPGLKCDIWTPTIKEMWYQIILKLEIGGSLNDDCREYNADKA 300
 DB 241 GSGTNGSGLVIGIEPGLKCDIWTPTIKEMWYQIILKLEIGGSLNDDCREYNADKA 300
 QY 301 IVDGTTLLRLPQKVFDAVVAVARASLIPEFSDGFWTGSQACWNTSETPMWYFPKISI 360
 DB 301 IVDGTTLLRLPQKVFDAVVAVARASLIPEFSDGFWTGSQACWNTSETPMWYFPKISI 360
 QY 361 YLRDENSRSFRITITLPQLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYI 420
 DB 361 YLRDENSRSFRITITLPQLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYI 420
 QY 421 RAOKRVGFPAASPCAEIAGAASEISGPFSTEDVASCNCPAOSLSEPLIMVSYALMSVCG 480
 DB 421 RAOKRVGFPAASPCAEIAGAASEISGPFSTEDVASCNCPAOSLSEPLIMVSYALMSVCG 480
 QY 481 AILVLIVLILLPFRCORRPRDPEVNDSSLVHRMK 518
 DB 481 AILVLIVLILLPFRCORRPRDPEVNDSSLVHRMK 518

RESULT 4
 ID AAY13799
 AAY13799 standard; Protein; 518 AA.
 AC AAY13799;
 XX 21-SEP-1999 (first entry)
 DT 21-SEP-1999 (first entry)
 DE Human aspartyl protease, CSP56.
 XX CSP56; human; aspartyl protease; diagnosis; neoplasia; tumour;
 KM breast tumour; colon tumour.
 KM
 XX Homo sapiens.
 OS
 XX MO9933963-A1.
 PN 08-JUL-1999.
 PD 08-JUL-1999.
 XX 14-DEC-1998; 98WO-US26547.
 PF 14-DEC-1998; 98WO-US26547.
 PR 31-DEC-1997; 97US-0070112.
 XX (CHIR) CHIRON CORP.
 PA
 XX Gliese KM, Xin H;
 PI
 XX WPI: 1999-430240/36.
 DR N-PSDB; AAX89297.
 XX Human CSP56 protein for diagnosis of neoplasia
 PT
 XX Claim 2; Fig 2A; 51pp; English.
 PS
 XX This represents a human CSP56 protein, a novel aspartyl protease. The
 CC CSP56 protein can be used in methods for diagnosing neoplasia, for
 CC determining the metastatic potential of a tumour, and for screening test
 CC compounds for the ability to suppress the metastatic potential of a
 CC tumour. The tumours are preferably from breast or colon.
 XX
 XX Sequence 518 AA;
 SQ

Query Match 100.0%; Score 518; DB 20; Length 518;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALRALLLPLLAQWMLRAAPELPAPFTLLPLRAAATNRVVAATPGGTPAERHADGL 60
 1 MGALRALLLPLLAQWMLRAAPELPAPFTLLPLRAAATNRVVAATPGGTPAERHADGL 60
 DB 1 MGALRALLLPLLAQWMLRAAPELPAPFTLLPLRAAATNRVVAATPGGTPAERHADGL 60

QY 61 ALALEPALASPAGANFLAMVDNLQDGRGYLLEMLIGTPPKQLIIVDTGSSNFAVAG 120
 61 ALALEPALASPAGANFLAMVDNLQDGRGYLLEMLIGTPPKQLIIVDTGSSNFAVAG 120
 DB 61 ALALEPALASPAGANFLAMVDNLQDGRGYLLEMLIGTPPKQLIIVDTGSSNFAVAG 120

QY 121 TPHSYIDTYFPTERSSTYRSKGFDTVYKYTGQSWTGFGVEDLVITIPKGFNTSFLVNIATI 180
 121 TPHSYIDTYFPTERSSTYRSKGFDTVYKYTGQSWTGFGVEDLVITIPKGFNTSFLVNIATI 180
 DB 121 TPHSYIDTYFPTERSSTYRSKGFDTVYKYTGQSWTGFGVEDLVITIPKGFNTSFLVNIATI 180

QY 181 FESSENFPLPGIKMNGIILGLAVATLAKPSSSLETFPDSLVTOANINPVFSMOCGAGLPVA 240
 181 FESSENFPLPGIKMNGIILGLAVATLAKPSSSLETFPDSLVTOANINPVFSMOCGAGLPVA 240
 DB 181 FESSENFPLPGIKMNGIILGLAVATLAKPSSSLETFPDSLVTOANINPVFSMOCGAGLPVA 240

QY 241 GSGTNGSLVLGIEPISLYKGDIMWYPIKEWYQIETIKLEIGGOSLNLDCREYNADKA 300
 241 GSGTNGSLVLGIEPISLYKGDIMWYPIKEWYQIETIKLEIGGOSLNLDCREYNADKA 300
 DB 241 GSGTNGSLVLGIEPISLYKGDIMWYPIKEWYQIETIKLEIGGOSLNLDCREYNADKA 300

QY 301 IVDSGTTLRLPQKVFAVEAVARASLIPEFSDGFWTGSQIACWTNSETPMWSPFKISI 360
 301 IVDSGTTLRLPQKVFAVEAVARASLIPEFSDGFWTGSQIACWTNSETPMWSPFKISI 360
 DB 301 IVDSGTTLRLPQKVFAVEAVARASLIPEFSDGFWTGSQIACWTNSETPMWSPFKISI 360

QY 361 YLRDSSRSRFRITLLPOLYIOPMMGAGLNYECYRFGISPSNNAIVGATWEGFYVIFD 420
 361 YLRDSSRSRFRITLLPOLYIOPMMGAGLNYECYRFGISPSNNAIVGATWEGFYVIFD 420
 DB 361 YLRDSSRSRFRITLLPOLYIOPMMGAGLNYECYRFGISPSNNAIVGATWEGFYVIFD 420

QY 421 RAQKRVGAASPCAEIAGAASEISGPFSTEDVASCNCPAQSISEPIIMIVSYALMSVCG 480
 421 RAQKRVGAASPCAEIAGAASEISGPFSTEDVASCNCPAQSISEPIIMIVSYALMSVCG 480
 DB 421 RAQKRVGAASPCAEIAGAASEISGPFSTEDVASCNCPAQSISEPIIMIVSYALMSVCG 480

QY 481 AILLVLIIVLLLPFCQRRPRDPEVNDSSILVRHRMK 518
 481 AILLVLIIVLLLPFCQRRPRDPEVNDSSILVRHRMK 518
 DB 481 AILLVLIIVLLLPFCQRRPRDPEVNDSSILVRHRMK 518

RESULT 5
 AAB44270
 ID AAB44270 standard; Protein; 518 AA.
 XX
 AC AAB44270;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Human PRO852 (UNQ418) protein sequence SEQ ID NO:196.
 XX
 KW Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;
 KW expressed sequence tag; detection; cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200053756-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 18-FEB-2000; 2000WO-US04341.
 XX
 PR 08-MAR-1999; 99WO-US05028.
 PR 12-MAR-1999; 99US-0123957.
 PR 29-MAR-1999; 99US-0126773.
 PR 21-APR-1999; 99US-0130232.
 PR 28-APR-1999; 99US-0131445.
 PR 14-MAY-1999; 99US-0134287.
 PR 23-JUN-1999; 99US-0141037.
 PR 26-JUL-1999; 99US-0145698.
 PR 29-OCT-1999; 99US-0162506.
 PR 30-NOV-1999; 99WO-US28313.

PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28565.
 PR 16-DEC-1999; 99WO-US30095.
 PR 30-DEC-1999; 99WO-US31243.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 XX
 PA (GERTH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein D, Deonoyers L, Eaton DL,
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerlitsen ME,
 PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ,
 PI Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA,
 PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI,
 XX
 DR WPI; 2000-611443/58.
 DR N-PSDB; AAC78500.
 XX
 PT Novel PRO polypeptides and polynucleotides used in detection methods,
 PT to target bioactive molecules to specific cells, and to modulate
 PT cellular activities -
 XX
 PS Claim 12; Fig 73; 636pp; English.
 XX
 CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed
 CC sequence tag) sequences which encode secreted or transmembrane PRO
 CC polypeptides. The PRO polynucleotides and polypeptides are used for cytosolic
 CC activity. The polynucleotides and polypeptides can be used for detecting
 CC the presence of PRO polypeptides in samples, for linking bioactive
 CC molecules to cells and for modulating biological activities of cells,
 CC using the polypeptides for specific targeting. The polypeptide targeting
 CC can be used to kill the target cells, e.g. for the treatment of cancers.
 CC The polypeptide pairs provide specific targeting of bioactive molecules
 CC to cells. AAC78600 to AAC78967 represent PCR primers and probes used in
 CC the isolation of the PRO polynucleotide sequences.
 XX
 SQ Sequence 518 AA;

Query Match 100.0%; Score 518; DB 21; Length 518;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALRALLLPLLAQWMLRAAPELPAPFTLLPLRAAATNRVVAATPGGTPAERHADGL 60
 1 MGALRALLLPLLAQWMLRAAPELPAPFTLLPLRAAATNRVVAATPGGTPAERHADGL 60
 DB 1 MGALRALLLPLLAQWMLRAAPELPAPFTLLPLRAAATNRVVAATPGGTPAERHADGL 60

QY 61 ALALEPALASPAGANFLAMVDNLQDGRGYLLEMLIGTPPKQLIIVDTGSSNFAVAG 120
 61 ALALEPALASPAGANFLAMVDNLQDGRGYLLEMLIGTPPKQLIIVDTGSSNFAVAG 120
 DB 61 ALALEPALASPAGANFLAMVDNLQDGRGYLLEMLIGTPPKQLIIVDTGSSNFAVAG 120

QY 121 TPHSYIDTYFPTERSSTYRSKGFDTVYKYTGQSWTGFGVEDLVITIPKGFNTSFLVNIATI 180
 121 TPHSYIDTYFPTERSSTYRSKGFDTVYKYTGQSWTGFGVEDLVITIPKGFNTSFLVNIATI 180
 DB 121 TPHSYIDTYFPTERSSTYRSKGFDTVYKYTGQSWTGFGVEDLVITIPKGFNTSFLVNIATI 180

QY 181 FESSENFPLPGIKMNGIILGLAVATLAKPSSSLETFPDSLVTOANINPVFSMOCGAGLPVA 240
 181 FESSENFPLPGIKMNGIILGLAVATLAKPSSSLETFPDSLVTOANINPVFSMOCGAGLPVA 240
 DB 181 FESSENFPLPGIKMNGIILGLAVATLAKPSSSLETFPDSLVTOANINPVFSMOCGAGLPVA 240

QY 241 GSGTNGSLVLGIEPISLYKGDIMWYPIKEWYQIETIKLEIGGOSLNLDCREYNADKA 300
 241 GSGTNGSLVLGIEPISLYKGDIMWYPIKEWYQIETIKLEIGGOSLNLDCREYNADKA 300
 DB 241 GSGTNGSLVLGIEPISLYKGDIMWYPIKEWYQIETIKLEIGGOSLNLDCREYNADKA 300

QY 301 IVDSGTTLRLPQKVFAVEAVARASLIPEFSDGFWTGSQIACWTNSETPMWSPFKISI 360
 301 IVDSGTTLRLPQKVFAVEAVARASLIPEFSDGFWTGSQIACWTNSETPMWSPFKISI 360
 DB 301 IVDSGTTLRLPQKVFAVEAVARASLIPEFSDGFWTGSQIACWTNSETPMWSPFKISI 360

QY 361 YLRDSSRSRFRITLLPOLYIOPMMGAGLNYECYRFGISPSNNAIVGATWEGFYVIFD 420
 361 YLRDSSRSRFRITLLPOLYIOPMMGAGLNYECYRFGISPSNNAIVGATWEGFYVIFD 420
 DB 361 YLRDSSRSRFRITLLPOLYIOPMMGAGLNYECYRFGISPSNNAIVGATWEGFYVIFD 420

QY 421 RAQKRVGAASPCAEIAGAASEISGPFSTEDVASCNCPAQSISEPIIMIVSYALMSVCG 480

DB 421 RAQKRVGFASPCAEIAGAAYSEISGPFSTEDVANSNCVPAQSLSPILMTVSYALMSVCG 480
 QY 481 AILVLIVLILLLPFCORRPRDPEVNDSSLVHRWK 518
 DB 481 AILVLIVLILLLPFCORRPRDPEVNDSSLVHRWK 518

RESULT 6

AY88424
 ID AAY88424 standard; Protein; 518 AA.

AC AAY88424;

DT 03-AUG-2000 (first entry)

DE Human aspartyl protease 1 (Asp1) amino acid sequence.

KW Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 1;

KM Alzheimer's disease; beta secretase site.

XX Homo sapiens.

OS MO200017369-A2.

PN 30-MAR-2000.

PD 23-SEP-1999; 99WO-US20881.

PF 24-SEP-1998; 98US-0101594.

PR (PDBA) PHARMACIA & UPJOHN CO.

PA Gurney ME, Bienkowski MJ, Heinrichson RL, Parodi LA, Yan R;

PI WPI; 2000-303209/26.

DR N-PSDB; AAA15661.

XX New enzyme designated human aspartase useful in research, into

FT Alzheimer's disease is capable of cleaving amyloid protein precursor at

PT the beta secretase site to produce amyloid beta peptide -

PS Claim 54; Fig 1; 183pp; English.

XX This sequence represents the human aspartyl protease amino acid sequence.

CC The invention relates to a protease capable of cleaving the beta

CC secretase site of amyloid precursor protein (APP). The protease contains

CC a sequence encoding the amino acid sequence DTG and a sequence encoding

CC DTG or DTG separated by 100-300 amino acids. When mutated the APP gene

CC causes an autosomal dominant form of Alzheimer's disease. APP localises

CC to the cell surface membrane and have a single C-terminal transmembrane

CC domain. Proteolytic processing of APP produces the amyloid beta protein,

CC which is possibly very important in Alzheimer's disease. The invention

CC includes a nucleotide sequence encoding the protease, a vector containing

CC the nucleotide sequence, and a cell line comprising the vector. Methods

CC for screening for inhibitors of beta secretase activity are also given in

CC the invention. The human aspartase protein and nucleotide sequences and

CC the methods for identifying inhibitors of the protease, are useful in the

CC treatment of and research in to Alzheimer's disease.

CC Sequence 518 AA;

CC

CC

CC

CC

CC

CC

CC

QY 121 TPHSYIDTFEPTERRSTYRSKGFDTWKYTGSGMTGVEGDLVTIPKGFNTSFLVNIATI 180

DB 121 TPHSYIDTFEPTERRSTYRSKGFDTWKYTGSGMTGVEGDLVTIPKGFNTSFLVNIATI 180

QY 181 FESNFFLPGLKMGIIIGLAVATLAKPSSSLETFPDSLVTOANI PNVSQMCGAGLPVA 240

DB 181 FESNFFLPGLKMGIIIGLAVATLAKPSSSLETFPDSLVTOANI PNVSQMCGAGLPVA 240

QY 241 GSGTNGSLVVGIEPISLVGMDIWTPTIKEMWYQIILILEIGGSLNDCERYNADKA 300

DB 241 GSGTNGSLVVGIEPISLVGMDIWTPTIKEMWYQIILILEIGGSLNDCERYNADKA 300

QY 301 IVDSGTTLRLPKVFPDVAEAVARASLIPEFSDGFWTGSOLA CWTNSETPWSYFPKISI 360

DB 301 IVDSGTTLRLPKVFPDVAEAVARASLIPEFSDGFWTGSOLA CWTNSETPWSYFPKISI 360

QY 361 YLRDENSRSRFRITILPOLYIQPMGAGLVNVECYRFGISPTNALVIGATVMEGFYIFD 420

DB 361 YLRDENSRSRFRITILPOLYIQPMGAGLVNVECYRFGISPTNALVIGATVMEGFYIFD 420

QY 421 RAQKRVGFASPCAEIAGAAYSEISGPFSTEDVANSNCVPAQSLSPILMTVSYALMSVCG 480

DB 421 RAQKRVGFASPCAEIAGAAYSEISGPFSTEDVANSNCVPAQSLSPILMTVSYALMSVCG 480

QY 481 AILVLIVLILLLPFCORRPRDPEVNDSSLVHRWK 518

DB 481 AILVLIVLILLLPFCORRPRDPEVNDSSLVHRWK 518

RESULT 7

AAE10628
 ID AAE10628 standard; Protein; 518 AA.

AC AAE10628;

DT 10-DEC-2001 (first entry)

DE Human aspartyl protease 1 (hu-Asp1) protein.

XX Human; aspartyl protease 1; Asp1; amyloid precursor protein; APP;

KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;

KW amyloid plaque; neuronal loss; proteolytic; neurotropic; neuroprotective;

XX chromosome 21.

OS Homo sapiens.

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QY 121 TPHSYIDTFEPTERRSTYRSKGFDTWKYTGSGMTGVEGDLVTIPKGFNTSFLVNIATI 180

DB 121 TPHSYIDTFEPTERRSTYRSKGFDTWKYTGSGMTGVEGDLVTIPKGFNTSFLVNIATI 180

QY 181 FESNFFLPGLKMGIIIGLAVATLAKPSSSLETFPDSLVTOANI PNVSQMCGAGLPVA 240

DB 181 FESNFFLPGLKMGIIIGLAVATLAKPSSSLETFPDSLVTOANI PNVSQMCGAGLPVA 240

QY 241 GSGTNGSLVVGIEPISLVGMDIWTPTIKEMWYQIILILEIGGSLNDCERYNADKA 300

DB 241 GSGTNGSLVVGIEPISLVGMDIWTPTIKEMWYQIILILEIGGSLNDCERYNADKA 300

QY 301 IVDSGTTLRLPKVFPDVAEAVARASLIPEFSDGFWTGSOLA CWTNSETPWSYFPKISI 360

DB 301 IVDSGTTLRLPKVFPDVAEAVARASLIPEFSDGFWTGSOLA CWTNSETPWSYFPKISI 360

QY 361 YLRDENSRSRFRITILPOLYIQPMGAGLVNVECYRFGISPTNALVIGATVMEGFYIFD 420

DB 361 YLRDENSRSRFRITILPOLYIQPMGAGLVNVECYRFGISPTNALVIGATVMEGFYIFD 420

QY 421 RAQKRVGFASPCAEIAGAAYSEISGPFSTEDVANSNCVPAQSLSPILMTVSYALMSVCG 480

DB 421 RAQKRVGFASPCAEIAGAAYSEISGPFSTEDVANSNCVPAQSLSPILMTVSYALMSVCG 480

QY 481 AILVLIVLILLLPFCORRPRDPEVNDSSLVHRWK 518

DB 481 AILVLIVLILLLPFCORRPRDPEVNDSSLVHRWK 518

RESULT 7

AAE10628
 ID AAE10628 standard; Protein; 518 AA.

AC AAE10628;

DT 10-DEC-2001 (first entry)

DE Human aspartyl protease 1 (hu-Asp1) protein.

XX Human; aspartyl protease 1; Asp1; amyloid precursor protein; APP;

KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;

KW amyloid plaque; neuronal loss; proteolytic; neurotropic; neuroprotective;

XX chromosome 21.

OS Homo sapiens.

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XX

XX

XX Polypeptide comprising fragments of human aspartyl protease with
 PT amyloid precursor protein processing activity and alpha-secretase
 PT activity, for identifying modulators useful in treating Alzheimer's
 PT disease -
 XX
 XX Claim 36; Fig 1; 187bp; English.
 XX
 CC The patent discloses human aspartyl protease 1 (hu-Asp1) or modified
 CC Asp1 proteins which lack transmembrane domain or amino terminal
 CC domain or cytoplasmic domain and retains alpha-secretase activity
 CC and amyloid protein precursor (APP) processing activity. The proteins
 CC of the invention are useful for assaying hu-Asp1 alpha-secretase
 CC activity, which in turn is useful for identifying modulators of
 CC hu-Asp1 alpha-secretase activity, where modulators that increase
 CC hu-Asp1 alpha-secretase activity are useful for treating Alzheimer's
 CC disease (AD) which causes progressive dementia with consequent
 CC formation of amyloid plaques, neurofibrillary tangles, gliosis and
 CC neuronal loss. Hu-Asp1 protease substrate is useful for assaying
 CC hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein with
 CC the substrate under acidic conditions and determining the level of
 CC hu-Asp1 proteolytic activity. The present sequence is Asp1 protein
 CC from human. Asp1 gene is localised on chromosome 21.
 XX
 SQ Sequence 518 AA;
 Query Match 100.0%; Score 518; DB 22; Length 518;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGALRALLLPLAOWMLRAPELAPAPFTLPLRVAAATNRVVAPTPGGTPAERHADGL 60
 DB 1 MGALRALLLPLAOWMLRAPELAPAPFTLPLRVAAATNRVVAPTPGGTPAERHADGL 60
 QY 61 ALALEPALASPAGANFLAMVDNLQDGRGYLEMLIGTPPOKQIIVDTGSSNFAVAG 120
 DB 61 ALALEPALASPAGANFLAMVDNLQDGRGYLEMLIGTPPOKQIIVDTGSSNFAVAG 120
 QY 121 TPHSYIDTYPTDERSSTYRSKGFDTVKYTOGSGTWGFGVEDLVITIPKGFNTSFLVNIATI 180
 DB 121 TPHSYIDTYPTDERSSTYRSKGFDTVKYTOGSGTWGFGVEDLVITIPKGFNTSFLVNIATI 180
 QY 181 FESNEFLIPGIRKNGILGLAVATLAKPSSSLETFPDSLVTOQININVSQMCGAGLPVA 240
 DB 181 FESNEFLIPGIRKNGILGLAVATLAKPSSSLETFPDSLVTOQININVSQMCGAGLPVA 240
 QY 241 GSGTNGSLVIGIEPSLYKGDIMWTPIKEWYQIETIKETIGGOSINLDCREYNADKA 300
 DB 241 GSGTNGSLVIGIEPSLYKGDIMWTPIKEWYQIETIKETIGGOSINLDCREYNADKA 300
 QY 301 IVDSTTLRLPQKVFDAVVEAVARASLIPFSDGFMFGSOLAQWNTSETPMSYFPKISI 360
 DB 301 IVDSTTLRLPQKVFDAVVEAVARASLIPFSDGFMFGSOLAQWNTSETPMSYFPKISI 360
 QY 361 YLRDSSRSFRITTLPOLYIOPMMGAGLNYECYRFGISPSSTNALVIGATWEGFYVIFD 420
 DB 361 YLRDSSRSFRITTLPOLYIOPMMGAGLNYECYRFGISPSSTNALVIGATWEGFYVIFD 420
 QY 421 RAQKRVGAAPCAEIAAGAAVSEISGPFSTEDVANCPAOSLSPIIMIVSYALMSYCG 480
 DB 421 RAQKRVGAAPCAEIAAGAAVSEISGPFSTEDVANCPAOSLSPIIMIVSYALMSYCG 480
 QY 481 AILVLIVLILPFCQRRPRDEPVNDESSLVRHRWK 518
 DB 481 AILVLIVLILPFCQRRPRDEPVNDESSLVRHRWK 518
 RESULT 8
 ID AAE10656 standard; Protein; 518 AA.
 XX
 AC AAE10656;
 XX

DT 10-DEC-2001 (first entry)
 XX
 DE Human-Asp 1 protein lacking TM domain and containing (His)6 tag.
 XX
 KW Human; aspartyl protease 1; Asp1; amyloid precursor protein; APP;
 KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
 KW amyloid plaque; neuronal loss; proteolytic; neuroprotective.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX GB2357767-A.
 PN 04-JUL-2001.
 PD
 PF 22-SEP-2000; 2000GB-0023315.
 PR 23-SEP-1999; 99US-0155493.
 PR 23-SEP-1999; 99US-0404133.
 PR 23-SEP-1999; 99WO-US20881.
 PR 13-OCT-1999; 99US-0416901.
 PR 06-DEC-1999; 99US-0169232.
 XX (PHDA) PHARMACIA & UPJOHN CO.
 PA
 PI Bienkowski MJ, Gurney M;
 XX WPI; 2001-444206/48.
 DR
 XX
 XX
 PT Polypeptide comprising fragments of human aspartyl protease with
 PT amyloid precursor protein processing activity and alpha-secretase
 PT activity, for identifying modulators useful in treating Alzheimer's
 PT disease -
 XX
 XX Example 14; Page 155-156; 187bp; English.
 PS
 CC The patent discloses human aspartyl protease 1 (hu-Asp1) or modified
 CC Asp1 proteins which lack transmembrane domain or amino terminal
 CC domain or cytoplasmic domain and retains alpha-secretase activity
 CC and amyloid protein precursor (APP) processing activity. The proteins
 CC of the invention are useful for assaying hu-Asp1 alpha-secretase
 CC activity, which in turn is useful for identifying modulators of
 CC hu-Asp1 alpha-secretase activity, where modulators that increase
 CC hu-Asp1 alpha-secretase activity are useful for treating Alzheimer's
 CC disease (AD) which causes progressive dementia with consequent
 CC formation of amyloid plaques, neurofibrillary tangles, gliosis and
 CC neuronal loss. Hu-Asp1 protease substrate is useful for assaying
 CC hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein with
 CC the substrate under acidic conditions and determining the level of
 CC hu-Asp1 proteolytic activity. The present sequence is human Asp 1
 CC protein lacking a transmembrane (TM) domain and containing (His)6
 CC tag. This sequence is generated from human Asp 1 protein by the
 CC deletion of its C-terminal TM domain and addition of hexa-histidine
 CC tag at its C-terminus.
 XX
 SQ Sequence 518 AA;
 Query Match 100.0%; Score 518; DB 22; Length 518;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGALRALLLPLAOWMLRAPELAPAPFTLPLRVAAATNRVVAPTPGGTPAERHADGL 60
 DB 1 MGALRALLLPLAOWMLRAPELAPAPFTLPLRVAAATNRVVAPTPGGTPAERHADGL 60
 QY 61 ALALEPALASPAGANFLAMVDNLQDGRGYLEMLIGTPPOKQIIVDTGSSNFAVAG 120
 DB 61 ALALEPALASPAGANFLAMVDNLQDGRGYLEMLIGTPPOKQIIVDTGSSNFAVAG 120
 QY 121 TPHSYIDTYPTDERSSTYRSKGFDTVKYTOGSGTWGFGVEDLVITIPKGFNTSFLVNIATI 180
 DB 121 TPHSYIDTYPTDERSSTYRSKGFDTVKYTOGSGTWGFGVEDLVITIPKGFNTSFLVNIATI 180

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QY 181 FESNFPLPGIKMNGIIGLAATLAKPSSSLETFPDSLVTOANI PNVSQMCGAGLPVA 240
DB 181 FESNFPLPGIKMNGIIGLAATLAKPSSSLETFPDSLVTOANI PNVSQMCGAGLPVA 240
QY 241 GSGTNGSLVVGIEPISLYKGDINTWTPKEEMYYOIELKIEIGOSINLDCREYNADKA 300
DB 241 GSGTNGSLVVGIEPISLYKGDINTWTPKEEMYYOIELKIEIGOSINLDCREYNADKA 300
QY 301 IVDSTTLRLPQKVFDAVEAVARASLIPEPSDGFMTGSQLACWTNSETPMSYFPKISI 360
DB 301 IVDSTTLRLPQKVFDAVEAVARASLIPEPSDGFMTGSQLACWTNSETPMSYFPKISI 360
QY 361 YLRDENSRSRFRITLLPOLYIOPMMGAGLNYECYRFGISPSSTNALVIGATWMEGFYIIFD 420
DB 361 YLRDENSRSRFRITLLPOLYIOPMMGAGLNYECYRFGISPSSTNALVIGATWMEGFYIIFD 420
QY 421 RAQKRVGPAASPCAIAGAAVSEISGPSTEDVANCVPAQSLSPILMIVSYALMSYCG 480
DB 421 RAQKRVGPAASPCAIAGAAVSEISGPSTEDVANCVPAQSLSPILMIVSYALMSYCG 480
QY 481 AILVLIVLLLPFCORRRPDEPVNDESSLVRRHWK 518
DB 481 AILVLIVLLLPFCORRRPDEPVNDESSLVRRHWK 518

RESULT 9
AAU29059
ID AAU29059 standard; Protein; 518 AA.
XX
AC AAU29059;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human PRO polypeptide sequence #36.
XX
KM PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200168848-A2.
XX
PD 20-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US06520.
XX
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 03-MAR-2000; 2000US-187202P.
PR 06-MAR-2000; 2000US-186968P.
PR 14-MAR-2000; 2000US-189320P.
PR 14-MAR-2000; 2000US-189328P.
PR 15-MAR-2000; 2000WO-US06884.
PR 21-MAR-2000; 2000US-190828P.
PR 21-MAR-2000; 2000US-191007P.
PR 21-MAR-2000; 2000US-191048P.
PR 21-MAR-2000; 2000US-191314P.
PR 28-MAR-2000; 2000US-192855P.
PR 29-MAR-2000; 2000US-193032P.
PR 29-MAR-2000; 2000US-193053P.
PR 30-MAR-2000; 2000WO-US08439.
PR 04-APR-2000; 2000US-194449P.
PR 04-APR-2000; 2000US-194447P.
PR 11-APR-2000; 2000US-195375P.
PR 11-APR-2000; 2000US-195375P.
PR 11-APR-2000; 2000US-196000P.
PR 11-APR-2000; 2000US-196187P.
PR 11-APR-2000; 2000US-196620P.
PR 11-APR-2000; 2000US-196620P.
PR 18-APR-2000; 2000US-198121P.
PR 18-APR-2000; 2000US-198585P.
PR 25-APR-2000; 2000US-199397P.

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PR 25-APR-2000; 2000US-199550P.
PR 25-APR-2000; 2000US-199654P.
PR 03-MAY-2000; 2000US-201516P.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000US-151264P.
PR 05-JUN-2000; 2000US-209833P.
PR 28-JUL-2000; 2000WO-US20710.
PR 22-AUG-2000; 2000US-0644848.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
XX
PA (GERTH ) GENENTECH INC.
XX
PI Baker KP, Chen J, Deeneyers L, Goddard A, Godowski PJ, Gurney AL,
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2001-602746/68.
DR N-PSDB; AAS45960.
XX
PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumours, such as prostate and breast tumours, in mammals and
PT to screen for modulators of the compounds -
XX
PS Claim 11; Fig 72; 774pp; English.
XX
CC Sequences AAU29024-AAU29338 represent PRO polypeptides of the invention.
CC The PRO polypeptides and their associated nucleic acids can be used to
CC detect the presence of a tumour in a mammal by comparing the level of
CC expression of a PRO polypeptide in a test sample of cells from the animal
CC and a control sample of normal cells, whereby a higher level of
CC expression in the test sample indicates the presence of a tumour in the
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC and rabbits but are preferably human. The polypeptides can be used to
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC when contacted with it. A specific polypeptide can be used to stimulate
CC the proliferation or differentiation of chondrocyte cells. The PRO
CC proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders.
XX
SQ Sequence 518 AA;
XX
Query Match 100.0%; Score 518; DB 22; Length 518;
Best local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGALRALLLPLAOWILRAAPBELAPAPFTLLVAATNRVVAPTGPGPARRHADGL 60
DB 1 MGALRALLLPLAOWILRAAPBELAPAPFTLLVAATNRVVAPTGPGPARRHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLEMLIGTPPQKIQILVDTGSSNFAVAG 120
DB 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLEMLIGTPPQKIQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTFPTERSSTYRSKGFDTVYKYGSTGWTGVEGDELVTIIPKGFNTSFLVNIATI 180
DB 121 TPHSYIDTFPTERSSTYRSKGFDTVYKYGSTGWTGVEGDELVTIIPKGFNTSFLVNIATI 180
QY 121 TPHSYIDTFPTERSSTYRSKGFDTVYKYGSTGWTGVEGDELVTIIPKGFNTSFLVNIATI 180
DB 121 TPHSYIDTFPTERSSTYRSKGFDTVYKYGSTGWTGVEGDELVTIIPKGFNTSFLVNIATI 180
QY 181 FESNFPLPGIKMNGIIGLAATLAKPSSSLETFPDSLVTOANI PNVSQMCGAGLPVA 240
DB 181 FESNFPLPGIKMNGIIGLAATLAKPSSSLETFPDSLVTOANI PNVSQMCGAGLPVA 240
QY 241 GSGTNGSLVVGIEPISLYKGDINTWTPKEEMYYOIELKIEIGOSINLDCREYNADKA 300
DB 241 GSGTNGSLVVGIEPISLYKGDINTWTPKEEMYYOIELKIEIGOSINLDCREYNADKA 300
QY 301 IVDSTTLRLPQKVFDAVEAVARASLIPEPSDGFMTGSQLACWTNSETPMSYFPKISI 360

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|||||
Db 301 IVDGTTLLRLPQKVFDAVEAVASLIPESDGFMTGSQLAQWTNSETPWSYFPKISI 360
QY 361 YLRDENSRSFRITILPOLYIQPMGAGLNYECYRFGISPTNALVIATWMEGYVIFD 420
Db 361 YLRDENSRSFRITILPOLYIQPMGAGLNYECYRFGISPTNALVIATWMEGYVIFD 420
QY 421 RAQKRVGFPAASPCAEIAGAASEISGPFSTEDVANSNCVPAQSISEPILMIVSYALMSVCG 480
Db 421 RAQKRVGFPAASPCAEIAGAASEISGPFSTEDVANSNCVPAQSISEPILMIVSYALMSVCG 480
QY 481 AILVLIVLILLLPRCQRRPRDPEVNVDESSLVHRMK 518
Db 481 AILVLIVLILLLPRCQRRPRDPEVNVDESSLVHRMK 518

RESULT 10
AA060658
ID AA060658 standard; Protein; 518 AA.
AC AA060658;
XX
XX 23-OCT-2001 (first entry)
DT
XX Human aspartyl protease 1 (Hu-Asp1) protein.
XX
XX Human; aspartyl protease 1; Asp 1; beta-amyloid precursor protein; APP;
XX beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
XX neurofibrillary tangle; neuronal loss; amyloid-beta peptide; neurotic;
XX neuroprotective; antilease therapy; gene therapy; chromosome 21.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..20
XX FT /label= Signal_peptide
XX FT 21..518
XX FT /note= "Mature human aspartyl protease 1 (Hu-Asp1)"
XX FT Domain 469..492
XX FT /label= Transmembrane_domain
XX
XX W0200150829-A2.
XX
XX 19-JUL-2001.
XX
XX 09-MAY-2001; 2001WO-1B00799.
XX
XX 09-MAY-2001; 2001WO-1B00799.
XX
XX (BIEN/) BIENKOWSKI M J.
XX (GURN/) GURNEY M E.
XX (HEIN/) HEINRIKSON R L.
XX (PARO/) PARODI L A.
XX (YANR/) YAN R.
XX
XX Bienkowski MJ, Gurney ME, Heinrichson RL, Parodi LA, Yan R;
XX WPI: 2001-483072/52.
XX DR N-PSDB; AAD13020.
XX
XX Novel purified polypeptide comprising fragment of mammalian aspartyl
XX protease 2, lacking Asp2 transmembrane domain and retaining beta
XX secretase activity of Asp2 useful for identifying inhibitors of Asp2
XX activity
XX
XX Example 2; Fig 1; 185bp; English.
XX
XX The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
XX precursor protein (APP) isoforms and their corresponding DNA molecules.
XX Human aspartyl proteases can act as beta-secretase proteases useful for
XX treating Alzheimer's disease. APP isoforms are useful for identifying
XX modulators of amyloid-beta peptide production, for use in designing
XX therapeutics for the treatment and prevention of Alzheimer's disease,

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CC dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
CC and neuronal loss. APP isoforms are also used in methods for identifying
CC inhibitors and modulators of human Asp2 activity. The invention relates
CC to a method for identifying agents that modulate the activity of human
CC aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
CC as a means to screen in cellular assays for the inhibitors of beta- and
CC gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
CC polymerase chain reactions (PCR). The probes are useful for detecting
CC Hu-Asp nucleic acids in in vitro assays and in Northern and Southern
CC blots. The present sequence is human aspartyl protease 1 (Hu-Asp1).
CC Hu-Asp 1 gene is localised on chromosome 21.
XX
XX Sequence 518 AA;
SQ
Query Match 100.0%; Score 518; DB 22; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGALARALLPLAOWMLRAAPBELAPAFLLPLRVAATNRVVAPTPGPTPAERHADGL 60
Db 1 MGALARALLPLAOWMLRAAPBELAPAFLLPLRVAATNRVVAPTPGPTPAERHADGL 60
QY 61 ALALEPALASPAAGANFLAWVDNIQSGSGRGYILEMLIGTPPOQLIIVDTGSSNFAVAG 120
Db 61 ALALEPALASPAAGANFLAWVDNIQSGSGRGYILEMLIGTPPOQLIIVDTGSSNFAVAG 120
QY 121 TPHSYITDYPPTBESSITYRSKGFDTVKYTOGSGWTFGVGEDLVITIPGPNFSPLVNIATI 180
Db 121 TPHSYITDYPPTBESSITYRSKGFDTVKYTOGSGWTFGVGEDLVITIPGPNFSPLVNIATI 180
QY 181 FESNFPLPGIKWNGILGLAVATLAKPSSLETFPDSLVTOQANIPNVFSMQMGAGLPVA 240
Db 181 FESNFPLPGIKWNGILGLAVATLAKPSSLETFPDSLVTOQANIPNVFSMQMGAGLPVA 240
QY 241 GSGTNGSLVIGIEPSLYKGDITWTPYIKBEWYQIETLKLEIGGSLNIDCREYNADKA 300
Db 241 GSGTNGSLVIGIEPSLYKGDITWTPYIKBEWYQIETLKLEIGGSLNIDCREYNADKA 300
QY 301 IVDGTTLLRLPQKVFDAVEAVASLIPESDGFMTGSQLAQWTNSETPWSYFPKISI 360
Db 301 IVDGTTLLRLPQKVFDAVEAVASLIPESDGFMTGSQLAQWTNSETPWSYFPKISI 360
QY 361 YLRDENSRSFRITILPOLYIQPMGAGLNYECYRFGISPTNALVIATWMEGYVIFD 420
Db 361 YLRDENSRSFRITILPOLYIQPMGAGLNYECYRFGISPTNALVIATWMEGYVIFD 420
QY 421 RAQKRVGFPAASPCAEIAGAASEISGPFSTEDVANSNCVPAQSISEPILMIVSYALMSVCG 480
Db 421 RAQKRVGFPAASPCAEIAGAASEISGPFSTEDVANSNCVPAQSISEPILMIVSYALMSVCG 480
QY 481 AILVLIVLILLLPRCQRRPRDPEVNVDESSLVHRMK 518
Db 481 AILVLIVLILLLPRCQRRPRDPEVNVDESSLVHRMK 518

RESULT 11
AA060602
ID AA060602 standard; Protein; 518 AA.
AC AA060602;
XX
XX 24-OCT-2001 (first entry)
DT
XX Human Aspartyl protease 1 (Asp1).
XX
XX Human; Aspartyl protease; Asp1; Asp2; beta-secretase; neurotropic;
XX neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
XX amyloid-beta; Abeta.
XX
XX Homo sapiens.
XX
XX W0200149098-A2.
XX

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PD 12-JUL-2001.
 XX
 PF 09-MAY-2001; 2001WO-IB00798.
 XX
 PR 09-MAY-2001; 2001WO-IB00798.
 XX
 PA (BIEN/) BIENKOWSKI M J.
 PA (GURN/) GURNEY M E.
 PA (HEIN/) HEINRIKSON R L.
 PA (PARO/) PARODI L A.
 PA (YANR/) YAN R.
 XX
 PI Bienkowski MJ, Gurney ME, Heinrichson RL, Parodi LA, Yan R;
 XX
 DR WPI: 2001-502548/55.
 DR N-PSDB; AAS11516.
 DR
 XX
 PT Novel purified polypeptide comprising fragment of mammalian aspartyl
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
 PT activity -
 XX
 PS Example 2; Fig 1; 185bp; English.
 XX
 CC The invention relates to a purified polypeptide comprising a fragment of
 CC mammalian aspartyl protease (Asp)2 protein which lacks the Asp2
 CC transmembrane domain and the Asp2 protein, and where the polypeptide and
 CC the fragment retain the beta-secretase activity of the mammalian Asp2
 CC protein. The invention also details polynucleotides for the Asp
 CC proteins and vectors expressing them, and a polypeptide (isotorm of
 CC amyloid protein precursor (APP) comprising the amino acid sequence of an
 CC APP or its fragment containing an APP cleavage site recognizable by a
 CC mammalian beta-secretase, and further comprising two lysine residues at
 CC the carboxyl terminus of the amino acid sequence of the mammalian APP or
 CC APP fragment. Also included in the invention are methods of identifying
 CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
 CC useful for treating Alzheimer's disease. APP is useful in methods for
 CC identifying inhibitors or modulators of human Asp2 activity and
 CC amyloid-beta (Abeta) peptide production. APP is also useful in designing
 CC therapeutics for the treatment or prevention of Alzheimer's disease.
 CC APP comprising the APP-Sw-beta-secretase peptide sequence (NMDA), which
 CC is associated with increased levels of Abeta processing is useful in
 CC assays relating the Alzheimer's research. The expression vector is useful
 CC for recombinantly expressing APP. Nucleic acids that hybridise to
 CC APP oligonucleotides are useful as probes or primers. The probes are
 CC useful for detecting Hu-Asp nucleic acids in vitro assays and in
 CC Northern and Southern blots. The present sequence is human Asp1.
 CC
 XX
 SQ Sequence 518 AA;
 Query Match 100.0%; Score 518; DB 22; Length 518;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGALRALLLPLLAQWLRAABELAPAPPTLPLRVAAATNRVAAPTGGTDAERHADGL 60
 DB 1 MGALRALLLPLLAQWLRAABELAPAPPTLPLRVAAATNRVAAPTGGTDAERHADGL 60
 QY 61 ALALEPALASPAGANFLAMVNDLQDSRGYYLEMLITGPQKQIIVDTGSSNPAVAG 120
 DB 61 ALALEPALASPAGANFLAMVNDLQDSRGYYLEMLITGPQKQIIVDTGSSNPAVAG 120
 QY 121 TPHSYIDYFDFERSSTYSKGFDTVVKYTGQSWTGFVGEDVLTIPKGFNTFLVNIAT 180
 DB 121 TPHSYIDYFDFERSSTYSKGFDTVVKYTGQSWTGFVGEDVLTIPKGFNTFLVNIAT 180
 QY 181 FESSENFLLPGIKWNGILGLAVATLAKPSSSLETFPDSLVTQANIPNVFSMOCGAGLPVA 240
 DB 181 FESSENFLLPGIKWNGILGLAVATLAKPSSSLETFPDSLVTQANIPNVFSMOCGAGLPVA 240
 QY 241 GSGTNGGSLVLCGIEPSLYKGDWTPPIKEENYQIETLKLGGGSLNDCREYNADKA 300
 DB 241 GSGTNGGSLVLCGIEPSLYKGDWTPPIKEENYQIETLKLGGGSLNDCREYNADKA 300

QY 301 IVDSGITLLRLPQKVFDAVEAVARASGLIPEFSDGFWTGSQACWINSFPMWYFKISI 360
 DB 301 IVDSGITLLRLPQKVFDAVEAVARASGLIPEFSDGFWTGSQACWINSFPMWYFKISI 360
 QY 361 YLRDENSRSFRITITLPOLYIOPMAGLWVECYRFGISPTNALVYGATWEGFYIFD 420
 DB 361 YLRDENSRSFRITITLPOLYIOPMAGLWVECYRFGISPTNALVYGATWEGFYIFD 420
 QY 421 RAQRVGFAPASPCAEIAGAASEISGPFSTEDVANSNCVPAQSISEPTLMTVSYALMSVCG 480
 DB 421 RAQRVGFAPASPCAEIAGAASEISGPFSTEDVANSNCVPAQSISEPTLMTVSYALMSVCG 480
 QY 481 AILLVLIVLLLPFCQRRPDPPEVNVDESGLVHRMK 518
 DB 481 AILLVLIVLLLPFCQRRPDPPEVNVDESGLVHRMK 518
 RESULT 12
 ID AAU07201 standard; Protein; 518 AA.
 XX
 AC AAU07201;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Human aspartyl protease 1 (Asp-1).
 XX
 KW Human; aspartyl protease 1; Asp-1; neurotropic; neuroprotective;
 KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;
 KW beta-secretase; Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 PN WC000149097-A2.
 XX
 PD 12-JUL-2001.
 XX
 PF 09-MAY-2001; 2001WO-IB00797.
 XX
 PR 09-MAY-2001; 2001WO-IB00797.
 XX
 PA (BIEN/) BIENKOWSKI M J.
 PA (GURN/) GURNEY M E.
 PA (HEIN/) HEINRIKSON R L.
 PA (PARO/) PARODI L A.
 PA (YANR/) YAN R.
 XX
 PI Bienkowski MJ, Gurney ME, Heinrichson RL, Parodi LA, Yan R;
 XX
 DR WPI: 2001-502548/55.
 DR N-PSDB; AAS11701.
 DR
 XX
 PT Novel purified polypeptide comprising fragment of mammalian aspartyl
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
 PT activity -
 XX
 PS Example 2; Fig 1; 185bp; English.
 XX
 CC The invention relates to a novel purified polypeptide comprising a
 CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
 CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
 CC and the fragment retain the beta-secretase activity of the mammalian Asp2
 CC protein. Also included is an isotorm of amyloid protein precursor (APP)
 CC comprising the amino acid sequence of a APP or its fragment containing
 CC an APP cleavage site recognizable by a mammalian beta-secretase, and
 CC further comprising two lysine residues at the carboxyl terminus of the
 CC amino acid sequence of the mammalian APP or APP fragment. The
 CC polypeptides are used for assaying for modulators of beta-secretase
 CC activity, identifying agents that inhibit the APP processing activity
 CC of human Asp2 aspartyl protease (Hu-Asp2); identifying agents that
 CC modulate the activity of Asp2; and for reducing cellular production of

CC amyloid beta (Abeta) from APP. Agents identified by the above methods
 CC are useful for treating Alzheimer's disease; and for identifying
 CC modulators of amyloid-beta (Abeta) peptide production, for use in
 CC designing therapeutics for the treatment or prevention of Alzheimer's
 CC disease. Probes and primers derived from Asp nucleic acid sequences
 CC are useful for detecting Hu-Asp nucleic acids in *in vitro* assays and in
 CC Northern and Southern blots. The present sequence represents the
 CC amino acid sequence of human Asp-1.
 XX
 SQ Sequence 518 AA;
 Query Match 100.0%; Score 518; DB 22; Length 518;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGALRALLLPLLAQWLRLAARAPETLPLRVAAATNRVAPTPGPGPAERHADGL 60
 DB 1 MGALRALLLPLLAQWLRLAARAPETLPLRVAAATNRVAPTPGPGPAERHADGL 60
 QY 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLEMLIGTPPKQLILVDTGSSNFAVAG 120
 DB 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLEMLIGTPPKQLILVDTGSSNFAVAG 120
 QY 121 TPHSYIDTYFDTERSSSTRSGKGFDTVTKYQSGWTGFGEDLVITIPKGFNTSFLVNIATI 180
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 QY 241 GSGTNGSLVLGIEPLSYKGDWYTPPIKEWYQIEILKLEIGGOSLNDCREYNADKA 300
 DB 241 GSGTNGSLVLGIEPLSYKGDWYTPPIKEWYQIEILKLEIGGOSLNDCREYNADKA 300
 QY 301 IVDGTTILRLPQKVFDAVVEAVARASLIPEPSDGFMTGSQLACTNSETPWSYFPKISI 360
 DB 301 IVDGTTILRLPQKVFDAVVEAVARASLIPEPSDGFMTGSQLACTNSETPWSYFPKISI 360
 QY 361 YLRDENSRSRRTITLPOLYTIOPMMGAGLNVCYRFGISPSNTNALVIGATMEGFFYFD 420
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 QY 421 RAQKRVGFASPCAEIAGAASEISGPSTEDVASNCVPAOSLSEPIIMIVSYALMSVCG 480
 DB 421 RAQKRVGFASPCAEIAGAASEISGPSTEDVASNCVPAOSLSEPIIMIVSYALMSVCG 480
 QY 481 AILLVLYLVLPPRCQRRPRDPEVNDSESLVRRHWK 518
 DB 481 AILLVLYLVLPPRCQRRPRDPEVNDSESLVRRHWK 518
 RESULT 13
 AAE02580
 ID AAE02580 standard; Protein; 518 AA.
 XX
 AC AAE02580;
 XX
 DT 10-AUG-2001 (first entry)
 XX
 DE Human aspartyl protease 1 (Asp 1).
 XX
 KW Human; alpha-secretase; amyloid precursor protein; APP; therapy;
 KW Alzheimer's disease; antialzheimer's; aspartyl protease 1; Asp 1;
 KW beta-secretase; chromosome 21.
 XX
 OS Homo sapiens.
 XX
 FH Key location/Qualifiers
 FT Peptide 1..20
 FT /label= Signal_peptide
 FT Peptide 22..62
 FT /label= Asp_1_prepropeptide

FT Peptide 23..62
 FT /label= Asp_1_propeptide
 FT Protein 63..518
 FT /label= Mature human Asp 1 protein
 FT /note= "Specifically claimed"
 FT Active-site 87..89
 FT /label= Active_site_1
 FT Active-site 110..113
 FT /label= Active_site_2
 FT Active-site 303..305
 FT /label= Active_site_3
 FT Domain 469..492
 FT /label= Transmembrane_domain
 FT Domain 493..518
 FT /label= Cytoplasmic_domain
 FT Region 497..518
 FT /note= "Peptide #1"
 XX
 PN WO200123533-A2.
 XX
 PD 05-APR-2001.
 XX
 PF 22-SEP-2000; 2000MO-US26080.
 XX
 PR 23-SEP-1999; 99US-015493.
 PR 23-SEP-1999; 99MO-US20881.
 PR 13-OCT-1999; 99US-0416901.
 PR 06-DEC-1999; 99US-0169232.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Gurney M, Bienkowski MJ;
 XX
 DR WPI: 2001-290516/30.
 DR N-PSDB; AAD06738.
 XX
 PT Enzymes that cleave the alpha-secretase site of the amyloid precursor
 PT protein, useful for the treatment of Alzheimer's disease -
 PS Claim 29; Fig 1; 189pp; English.
 XX
 CC The present invention relates to enzymes for cleaving the alpha-
 CC secretase site of the amyloid precursor protein (APP) and methods of
 CC identifying those enzymes. The methods may be used to identify enzymes
 CC that may be used to cleave the alpha-secretase cleavage site of the APP
 CC protein. The enzymes may be used to treat or modulate the progress of
 CC Alzheimer's disease. The present sequence is human aspartyl protease 1
 CC (Asp 1). Asp 1 has alpha-secretase protease and beta-secretase
 CC protease activities. Asp 1 gene is located on chromosome 21.
 XX
 SQ Sequence 518 AA;
 Query Match 100.0%; Score 518; DB 22; Length 518;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGALRALLLPLLAQWLRLAARAPETLPLRVAAATNRVAPTPGPGPAERHADGL 60
 DB 1 MGALRALLLPLLAQWLRLAARAPETLPLRVAAATNRVAPTPGPGPAERHADGL 60
 QY 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLEMLIGTPPKQLILVDTGSSNFAVAG 120
 DB 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLEMLIGTPPKQLILVDTGSSNFAVAG 120
 QY 121 TPHSYIDTYFDTERSSSTRSGKGFDTVTKYQSGWTGFGEDLVITIPKGFNTSFLVNIATI 180
 DB 121 TPHSYIDTYFDTERSSSTRSGKGFDTVTKYQSGWTGFGEDLVITIPKGFNTSFLVNIATI 180
 QY 181 FESSENFPLPGIKKNGIILGLAVATLAKPSSSLETFPDSLVTQANI PNVSQMCGAGLPVA 240
 DB 181 FESSENFPLPGIKKNGIILGLAVATLAKPSSSLETFPDSLVTQANI PNVSQMCGAGLPVA 240
 QY 241 GSGTNGSLVLGIEPLSYKGDWYTPPIKEWYQIEILKLEIGGOSLNDCREYNADKA 300

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Db 301 IVDGTTLLRLPQKVPDAVVEAVARASLIPEFSDGFWTGSQIACWTNSETPMSTYFPKISI 360
Qy 361 YLRDENSRSRFRITLLPOLYIOPMAGLANECYRFGISPSSTNALVIGATWEGFYIFD 420
Db 361 YLRDENSRSRFRITLLPOLYIOPMAGLANECYRFGISPSSTNALVIGATWEGFYIFD 420
Qy 421 RAQKRVGFAPSPCAEIAAGAAVSEISGPFSTEDVASCNCPAQSLSEPIIMIVSYALMSVCG 480
Db 421 RAQKRVGFAPSPCAEIAAGAAVSEISGPFSTEDVASCNCPAQSLSEPIIMIVSYALMSVCG 480
Qy 481 ALLVLIIVLLLPFCORRRPDPPEVNDSSLVHRMK 518
Db 481 ALLVLIIVLLLPFCORRRPDPPEVNDSSLVHRMK 518

RESULT 14
ID AAE02608 standard; Protein; 518 AA.
AC AAE02608;
XX
XX 10-AUG-2001 (first entry)
DE Human Aspartyl protease-1 (Asp-1) deltatm (His)6 protein.
XX
KM Human; alpha-secretase; amyloid precursor protein; APP; therapy;
KM Alzheimer's disease; antialzheimer's; aspartyl protease 1; Asp1;
KM beta-secretase; Asp-1 deltatm (His)6 protein.
XX
OS Homo sapiens.
XX Synthetic.
XX MO200123533-A2.
XX
XX 05-APR-2001.
PF 22-SEP-2000; 2000WO-US26080.
XX
PR 23-SEP-1999; 99US-0155493.
PR 23-SEP-1999; 99WO-US20881.
PR 13-OCT-1999; 98US-0416901.
PR 06-DEC-1999; 99US-0169232.
XX
XX (PHAA ) PHARMACIA & UPJOHN CO.
XX
XX Gurney M, Bienkowski MJ;
XX WPI; 2001-290516/30.
XX
XX Enzymes that cleave the alpha-secretase site of the amyloid precursor
XX protein, useful for the treatment of Alzheimer's disease -
XX
XX Example 14; Page 183-184; 189pp; English.
XX
CC The present invention relates to enzymes for cleaving the alpha-
CC secretase site of the amyloid precursor protein (APP) and methods of
CC identifying those enzymes. The method may be used to identify enzymes
CC that may be used to cleave the alpha-secretase cleavage site of the APP
CC protein. The enzymes may be used to treat or modulate the progress of
CC Alzheimer's disease. The present sequence is human Aspartyl protease-1
CC (Asp-1) deltatm (His)6 protein which is used for the expression of
CC pre-pro-human-Aspartyl protease 1 (Asp1). This protein is obtained by
CC replacing C-terminal transmembrane and cytoplasmic domains with a
CC hexahistidine purification tag in the human Aspartyl protease 1.
XX
XX Sequence 518 AA;
SQ

```

Query Match

100.0%; Score 518; DB 22; Length 518;

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 ALALEPALASPAGANFLAMVDNLQSGRGYILEMLIGTPQQLVDTGSSNPAVAG 120
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Db 121 TPHSYIDTTPDTESSSTYRSKGFVYKYTGQSGMTGSGEDLVITPKGFNTSFLVNIATI 180
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Db 361 YLRDENSRSRFRITLLPOLYIOPMAGLANECYRFGISPSSTNALVIGATWEGFYIFD 420
Qy 421 RAQKRVGFAPSPCAEIAAGAAVSEISGPFSTEDVASCNCPAQSLSEPIIMIVSYALMSVCG 480
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Qy 481 ALLVLIIVLLLPFCORRRPDPPEVNDSSLVHRMK 518
Db 481 ALLVLIIVLLLPFCORRRPDPPEVNDSSLVHRMK 518

RESULT 15
ID ABB78589 standard; Protein; 518 AA.
AC ABB78589;
XX
XX 16-JUL-2002 (first entry)
DE Human Asp-1 protein sequence SEQ ID NO:2.
XX
KM Human; Asp-1; Asp-2; aspartyl protease; enzyme; Alzheimer's disease;
KM proteolytic; chromosome 21.
XX
XX Homo sapiens.
XX
XX GB2367060-A.
XX
XX 27-MAR-2002.
XX
XX 29-OCT-2001; 2001GB-0025934.
XX
PR 23-SEP-1999; 99US-155493P.
PR 23-SEP-1999; 99US-0404133.
PR 23-SEP-1999; 99WO-US20881.
PR 13-OCT-1999; 99US-0416901.
PR 06-DEC-1999; 99US-169232P.
PR 22-SEP-2000; 2000GB-0023315.
XX
XX (PHAA ) PHARMACIA & UPJOHN CO.
XX
XX Bienkowski MJ, Gurney M;
XX WPI; 2002-396337/43.
XX

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DR N-PSDB; ABL52456.

XX Human aspartyl protease 1 substrates useful in assays to detect
PT aspartyl protease activity, e.g. for the diagnosis of Alzheimer's
PT disease -
XX
XX
PS Claim 7; Fig 1; 182pp; English.

XX
CC The present invention describes a human aspartyl protease 1 (hu-Asp1)
CC substrate (I) which comprises a peptide of no more than 50 amino acids,
CC and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
CC Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1
CC proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with
CC (I) under acidic conditions; and (b) determining the level of hu-Asp1
CC proteolytic activity; (2) a purified polynucleotide (III) comprising a
CC nucleotide sequence that hybridises under stringent conditions to the
CC non-coding strand complementary to a defined 1804 nucleotide sequence
CC (see ABL52456) where the nucleotide sequence encodes a polypeptide having
CC Asp1 proteolytic activity and lacks nucleotides encoding a transmembrane
CC domain; (3) a purified polynucleotide (III') comprising a sequence that
CC hybridises under stringent conditions to (III) (the nucleotide sequence
CC encodes a polypeptide further lacking a pro-peptide domain corresponding
CC to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV)
CC comprising (III) or (III') and (5) a host cell (V) transformed or
CC transfected with (III), (III') and/or (IV). The hu-Asp1 protease
CC substrate (I) may be used as an enzyme substrate in assays to detect
CC aspartyl protease activity, (II) and therefore diagnose diseases
CC associated with aberrant hu-Asp1 expression and activity such as
CC Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while
CC hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
CC sequence represents hu-Asp1 from the present invention.
XX
SQ Sequence 518 AA;

Query Match 100.0%; Score 518; DB 23; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MGALABALLLPLQMLRAAPLAPFTLLRVAATNRVAPTPGPTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLEMLIGTPPKQLIIVDTGSSNFAVAG 120
DB 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLEMLIGTPPKQLIIVDTGSSNFAVAG 120
QY 121 TPHSVYIDYPTERTSSTRSGFDVTYKYGSGTGFVGEDLVITPKGFNTSFLVNIATI 180
DB 121 TPHSVYIDYPTERTSSTRSGFDVTYKYGSGTGFVGEDLVITPKGFNTSFLVNIATI 180
QY 181 FESENFPLPGIKMNGILGLAYATLAKPSSLETFFDSLVTQANIPIVFSMOMCGALPVA 240
DB 181 FESENFPLPGIKMNGILGLAYATLAKPSSLETFFDSLVTQANIPIVFSMOMCGALPVA 240
QY 241 GSGTNGGSLVIGLIEPSLYKGDWYTPIKEWYQIEILKLEIGQSLNLDCREYNADKA 300
DB 241 GSGTNGGSLVIGLIEPSLYKGDWYTPIKEWYQIEILKLEIGQSLNLDCREYNADKA 300
QY 301 IVDGGTTLRLPQKVFDAVVAARASLIPERSDGFMTGSOLACWTNSETPWSYFPKISI 360
DB 301 IVDGGTTLRLPQKVFDAVVAARASLIPERSDGFMTGSOLACWTNSETPWSYFPKISI 360
QY 361 YLRDENSRSFRITLIPOLYIOPMMGAGLANECYRFGISPTNALVIGATWMEGFYVFD 420
DB 361 YLRDENSRSFRITLIPOLYIOPMMGAGLANECYRFGISPTNALVIGATWMEGFYVFD 420
QY 421 RAQRVGFPAASPCAEIAAGAAVSEISGPSTEDVANSVCVPAQSLSEPIIMIVSYALMSYCG 480
DB 421 RAQRVGFPAASPCAEIAAGAAVSEISGPSTEDVANSVCVPAQSLSEPIIMIVSYALMSYCG 480
QY 481 AILLVLLVLLLPFCORRRPRDPEVNDSSIVRRMK 518
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OM protein - protein search, using sw model

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Title: US-09-668-314C-2

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SUMMARIES

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6	59	11.4	514	4	US-09-912-484-2
7	22	4.2	25	4	US-09-548-372D-33
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9	12	2.3	425	4	US-09-548-372D-28
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13	12	2.3	433	4	US-09-548-372D-26
14	12	2.3	433	4	US-09-548-367D-26
15	12	2.3	434	4	US-09-548-372D-53
16	12	2.3	434	4	US-09-548-367D-53
17	12	2.3	446	4	US-09-548-372D-22
18	12	2.3	446	4	US-09-548-367D-22
19	12	2.3	453	4	US-09-548-372D-30
20	12	2.3	453	4	US-09-548-367D-30
21	12	2.3	459	4	US-09-548-372D-24
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23	12	2.3	459	4	US-09-548-367D-24
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26	12	2.3	476	4	US-09-548-372D-73
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31	12	2.3	501	4	US-09-548-372D-4	Sequence 4, Appl
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93	7	1.4	160	4	US-08-468-570-74	Sequence 74, Appl
94	7	1.4	160	4	US-08-468-570-76	Sequence 76, Appl
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102	7	1.4	192	5	PCT-US95-10398-76	Sequence 76, Appl	175	6	1.2	25	3	US-09-023-339-5	Sequence 5, Appl
103	7	1.4	234	1	US-08-298-557-5	Sequence 5, Appl	176	6	1.2	25	3	US-09-375-419-34	Sequence 34, Appl
104	7	1.4	238	1	US-08-240-124-2	Sequence 2, Appl	177	6	1.2	27	1	US-07-668-648-12	Sequence 12, Appl
105	7	1.4	238	1	US-08-453-943-2	Sequence 2, Appl	178	6	1.2	27	1	US-08-429-998-12	Sequence 12, Appl
106	7	1.4	238	1	US-09-057-121-2	Sequence 2, Appl	179	6	1.2	27	2	US-08-431-333-12	Sequence 12, Appl
107	7	1.4	238	4	US-09-358-734-2	Sequence 29, Appl	180	6	1.2	27	4	US-08-789-333F-35	Sequence 35, Appl
108	7	1.4	268	4	US-09-651-656-29	Sequence 29, Appl	181	6	1.2	27	4	US-09-169-015-45	Sequence 45, Appl
109	7	1.4	279	4	US-09-650-855-29	Sequence 29, Appl	182	6	1.2	27	4	US-09-133-944-34	Sequence 34, Appl
110	7	1.4	279	1	US-08-325-286-8	Sequence 8, Appl	183	6	1.2	27	4	US-09-208-827-37	Sequence 37, Appl
111	7	1.4	306	1	US-08-454-196-11	Sequence 11, Appl	184	6	1.2	27	4	US-08-787-738B-35	Sequence 35, Appl
112	7	1.4	306	2	US-08-286-819A-33	Sequence 33, Appl	185	6	1.2	27	4	US-09-157-748-35	Sequence 35, Appl
113	7	1.4	306	3	US-08-980-357-33	Sequence 33, Appl	186	6	1.2	27	5	PCT-US91-02321-12	Sequence 12, Appl
114	7	1.4	306	3	US-09-064-033-11	Sequence 11, Appl	187	6	1.2	29	1	US-07-746-705A-2	Sequence 1, Appl
115	7	1.4	320	1	US-08-362-739-2	Sequence 2, Appl	188	6	1.2	29	2	US-08-380-182-1	Sequence 8, Appl
116	7	1.4	330	4	US-09-187-710-2	Sequence 2, Appl	189	6	1.2	32	1	US-08-085-122-8	Sequence 8, Appl
117	7	1.4	354	1	US-08-222-289-2	Sequence 2, Appl	190	6	1.2	32	2	US-08-319-052-18	Sequence 18, Appl
118	7	1.4	354	2	US-08-646-590B-36	Sequence 36, Appl	191	6	1.2	32	4	US-08-442-108B-18	Sequence 18, Appl
119	7	1.4	363	4	US-09-412-184-36	Sequence 36, Appl	192	6	1.2	32	5	PCT-US95-15696-3	Sequence 3, Appl
120	7	1.4	397	3	US-09-079-415-2	Sequence 3, Appl	193	6	1.2	36	4	US-08-789-333F-22	Sequence 22, Appl
121	7	1.4	409	1	US-09-640-305-6	Sequence 6, Appl	194	6	1.2	36	4	US-09-169-015-32	Sequence 32, Appl
122	7	1.4	409	1	US-08-360-673-6	Sequence 6, Appl	195	6	1.2	36	4	US-09-133-944-21	Sequence 21, Appl
123	7	1.4	410	1	US-08-088-633-2	Sequence 2, Appl	196	6	1.2	36	4	US-09-208-827-23	Sequence 23, Appl
124	7	1.4	410	1	US-08-245-756-2	Sequence 2, Appl	197	6	1.2	36	4	US-08-787-738B-22	Sequence 22, Appl
125	7	1.4	410	1	US-08-441-750-2	Sequence 2, Appl	198	6	1.2	36	4	US-09-157-748-24	Sequence 24, Appl
126	7	1.4	410	5	PCT-US92-02521-2	Sequence 2, Appl	199	6	1.2	38	2	US-08-622-753A-2	Sequence 2, Appl
127	7	1.4	453	1	US-07-937-609-27	Sequence 27, Appl	200	6	1.2	38	2	US-08-622-753A-6	Sequence 6, Appl
128	7	1.4	453	1	US-07-978-892A-5	Sequence 5, Appl	201	6	1.2	38	2	US-08-622-753A-8	Sequence 8, Appl
129	7	1.4	453	1	US-08-570-157-4	Sequence 4, Appl	202	6	1.2	38	2	US-08-622-753A-19	Sequence 19, Appl
130	7	1.4	453	4	US-08-029-170-27	Sequence 27, Appl	203	6	1.2	40	2	US-08-727-68B-19	Sequence 19, Appl
131	7	1.4	453	4	US-09-076-510-4	Sequence 4, Appl	204	6	1.2	41	2	US-08-640-847C-39	Sequence 39, Appl
132	7	1.4	453	4	US-08-674-168-29	Sequence 29, Appl	205	6	1.2	42	4	US-09-227-357-221	Sequence 221, App
133	7	1.4	550	1	US-08-985-908-19	Sequence 19, Appl	206	6	1.2	43	4	US-09-149-476-524	Sequence 524, App
134	7	1.4	550	3	US-08-852-730-4	Sequence 4, Appl	207	6	1.2	47	2	US-08-142-551B-127	Sequence 127, App
135	7	1.4	550	3	US-08-985-916-11	Sequence 5, Appl	208	6	1.2	47	4	US-08-977-378-13	Sequence 13, Appl
136	7	1.4	589	2	US-08-756-317-5	Sequence 5, Appl	209	6	1.2	47	4	US-09-453-322B-11	Sequence 11, Appl
137	7	1.4	601	2	US-08-756-317-15	Sequence 15, Appl	210	6	1.2	48	2	US-08-758-307B-2	Sequence 2, Appl
138	7	1.4	604	1	US-08-064-271-10	Sequence 10, Appl	211	6	1.2	50	4	US-08-861-572-1	Sequence 1, Appl
139	7	1.4	604	1	US-08-487-753-4	Sequence 4, Appl	212	6	1.2	50	4	US-09-586-562C-8	Sequence 8, Appl
140	7	1.4	604	1	US-08-487-753-5	Sequence 5, Appl	213	6	1.2	50	4	US-09-586-562C-8	Sequence 8, Appl
141	7	1.4	604	2	US-08-480-065-4	Sequence 4, Appl	214	6	1.2	51	4	US-08-927-219-49	Sequence 49, Appl
142	7	1.4	604	2	US-08-480-065-5	Sequence 5, Appl	215	6	1.2	55	1	US-08-209-947-10	Sequence 10, Appl
143	7	1.4	604	3	US-08-487-744-4	Sequence 4, Appl	216	6	1.2	55	1	US-08-458-298-10	Sequence 10, Appl
144	7	1.4	604	3	US-08-487-744-5	Sequence 5, Appl	217	6	1.2	59	1	US-08-313-050-16	Sequence 16, Appl
145	7	1.4	604	3	US-08-487-744-5	Sequence 5, Appl	218	6	1.2	60	1	US-08-117-083-20	Sequence 20, Appl
146	7	1.4	604	3	US-08-930-589A-18	Sequence 18, Appl	219	6	1.2	68	4	US-09-220-528-50	Sequence 50, Appl
147	7	1.4	604	4	US-09-599-781-18	Sequence 18, Appl	220	6	1.2	73	2	US-08-530-569B-5	Sequence 5, Appl
148	7	1.4	604	5	PCT-US93-09167-4	Sequence 4, Appl	221	6	1.2	75	3	US-09-042-012-8	Sequence 8, Appl
149	7	1.4	604	5	PCT-US93-09167-5	Sequence 5, Appl	222	6	1.2	75	4	US-09-305-086-2	Sequence 2, Appl
150	7	1.4	638	4	US-09-376-781-6	Sequence 6, Appl	223	6	1.2	75	4	US-08-817-811-97	Sequence 97, Appl
151	7	1.4	654	3	US-08-560-005-10	Sequence 10, Appl	224	6	1.2	75	4	US-09-457-324-8	Sequence 8, Appl
152	7	1.4	654	4	US-09-418-540-10	Sequence 10, Appl	225	6	1.2	76	4	US-08-817-811-21	Sequence 21, Appl
153	7	1.4	668	4	US-09-436-605-2	Sequence 2, Appl	226	6	1.2	78	4	US-08-817-811-20	Sequence 20, Appl
154	7	1.4	802	1	US-08-261-465-2	Sequence 2, Appl	227	6	1.2	78	4	US-08-817-811-96	Sequence 96, Appl
155	7	1.4	802	2	US-08-326-286-4	Sequence 6, Appl	228	6	1.2	79	4	US-08-817-811-19	Sequence 19, Appl
156	7	1.4	802	2	US-08-326-286-4	Sequence 4, Appl	229	6	1.2	79	4	US-08-817-811-95	Sequence 95, Appl
157	7	1.4	993	4	US-09-060-410-4	Sequence 4, Appl	230	6	1.2	87	4	US-09-220-528-115	Sequence 115, App
158	7	1.4	994	4	US-08-542-635-2	Sequence 2, Appl	231	6	1.2	91	4	US-08-591-498-3	Sequence 3, Appl
159	7	1.4	2584	3	US-08-936-135-4	Sequence 4, Appl	232	6	1.2	107	4	US-09-220-528-52	Sequence 52, Appl
160	7	1.4	2588	3	US-08-936-135-2	Sequence 2, Appl	233	6	1.2	108	4	US-09-149-476-552	Sequence 552, App
161	7	1.4	3218	1	US-08-764-100-27	Sequence 27, Appl	234	6	1.2	110	3	US-08-950-720A-11	Sequence 11, Appl
162	6	1.2	12	4	US-08-679-493A-109	Sequence 109, App	235	6	1.2	110	3	US-08-589-028-2	Sequence 2, Appl
163	6	1.2	12	4	US-08-469-260A-446	Sequence 446, App	236	6	1.2	110	3	US-08-589-028-4	Sequence 4, Appl
164	6	1.2	14	4	US-09-369-364A-28	Sequence 28, App	237	6	1.2	110	3	US-08-784-582-2	Sequence 2, Appl
165	6	1.2	19	4	US-09-369-364A-24	Sequence 24, Appl	238	6	1.2	110	3	US-08-784-582-2	Sequence 2, Appl
166	6	1.2	21	1	US-08-672-571A-9	Sequence 9, Appl	239	6	1.2	110	3	US-08-785-271-2	Sequence 2, Appl
167	6	1.2	21	3	US-08-753-007A-24	Sequence 24, Appl	240	6	1.2	110	5	PCT-US95-08596-2	Sequence 2, Appl
168	6	1.2	21	4	US-09-398-496-24	Sequence 24, Appl	241	6	1.2	111	4	US-09-227-357-235	Sequence 235, App
169	6	1.2	22	2	US-08-902-515-6	Sequence 6, Appl	242	6	1.2	111	4	US-08-052-472B-11	Sequence 11, Appl
170	6	1.2	22	4	US-08-977-378-22	Sequence 22, Appl	243	6	1.2	113	1	US-09-127-946-2	Sequence 1, Appl
171	6	1.2	24	2	US-08-480-190-249	Sequence 249, App	244	6	1.2	113	4	US-09-097-889-20	Sequence 20, Appl
172	6	1.2	24	2	US-08-488-379-249	Sequence 249, App	245	6	1.2	115	4	US-08-434-705B-6	Sequence 6, Appl
173	6	1.2	24	5	PCT-US93-07545-249	Sequence 249, App	246	6	1.2	116	1		

247	6	1.2	116	2	US-09-086-201-6	Sequence 6, Appli	320	6	1.2	225	4	US-09-040-483-1	Sequence 1, Appli
248	6	1.2	117	5	PCT-US96-08730-11	Sequence 11, Appl	321	6	1.2	225	4	US-08-821-994-49	Sequence 49, Appl
249	6	1.2	122	4	US-09-071-035-170	Sequence 170, App	322	6	1.2	225	4	US-09-370-861A-3	Sequence 3, Appl
250	6	1.2	124	4	US-08-981-189B-15	Sequence 15, Appl	323	6	1.2	225	4	US-08-832-488-2	Sequence 2, Appl
251	6	1.2	125	1	US-07-624-742-3	Sequence 3, Appli	324	6	1.2	226	2	US-08-572-447C-15	Sequence 15, Appl
252	6	1.2	125	2	US-08-468-819-2	Sequence 2, Appli	325	6	1.2	226	2	US-09-267-747-15	Sequence 15, Appl
253	6	1.2	126	3	US-08-513-974B-28	Sequence 28, Appl	326	6	1.2	226	6	5498600-2	Patent No. 5498600
254	6	1.2	126	3	US-08-776-971-23	Sequence 23, Appl	327	6	1.2	220	2	US-08-637-759B-457	Sequence 457, App
255	6	1.2	129	1	US-08-434-705B-4	Sequence 4, Appli	328	6	1.2	220	3	US-08-871-155A-457	Sequence 457, App
256	6	1.2	129	2	US-09-086-201-4	Sequence 4, Appli	329	6	1.2	220	4	US-08-821-994-50	Sequence 50, Appl
257	6	1.2	131	2	US-08-647-960-9	Sequence 9, Appli	330	6	1.2	230	4	US-08-818-112-65	Sequence 65, Appl
258	6	1.2	136	4	US-08-905-223-287	Sequence 287, App	331	6	1.2	220	4	US-08-818-111-65	Sequence 65, Appl
259	6	1.2	144	3	US-08-513-974B-366	Sequence 366, App	332	6	1.2	220	4	US-09-201-945-457	Sequence 457, App
260	6	1.2	144	3	US-08-513-974B-369	Sequence 369, App	333	6	1.2	220	4	US-09-056-556-65	Sequence 65, Appl
261	6	1.2	144	3	US-08-776-971-106	Sequence 106, App	334	6	1.2	230	4	US-09-072-596-66	Sequence 66, Appl
262	6	1.2	144	4	US-08-776-971-109	Sequence 109, App	335	6	1.2	233	4	US-09-214-631-7	Sequence 7, Appli
263	6	1.2	156	4	US-09-064-922-2	Sequence 2, Appli	336	6	1.2	235	1	US-07-940-605A-12	Sequence 12, Appl
264	6	1.2	156	4	US-09-134-001C-5172	Sequence 5172, Ap	337	6	1.2	225	2	US-08-690-096-12	Sequence 12, Appl
265	6	1.2	157	4	US-09-149-476-50	Sequence 350, App	338	6	1.2	237	4	US-09-220-528-32	Sequence 32, Appl
266	6	1.2	164	4	US-08-858-207A-502	Sequence 502, App	339	6	1.2	237	4	US-09-227-357-154	Sequence 154, App
267	6	1.2	169	1	US-08-233-788A-53	Sequence 53, Appl	340	6	1.2	238	4	US-09-149-476-485	Sequence 485, App
268	6	1.2	171	4	US-09-134-001C-5205	Sequence 5205, Ap	341	6	1.2	241	4	US-08-634-475-7	Sequence 7, Appli
269	6	1.2	173	1	US-08-157-005-8	Sequence 8, Appli	342	6	1.2	241	4	US-09-709-791-7	Sequence 7, Appli
270	6	1.2	173	1	US-08-062-472B-6	Sequence 6, Appli	343	6	1.2	241	4	US-09-153-599A-5	Sequence 5, Appli
271	6	1.2	173	2	US-08-799-464A-24	Sequence 24, Appl	344	6	1.2	241	6	5175255-2	Patent No. 5175255
272	6	1.2	173	4	US-08-747-863-8	Sequence 8, Appli	345	6	1.2	243	1	5175255-8	Patent No. 5175255
273	6	1.2	173	4	US-09-565-864-8	Sequence 8, Appli	346	6	1.2	243	1	US-08-021-608D-6	Sequence 6, Appli
274	6	1.2	173	5	PCT-US95-09927-24	Sequence 24, Appl	347	6	1.2	243	1	US-08-726-160-6	Sequence 6, Appli
275	6	1.2	173	5	PCT-US95-09927-24	Sequence 24, Appl	348	6	1.2	243	5	PCT-US94-01780-6	Sequence 6, Appli
276	6	1.2	174	1	US-08-131-625B-14	Sequence 14, Appl	349	6	1.2	243	1	US-08-910-973-22	Sequence 22, Appl
277	6	1.2	174	2	US-08-799-464A-11	Sequence 11, Appl	350	6	1.2	244	3	US-09-003-287-6	Sequence 6, Appli
278	6	1.2	174	2	US-09-113-750A-41	Sequence 41, Appl	351	6	1.2	244	3	US-09-003-287-8	Sequence 8, Appli
279	6	1.2	174	5	PCT-US95-09927-11	Sequence 11, Appl	352	6	1.2	244	4	US-09-518-988-2	Sequence 2, Appli
280	6	1.2	174	5	PCT-US95-10904-17	Sequence 17, Appl	353	6	1.2	244	4	US-09-499-927-22	Sequence 22, Appl
281	6	1.2	174	5	PCT-US95-10904-43	Sequence 43, Appl	354	6	1.2	246	4	US-08-634-475-3	Sequence 3, Appli
282	6	1.2	174	5	PCT-US95-10904-45	Sequence 45, Appl	355	6	1.2	246	4	US-09-709-791-3	Sequence 3, Appli
283	6	1.2	174	5	PCT-US95-10904-47	Sequence 47, Appl	356	6	1.2	247	1	US-08-324-977-44	Sequence 44, Appl
284	6	1.2	174	5	PCT-US95-10904-49	Sequence 49, Appl	357	6	1.2	247	2	US-08-384-616-44	Sequence 44, Appl
285	6	1.2	174	5	PCT-US95-10904-51	Sequence 51, Appl	358	6	1.2	247	2	US-08-904-686A-44	Sequence 44, Appl
286	6	1.2	175	4	US-08-887-534A-14	Sequence 14, Appl	359	6	1.2	247	4	US-09-315-850-44	Sequence 44, Appl
287	6	1.2	177	4	US-09-263-933-25	Sequence 25, Appl	360	6	1.2	247	4	US-09-724-864-49	Sequence 49, Appl
288	6	1.2	179	4	US-09-064-922-5	Sequence 5, Appli	361	6	1.2	249	4	US-09-318-191-34	Sequence 34, Appl
289	6	1.2	181	4	US-09-220-528-10	Sequence 40, Appl	362	6	1.2	249	4	US-09-318-191-34	Sequence 34, Appl
290	6	1.2	184	2	US-08-737-825-50	Sequence 10, Appl	363	6	1.2	254	4	US-09-134-001C-3536	Sequence 3536, Ap
291	6	1.2	184	3	US-08-741-411-7	Sequence 7, Appli	364	6	1.2	259	4	US-09-006-353A-2	Sequence 2, Appli
292	6	1.2	185	3	US-08-984-295-1	Sequence 1, Appli	365	6	1.2	259	4	US-09-632-947B-3	Sequence 3, Appli
293	6	1.2	186	4	US-09-149-476-394	Sequence 394, App	366	6	1.2	259	4	US-09-573-986-2	Sequence 2, Appli
294	6	1.2	188	3	US-08-855-531D-37	Sequence 37, Appl	367	6	1.2	261	4	US-08-163-919A-2	Sequence 2, Appli
295	6	1.2	188	4	US-08-855-526B-37	Sequence 37, Appl	368	6	1.2	261	5	PCT-US94-14073-2	Sequence 2, Appli
296	6	1.2	188	4	US-09-134-001C-3152	Sequence 3152, Ap	369	6	1.2	264	4	US-08-469-260A-76	Sequence 76, Appl
297	6	1.2	192	1	US-08-086-428B-64	Sequence 64, Appl	370	6	1.2	266	4	US-08-904-234-3	Sequence 3, Appli
298	6	1.2	192	2	US-08-468-570-64	Sequence 64, Appl	371	6	1.2	268	4	US-09-403-768-2	Sequence 2, Appli
299	6	1.2	192	2	US-08-290-665A-64	Sequence 64, Appl	372	6	1.2	270	2	US-08-773-368-1	Sequence 1, Appli
300	6	1.2	192	5	PCT-US95-10398-64	Sequence 64, Appl	373	6	1.2	270	3	US-09-199-887-1	Sequence 1, Appli
301	6	1.2	196	3	US-07-998-289B-4	Sequence 4, Appli	374	6	1.2	270	4	US-09-013-881-6	Sequence 6, Appli
302	6	1.2	205	1	US-08-321-162-2	Sequence 2, Appli	375	6	1.2	271	2	US-08-467-265-2	Sequence 2, Appli
303	6	1.2	205	1	US-08-448-736-1	Sequence 1, Appli	376	6	1.2	271	4	US-08-467-265-2	Sequence 2, Appli
304	6	1.2	205	1	US-08-441-216-2	Sequence 2, Appli	377	6	1.2	271	4	US-09-407-891-2	Sequence 2, Appli
305	6	1.2	205	1	US-08-452-779-1	Sequence 1, Appli	378	6	1.2	274	4	US-09-570-367C-19	Sequence 19, Appl
306	6	1.2	205	1	US-08-299-567-4	Sequence 4, Appli	379	6	1.2	276	4	US-09-041-886-27	Sequence 27, Appl
307	6	1.2	205	2	US-08-445-065-1	Sequence 1, Appli	380	6	1.2	277	4	US-09-042-785A-10	Sequence 10, Appl
308	6	1.2	205	3	US-08-445-065-12	Sequence 12, Appl	381	6	1.2	277	4	US-09-006-353A-10	Sequence 10, Appl
309	6	1.2	205	3	US-08-959-524-1	Sequence 1, Appli	382	6	1.2	277	4	US-08-114-944D-2	Sequence 2, Appli
310	6	1.2	205	3	US-08-959-524-12	Sequence 12, Appl	383	6	1.2	277	4	US-09-573-986-10	Sequence 10, Appl
311	6	1.2	205	4	US-09-214-631-10	Sequence 10, Appl	384	6	1.2	278	4	US-09-570-367C-2	Sequence 2, Appli
312	6	1.2	206	4	US-09-134-001C-5047	Sequence 5047, Ap	385	6	1.2	278	4	US-09-570-367C-21	Sequence 21, Appl
313	6	1.2	220	4	US-09-220-528-26	Sequence 26, Appl	386	6	1.2	281	2	US-08-822-701-9	Sequence 9, Appli
314	6	1.2	223	4	US-09-124-238A-34	Sequence 34, Appl	387	6	1.2	281	3	US-08-935-855-9	Sequence 9, Appli
315	6	1.2	223	4	US-09-721-975-34	Sequence 34, Appl	388	6	1.2	282	1	US-08-445-847A-1	Sequence 1, Appli
316	6	1.2	225	1	US-07-991-667B-3	Sequence 3, Appli	389	6	1.2	298	4	US-08-767-942B-25	Sequence 25, Appl
317	6	1.2	225	1	US-08-107-755A-3	Sequence 3, Appli	390	6	1.2	298	4	US-09-177-165A-23	Sequence 23, Appl
318	6	1.2	225	2	US-08-544-332-9	Sequence 3, Appli	391	6	1.2	299	4	US-09-153-927-3	Sequence 3, Appli
319	6	1.2	225	3	US-09-248-335-40	Sequence 40, Appl	392	6	1.2	299	4	US-09-134-618-4	Sequence 4, Appli

393	6	1.2	299	4	US-09-370-398-2	Sequence 2, Appli	466	6	1.2	361	2	US-09-128-369-3	Sequence 3, Appli
394	6	1.2	301	3	US-08-829-525-24	Sequence 24, Appl	467	6	1.2	362	4	US-09-542-733-2	Sequence 2, Appli
395	6	1.2	301	4	US-08-609-583A-24	Sequence 24, Appl	468	6	1.2	363	4	US-08-196-989B-4	Sequence 4, Appli
396	6	1.2	301	4	US-08-937-399-24	Sequence 24, Appl	469	6	1.2	363	2	US-08-760-936-4	Sequence 4, Appli
397	6	1.2	301	4	US-09-310-367-24	Sequence 24, Appl	470	6	1.2	364	4	US-09-045-583-2	Sequence 2, Appli
398	6	1.2	301	4	US-09-288-143-98	Sequence 98, Appl	471	6	1.2	364	4	US-09-534-183-2	Sequence 2, Appli
399	6	1.2	301	4	US-09-033-317-24	Sequence 24, Appl	472	6	1.2	367	4	US-09-457-302-1	Sequence 1, Appli
400	6	1.2	303	4	US-08-985-950-2	Sequence 2, Appli	473	6	1.2	368	3	US-08-445-640-12	Sequence 12, Appl
401	6	1.2	307	4	US-08-858-207A-481	Sequence 481, App	474	6	1.2	368	3	US-08-170-558-12	Sequence 12, Appl
402	6	1.2	314	4	US-09-134-001C-2983	Sequence 2983, Ap	475	6	1.2	368	3	US-08-447-314-12	Sequence 12, Appl
403	6	1.2	316	1	US-08-464-400-2	Sequence 2, Appli	476	6	1.2	368	3	US-08-445-461-12	Sequence 12, Appl
404	6	1.2	316	3	US-08-875-273A-2	Sequence 2, Appli	477	6	1.2	360	1	US-07-669-171-2	Sequence 2, Appli
405	6	1.2	316	4	US-09-123-386-2	Sequence 2, Appli	478	6	1.2	330	1	US-08-132-405-1	Sequence 1, Appli
406	6	1.2	316	5	PCT-US95-01827A-2	Sequence 2, Appli	479	6	1.2	330	1	US-08-395-939A-1	Sequence 1, Appli
407	6	1.2	317	2	US-08-864-799-4	Sequence 4, Appli	480	6	1.2	330	5	PCT-US91-01861-1	Sequence 1, Appli
408	6	1.2	317	2	US-08-864-799-5	Sequence 5, Appli	481	6	1.2	330	6	5168051-2	Patent No. 5168051
409	6	1.2	318	4	US-09-605-785-339	Sequence 339, App	482	6	1.2	334	4	US-09-385-028-8	Sequence 8, Appli
410	6	1.2	318	4	US-09-439-313-339	Sequence 339, App	483	6	1.2	334	5	PCT-US94-03705-5	Sequence 5, Appli
411	6	1.2	318	4	US-09-352-616A-339	Sequence 339, App	484	6	1.2	335	2	US-08-723-938-3	Sequence 3, Appli
412	6	1.2	320	1	US-07-613-083B-1	Sequence 1, Appli	485	6	1.2	335	2	US-09-080-538-3	Sequence 3, Appli
413	6	1.2	323	4	US-09-457-646-30	Sequence 30, Appl	486	6	1.2	336	4	US-08-208-007A-13	Sequence 13, Appl
414	6	1.2	326	4	US-09-134-001C-4837	Sequence 4837, Ap	487	6	1.2	336	4	US-09-032-523-9	Sequence 9, Appli
415	6	1.2	329	4	US-09-413-231-5	Sequence 5, Appli	488	6	1.2	336	4	US-08-915-095A-13	Sequence 13, Appl
416	6	1.2	329	4	US-09-413-231-9	Sequence 9, Appli	489	6	1.2	336	4	US-08-798-096-13	Sequence 13, Appl
417	6	1.2	330	2	US-08-788-750-2	Sequence 2, Appli	490	6	1.2	336	4	US-08-798-095A-13	Sequence 13, Appl
418	6	1.2	330	4	US-09-152-060-104	Sequence 104, App	491	6	1.2	337	4	US-09-459-133-2	Sequence 2, Appli
419	6	1.2	333	4	US-09-171-710-2	Sequence 2, Appli	492	6	1.2	338	1	US-08-091-519-2	Sequence 2, Appli
420	6	1.2	337	4	US-09-044-404A-2	Sequence 2, Appli	493	6	1.2	338	1	US-08-176-413-5	Sequence 5, Appli
421	6	1.2	337	4	US-09-457-646-32	Sequence 32, Appl	494	6	1.2	338	1	US-08-328-314-2	Sequence 2, Appli
422	6	1.2	340	1	US-08-118-270-49	Sequence 49, Appl	495	6	1.2	338	1	US-08-507-931-2	Sequence 2, Appli
423	6	1.2	340	5	PCT-US93-08528-49	Sequence 49, Appl	496	6	1.2	338	1	US-08-731-045-2	Sequence 2, Appli
424	6	1.2	343	4	US-08-469-260A-608	Sequence 608, App	497	6	1.2	338	1	US-08-442-043-2	Sequence 2, Appli
425	6	1.2	346	3	US-08-988-111-2	Sequence 2, Appli	498	6	1.2	338	2	US-08-371-177-17	Sequence 17, Appl
426	6	1.2	346	3	US-09-387-922-2	Sequence 2, Appli	499	6	1.2	338	2	US-08-288-663A-1	Sequence 1, Appli
427	6	1.2	348	1	US-08-458-489-10	Sequence 10, Appl	500	6	1.2	338	2	US-08-902-655A-2	Sequence 2, Appli
428	6	1.2	348	1	US-08-458-686-10	Sequence 10, Appl	501	6	1.2	338	3	US-09-116-622-2	Sequence 3, Appli
429	6	1.2	348	1	US-07-843-350C-10	Sequence 10, Appl	502	6	1.2	338	4	US-09-219-777-2	Sequence 2, Appli
430	6	1.2	349	4	US-09-033-523-3	Sequence 3, Appli	503	6	1.2	338	4	US-09-599-661-1	Sequence 2, Appli
431	6	1.2	349	4	US-09-134-001C-4004	Sequence 4004, Ap	504	6	1.2	338	4	US-09-173-151A-26	Sequence 26, Appl
432	6	1.2	355	4	US-09-330-611-16	Sequence 16, Appl	505	6	1.2	338	4	US-09-347-878-11	Sequence 11, Appl
433	6	1.2	357	3	US-09-116-115-17	Sequence 17, Appl	506	6	1.2	338	5	PCT-US91-03478-2	Sequence 2, Appli
434	6	1.2	357	4	US-09-541-762-17	Sequence 17, Appl	507	6	1.2	338	5	PCT-US94-14919-5	Sequence 5, Appli
435	6	1.2	364	1	US-08-680-726A-56	Sequence 56, Appl	508	6	1.2	402	1	US-08-553-703A-1	Sequence 1, Appli
436	6	1.2	364	4	US-09-092-409-56	Sequence 56, Appl	509	6	1.2	402	1	US-08-553-703A-4	Sequence 4, Appli
437	6	1.2	368	2	US-08-824-878-3	Sequence 3, Appli	510	6	1.2	402	2	US-09-006-021-1	Sequence 1, Appli
438	6	1.2	368	2	US-08-824-878-3	Sequence 3, Appli	511	6	1.2	402	2	US-09-006-021-4	Sequence 4, Appli
439	6	1.2	369	1	US-08-700-359-21	Sequence 21, Appl	512	6	1.2	405	5	PCT-US93-11404-2	Sequence 2, Appli
440	6	1.2	370	4	US-09-172-353-2	Sequence 2, Appli	513	6	1.2	408	1	US-07-841-646-7	Sequence 7, Appli
441	6	1.2	370	4	US-09-172-353-3	Sequence 3, Appli	514	6	1.2	408	1	US-07-718-274A-6	Sequence 6, Appli
442	6	1.2	370	4	US-09-172-353-7	Sequence 7, Appli	515	6	1.2	408	1	US-07-901-703-19	Sequence 19, Appl
443	6	1.2	370	4	US-08-776-971-140	Sequence 140, App	516	6	1.2	408	1	US-08-149-106-6	Sequence 6, Appli
444	6	1.2	371	4	US-09-199-637A-295	Sequence 295, App	517	6	1.2	408	1	US-08-147-023-7	Sequence 7, Appli
445	6	1.2	372	4	US-09-092-315-13	Sequence 13, Appl	518	6	1.2	408	1	US-08-298-021-6	Sequence 6, Appli
446	6	1.2	373	2	US-08-824-878-1	Sequence 1, Appli	519	6	1.2	408	1	US-08-050-132A-4	Sequence 4, Appli
447	6	1.2	373	4	US-09-353-688-1	Sequence 1, Appli	520	6	1.2	408	1	US-08-447-570-7	Sequence 7, Appli
448	6	1.2	374	3	US-09-046-736-4	Sequence 4, Appli	521	6	1.2	408	2	US-08-459-346-11	Sequence 11, Appl
449	6	1.2	374	4	US-08-821-994-68	Sequence 68, Appl	522	6	1.2	408	2	US-08-449-700-7	Sequence 7, Appli
450	6	1.2	376	1	US-08-614-801A-6	Sequence 6, Appli	523	6	1.2	408	2	US-07-989-847-4	Sequence 4, Appli
451	6	1.2	376	2	US-08-997-080-89	Sequence 89, Appl	524	6	1.2	408	2	US-08-449-699A-7	Sequence 7, Appli
452	6	1.2	376	3	US-08-997-362-89	Sequence 89, Appl	525	6	1.2	408	3	US-08-750-222A-4	Sequence 4, Appli
453	6	1.2	376	3	US-08-873-970-89	Sequence 89, Appl	526	6	1.2	408	3	US-08-815-522B-4	Sequence 4, Appli
454	6	1.2	376	3	US-08-751-512-8	Sequence 8, Appli	527	6	1.2	408	3	US-08-889-419-11	Sequence 11, Appl
455	6	1.2	376	4	US-09-095-855-89	Sequence 89, Appl	528	6	1.2	408	3	US-08-458-434A-2	Sequence 2, Appli
456	6	1.2	376	4	US-09-324-542-89	Sequence 89, Appl	529	6	1.2	408	4	US-07-721-847A-6	Sequence 6, Appli
457	6	1.2	376	4	US-09-205-426-89	Sequence 89, Appl	530	6	1.2	408	4	US-08-469-411-4	Sequence 4, Appli
458	6	1.2	377	1	US-08-227-108-17	Sequence 17, Appl	531	6	1.2	408	4	US-08-925-779-6	Sequence 6, Appli
459	6	1.2	377	2	US-08-553-367A-4	Sequence 4, Appli	532	6	1.2	408	4	US-08-254-353A-11	Sequence 4, Appli
460	6	1.2	377	2	US-09-073-674-17	Sequence 17, Appl	533	6	1.2	408	4	US-08-402-542-11	Sequence 11, Appl
461	6	1.2	377	4	US-09-295-306-4	Sequence 4, Appli	534	6	1.2	408	5	PCT-US91-03540A-9	Sequence 9, Appli
462	6	1.2	377	4	US-09-734-719-4	Sequence 4, Appli	535	6	1.2	408	5	PCT-US92-05374A-4	Sequence 4, Appli
463	6	1.2	378	4	US-09-045-583-5	Sequence 5, Appli	536	6	1.2	408	5	PCT-US93-05446-19	Sequence 19, Appl
464	6	1.2	378	4	US-09-534-185-5	Sequence 5, Appli	537	6	1.2	408	5	PCT-US93-07189-11	Sequence 11, Appl
465	6	1.2	381	2	US-08-867-057-3	Sequence 3, Appli	538	6	1.2	408	5	PCT-US95-07084-4	Sequence 4, Appli

539	6	1.2	408	6	516058-6	Patent No. 516058	612	6	1.2	453	1	US-08-446-380-12	Sequence 12, Appl
540	6	1.2	409	6	5168050-4	Patent No. 5168050	613	6	1.2	453	1	US-08-446-574-12	Sequence 12, Appl
541	6	1.2	412	1	US-08-208-007A-12	Sequence 12, Appl	614	6	1.2	453	1	US-08-446-382-12	Sequence 12, Appl
542	6	1.2	412	4	US-08-974-691-4	Sequence 4, Appl	615	6	1.2	453	1	US-08-445-801-12	Sequence 12, Appl
543	6	1.2	412	4	US-08-915-095A-12	Sequence 12, Appl	616	6	1.2	453	1	US-08-275-487-12	Sequence 12, Appl
544	6	1.2	412	4	US-08-798-096-12	Sequence 12, Appl	617	6	1.2	453	5	PCT-US95-08919-12	Sequence 12, Appl
545	6	1.2	412	4	US-08-798-095A-12	Sequence 12, Appl	618	6	1.2	454	3	US-08-446-100-27	Sequence 28, Appl
546	6	1.2	416	1	US-08-073-807A-2	Sequence 2, Appl	619	6	1.2	454	3	US-08-446-100-27	Sequence 28, Appl
547	6	1.2	416	1	US-08-117-083-62	Sequence 62, Appl	620	6	1.2	454	3	US-08-446-100-28	Sequence 29, Appl
548	6	1.2	419	4	US-08-974-691-3	Sequence 3, Appl	621	6	1.2	454	3	US-08-446-100-29	Sequence 29, Appl
549	6	1.2	419	4	US-09-705-448-10	Sequence 10, Appl	622	6	1.2	454	3	US-08-446-100-30	Sequence 30, Appl
550	6	1.2	420	4	US-09-008-271A-4	Sequence 4, Appl	623	6	1.2	454	3	US-08-446-100-31	Sequence 31, Appl
551	6	1.2	420	4	US-08-974-691-8	Sequence 8, Appl	624	6	1.2	455	1	US-08-035-928-2	Sequence 2, Appl
552	6	1.2	420	4	US-09-705-448-1	Sequence 1, Appl	625	6	1.2	457	4	US-09-124-238A-1	Sequence 1, Appl
553	6	1.2	421	4	US-08-759-628-5	Sequence 5, Appl	626	6	1.2	457	4	US-09-124-238A-10	Sequence 10, Appl
554	6	1.2	424	4	US-09-661-711A-14	Sequence 14, Appl	627	6	1.2	457	4	US-09-134-001C-3838	Sequence 3838, Ap
555	6	1.2	425	4	US-09-092-315-6	Sequence 6, Appl	628	6	1.2	457	4	US-09-721-975-1	Sequence 1, Appl
556	6	1.2	427	4	US-08-065-844A-2	Sequence 2, Appl	629	6	1.2	457	4	US-09-721-975-10	Sequence 10, Appl
557	6	1.2	428	1	US-07-973-324A-4	Sequence 4, Appl	630	6	1.2	458	4	US-09-504-358-2	Sequence 2, Appl
558	6	1.2	428	1	US-08-343-380-4	Sequence 4, Appl	631	6	1.2	458	4	US-08-487-596-16	Sequence 16, Appl
559	6	1.2	428	4	US-09-435-4	Sequence 4, Appl	632	6	1.2	458	4	US-09-594-114-2	Sequence 2, Appl
560	6	1.2	428	4	US-09-072-917A-4	Sequence 4, Appl	633	6	1.2	461	4	US-08-672-571A-3	Sequence 3, Appl
561	6	1.2	429	1	US-08-745-977-4	Sequence 4, Appl	634	6	1.2	461	4	US-09-102-528-25	Sequence 25, Appl
562	6	1.2	429	2	US-08-677-049-5	Sequence 5, Appl	635	6	1.2	462	1	US-08-299-351-1	Sequence 1, Appl
563	6	1.2	429	2	US-09-040-639A-4	Sequence 4, Appl	636	6	1.2	462	2	US-08-371-377-18	Sequence 18, Appl
564	6	1.2	430	4	US-08-686-968C-3	Sequence 3, Appl	637	6	1.2	462	2	US-09-309-572-10	Sequence 10, Appl
565	6	1.2	431	1	US-08-090-523-2	Sequence 2, Appl	638	6	1.2	464	6	5225348-1	Patent No. 5225348
566	6	1.2	431	1	US-08-090-523-4	Sequence 4, Appl	639	6	1.2	464	4	US-09-092-315-1	Sequence 1, Appl
567	6	1.2	431	1	US-08-398-627-2	Sequence 2, Appl	640	6	1.2	467	3	US-09-046-736-2	Sequence 2, Appl
568	6	1.2	431	1	US-08-398-627-4	Sequence 4, Appl	641	6	1.2	470	1	US-08-471-936-2	Sequence 2, Appl
569	6	1.2	431	1	US-08-406-858-2	Sequence 2, Appl	642	6	1.2	470	2	US-08-894-840-2	Sequence 2, Appl
570	6	1.2	431	1	US-08-406-858-4	Sequence 4, Appl	643	6	1.2	470	3	US-09-139-675-2	Sequence 2, Appl
571	6	1.2	431	1	US-08-469-202-14	Sequence 14, Appl	644	6	1.2	476	4	US-09-092-315-5	Sequence 5, Appl
572	6	1.2	431	2	US-08-484-434C-14	Sequence 14, Appl	645	6	1.2	478	4	US-09-092-315-7	Sequence 7, Appl
573	6	1.2	431	4	US-09-038-832-2	Sequence 2, Appl	646	6	1.2	479	1	US-08-583-218-5	Sequence 5, Appl
574	6	1.2	431	4	US-09-038-832-4	Sequence 4, Appl	647	6	1.2	480	4	US-09-305-681-2	Sequence 2, Appl
575	6	1.2	431	5	PCT-US91-04036-2	Sequence 2, Appl	648	6	1.2	480	4	US-09-305-681-4	Sequence 4, Appl
576	6	1.2	431	5	PCT-US91-04036-4	Sequence 4, Appl	649	6	1.2	484	4	US-09-155-183-4	Sequence 4, Appl
577	6	1.2	431	5	PCT-US94-05275-2	Sequence 2, Appl	650	6	1.2	488	4	US-09-444-728-2	Sequence 2, Appl
578	6	1.2	431	5	PCT-US94-05275-4	Sequence 4, Appl	651	6	1.2	489	1	US-08-318-831-4	Sequence 4, Appl
579	6	1.2	433	4	US-09-705-448-3	Sequence 3, Appl	652	6	1.2	489	4	US-09-986-536-2	Sequence 2, Appl
580	6	1.2	434	1	US-07-923-632C-6	Sequence 6, Appl	653	6	1.2	490	1	US-08-672-571A-1	Sequence 1, Appl
581	6	1.2	434	1	US-08-184-237-6	Sequence 6, Appl	654	6	1.2	493	2	US-09-031-592-10	Sequence 10, Appl
582	6	1.2	434	2	US-08-482-920-6	Sequence 6, Appl	655	6	1.2	493	4	US-09-299-549-10	Sequence 10, Appl
583	6	1.2	434	3	US-08-484-341-6	Sequence 6, Appl	656	6	1.2	494	1	US-09-610-417-10	Sequence 10, Appl
584	6	1.2	434	4	US-09-252-292C-26	Sequence 26, Appl	657	6	1.2	494	1	US-08-275-488A-4	Sequence 4, Appl
585	6	1.2	434	4	US-08-483-502-6	Sequence 6, Appl	658	6	1.2	494	1	US-08-446-380-4	Sequence 4, Appl
586	6	1.2	434	4	US-09-726-651A-6	Sequence 6, Appl	659	6	1.2	494	1	US-08-446-374-4	Sequence 4, Appl
587	6	1.2	437	4	US-09-353-332-2	Sequence 2, Appl	660	6	1.2	494	1	US-08-446-382-4	Sequence 4, Appl
588	6	1.2	438	1	US-07-923-095-2	Sequence 2, Appl	661	6	1.2	494	1	US-08-445-801-4	Sequence 4, Appl
589	6	1.2	438	1	US-08-229-511-2	Sequence 2, Appl	662	6	1.2	494	1	US-08-375-487-4	Sequence 4, Appl
590	6	1.2	438	1	US-08-314-979-2	Sequence 2, Appl	663	6	1.2	494	5	PCT-US95-08919-4	Sequence 4, Appl
591	6	1.2	438	1	US-08-436-716-2	Sequence 4, Appl	664	6	1.2	495	3	US-09-079-415-4	Sequence 3, Appl
592	6	1.2	440	1	US-08-759-628-4	Sequence 4, Appl	665	6	1.2	500	2	US-09-031-392-7	Sequence 7, Appl
593	6	1.2	440	4	US-09-092-315-3	Sequence 3, Appl	666	6	1.2	500	4	US-09-299-549-7	Sequence 7, Appl
594	6	1.2	444	4	US-09-252-292C-27	Sequence 27, Appl	667	6	1.2	500	4	US-08-960-190A-25	Sequence 25, Appl
595	6	1.2	445	4	US-08-974-691-6	Sequence 6, Appl	668	6	1.2	502	4	US-09-610-417-7	Sequence 7, Appl
596	6	1.2	449	1	US-08-570-157-1	Sequence 1, Appl	669	6	1.2	502	4	US-08-334-179A-14	Sequence 14, Appl
597	6	1.2	449	4	US-09-076-510-1	Sequence 1, Appl	670	6	1.2	511	4	US-09-305-681-4	Sequence 4, Appl
598	6	1.2	450	4	US-09-071-035-222	Sequence 322, App	671	6	1.2	511	4	US-09-305-681-6	Sequence 6, Appl
599	6	1.2	451	4	US-08-974-691-2	Sequence 2, Appl	672	6	1.2	521	4	US-09-661-711A-18	Sequence 18, Appl
600	6	1.2	451	4	US-09-342-647-10	Sequence 10, Appl	673	6	1.2	525	1	US-08-681-129-2	Sequence 2, Appl
601	6	1.2	452	1	US-08-275-488A-2	Sequence 2, Appl	674	6	1.2	525	4	US-09-369-364A-21	Sequence 21, Appl
602	6	1.2	452	1	US-08-275-490-2	Sequence 2, Appl	675	6	1.2	529	1	US-08-172-331B-14	Sequence 14, Appl
603	6	1.2	452	1	US-08-446-380-2	Sequence 2, Appl	676	6	1.2	529	1	US-08-706-037-25	Sequence 25, Appl
604	6	1.2	452	1	US-08-446-374-2	Sequence 2, Appl	677	6	1.2	529	2	US-09-005-397-25	Sequence 25, Appl
605	6	1.2	452	1	US-08-446-382-2	Sequence 2, Appl	678	6	1.2	529	2	US-09-032-315-5	Sequence 5, Appl
606	6	1.2	452	1	US-08-445-801-2	Sequence 2, Appl	679	6	1.2	529	2	US-08-993-318A-5	Sequence 5, Appl
607	6	1.2	452	1	US-08-275-487-2	Sequence 2, Appl	680	6	1.2	529	4	US-09-399-886-5	Sequence 5, Appl
608	6	1.2	452	5	US-09-333-872A-15	Sequence 15, Appl	681	6	1.2	529	4	US-09-576-260-5	Sequence 5, Appl
609	6	1.2	452	5	PCT-US95-08919-2	Sequence 2, Appl	682	6	1.2	530	4	US-09-576-261-5	Sequence 5, Appl
610	6	1.2	453	1	US-08-275-488A-12	Sequence 12, Appl	683	6	1.2	530	2	US-08-752-307B-2	Sequence 2, Appl
611	6	1.2	453	1	US-08-275-490-12	Sequence 12, Appl	684	6	1.2	530	4	US-09-707-802-2	Sequence 2, Appl

685	6	1.2	530	4	US-09-991-326-2	Sequence 2, Appli	758	6	1.2	605	1	US-08-190-802A-49	Sequence 49, Appli
686	6	1.2	531	4	US-09-661-711A-16	Sequence 16, Appl	759	6	1.2	605	4	US-09-063-950-5	Sequence 5, Appli
687	6	1.2	533	1	US-08-368-071-10	Sequence 10, Appl	760	6	1.2	605	4	US-08-477-346-49	Sequence 49, Appl
688	6	1.2	533	1	US-08-458-161-10	Sequence 10, Appl	761	6	1.2	605	4	US-08-473-089-49	Sequence 49, Appl
689	6	1.2	533	5	PCT-US93-02172-10	Sequence 2, Appli	762	6	1.2	605	4	US-08-487-072A-49	Sequence 49, Appl
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691	6	1.2	539	3	US-09-150-476B-2	Sequence 2, Appli	764	6	1.2	609	4	US-09-271-778-1	Sequence 1, Appli
692	6	1.2	539	3	US-09-190-889A-2	Sequence 2, Appli	765	6	1.2	609	4	US-09-788-871-1	Sequence 1, Appli
693	6	1.2	539	4	US-09-190-938B-2	Sequence 2, Appli	766	6	1.2	610	1	US-07-821-717B-6	Sequence 6, Appli
694	6	1.2	539	5	PCT-US95-09261-2	Sequence 2, Appli	767	6	1.2	610	1	US-08-119-262B-6	Sequence 6, Appli
695	6	1.2	543	4	US-09-362-123A-4	Sequence 4, Appli	768	6	1.2	610	1	US-08-135-822A-11	Sequence 11, Appl
696	6	1.2	544	1	US-08-264-002-7	Sequence 7, Appli	769	6	1.2	610	1	US-08-234-265A-11	Sequence 11, Appl
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698	6	1.2	549	2	US-08-676-279-59	Sequence 59, Appl	771	6	1.2	620	1	US-08-706-037-27	Sequence 27, Appl
699	6	1.2	551	4	US-09-661-711A-12	Sequence 12, Appl	772	6	1.2	620	1	US-08-940-661A-2	Sequence 2, Appli
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701	6	1.2	556	4	US-08-462-467B-24	Sequence 24, Appl	774	6	1.2	620	2	US-09-005-397-27	Sequence 27, Appl
702	6	1.2	556	4	US-08-462-467B-26	Sequence 26, Appl	775	6	1.2	620	2	US-08-939-218A-2	Sequence 2, Appli
703	6	1.2	559	4	US-09-271-437-4	Sequence 4, Appli	776	6	1.2	620	4	US-09-232-200-61	Sequence 61, Appl
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705	6	1.2	563	4	US-09-211-704A-2	Sequence 2, Appli	778	6	1.2	620	4	US-09-232-197-61	Sequence 61, Appl
706	6	1.2	565	4	US-08-937-067-8	Sequence 8, Appli	779	6	1.2	620	4	US-09-232-197-93	Sequence 93, Appl
707	6	1.2	566	4	US-09-134-001C-3431	Sequence 3431, Ap	780	6	1.2	620	4	US-09-232-201-61	Sequence 61, Appl
708	6	1.2	569	4	US-08-686-968C-227	Sequence 227, App	781	6	1.2	620	4	US-09-232-201-93	Sequence 93, Appl
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710	6	1.2	572	2	US-08-993-318A-7	Sequence 7, Appli	783	6	1.2	621	4	US-09-898-297-1	Sequence 1, Appli
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712	6	1.2	572	4	US-09-396-260-7	Sequence 7, Appli	785	6	1.2	623	4	US-09-232-197-67	Sequence 67, Appl
713	6	1.2	572	4	US-09-576-281-7	Sequence 7, Appli	786	6	1.2	623	4	US-09-232-201-67	Sequence 67, Appl
714	6	1.2	573	2	US-08-991-531-1	Sequence 1, Appli	787	6	1.2	623	3	US-08-996-139-15	Sequence 15, Appl
715	6	1.2	573	2	US-09-033-315-10	Sequence 10, Appl	788	6	1.2	625	4	US-08-995-659-15	Sequence 15, Appl
716	6	1.2	573	2	US-08-993-318A-10	Sequence 10, Appl	789	6	1.2	625	4	US-09-215-449A-15	Sequence 15, Appl
717	6	1.2	573	3	US-09-028-887-1	Sequence 1, Appli	790	6	1.2	625	4	US-09-577-780-15	Sequence 15, Appl
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719	6	1.2	573	4	US-09-396-260-10	Sequence 10, Appl	792	6	1.2	628	1	US-08-250-740-33	Sequence 33, Appl
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732	6	1.2	584	2	US-08-928-692-13	Sequence 13, Appl	805	6	1.2	654	4	US-09-315-127-11	Sequence 11, Appl
733	6	1.2	584	2	US-08-339-972-13	Sequence 13, Appl	806	6	1.2	654	4	US-09-315-127-12	Sequence 12, Appl
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736	6	1.2	586	4	US-09-504-358-20	Sequence 20, Appl	809	6	1.2	668	4	US-09-149-879-13	Sequence 13, Appl
737	6	1.2	586	4	US-09-954-314-20	Sequence 20, Appl	810	6	1.2	669	4	US-09-071-035-264	Sequence 264, App
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741	6	1.2	591	4	US-09-352-159-44	Sequence 44, Appl	814	6	1.2	687	1	US-08-204-656B-10	Sequence 10, Appl
742	6	1.2	591	4	US-09-352-159-46	Sequence 46, Appl	815	6	1.2	687	1	US-08-470-702-10	Sequence 10, Appl
743	6	1.2	598	4	US-09-352-159-42	Sequence 42, Appl	816	6	1.2	687	1	US-08-467-831-10	Sequence 10, Appl
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745	6	1.2	600	4	US-09-352-159-38	Sequence 38, Appl	818	6	1.2	696	3	US-08-906-865-4	Sequence 4, Appli
746	6	1.2	600	4	US-09-423-468A-13	Sequence 13, Appl	819	6	1.2	696	4	US-09-129-668-4	Sequence 4, Appli
747	6	1.2	601	4	US-09-398-395A-42	Sequence 42, Appl	820	6	1.2	699	1	US-08-348-006B-7	Sequence 7, Appli
748	6	1.2	604	1	US-08-224-657-84	Sequence 84, Appl	821	6	1.2	699	2	US-08-800-825A-7	Sequence 7, Appli
749	6	1.2	604	1	US-08-224-657-95	Sequence 95, Appl	822	6	1.2	699	2	US-09-158-657-7	Sequence 7, Appli
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755	6	1.2	604	4	US-09-354-138-84	Sequence 84, Appl	828	6	1.2	702	4	US-09-232-197-102	Sequence 102, App
756	6	1.2	604	4	US-09-354-138-95	Sequence 95, Appl	829	6	1.2	702	4	US-09-232-201-102	Sequence 102, App
757	6	1.2	604	4	US-09-354-138-98	Sequence 98, Appl	830	6	1.2	718	2	US-08-560-398-12	Sequence 12, Appl

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832	6	1.2	739	3	US-08-510-646B-33	Sequence 33, Appli	905	6	1.2	1097	2	US-08-680-326-39	Sequence 33, Appli
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837	6	1.2	775	4	US-09-308-179B-1	Sequence 1, Appli	910	6	1.2	1156	4	US-09-001-882-10	Sequence 10, Appli
838	6	1.2	795	4	US-07-716-827C-5	Sequence 5, Appli	911	6	1.2	1156	4	US-09-002-285-70	Sequence 70, Appli
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887	6	1.2	933	4	US-08-370-193A-8	Sequence 8, Appli	960	6	1.2	1528	2	US-08-462-109A-6	Sequence 6, Appli
888	6	1.2	933	1	US-08-271-438A-9	Sequence 9, Appli	961	6	1.2	1528	2	US-08-460-907B-6	Sequence 6, Appli
889	6	1.2	935	4	US-09-271-438A-3	Sequence 3, Appli	962	6	1.2	1528	3	US-08-463-179A-6	Sequence 6, Appli
890	6	1.2	935	4	US-09-271-438A-8	Sequence 8, Appli	963	6	1.2	1528	3	US-08-461-184B-6	Sequence 6, Appli
891	6	1.2	979	4	US-09-323-872A-55	Sequence 55, Appli	964	6	1.2	1531	1	US-08-141-893-2	Sequence 2, Appli
892	6	1.2	989	4	US-09-199-637A-273	Sequence 273, App	965	6	1.2	1531	1	US-08-463-092B-2	Sequence 2, Appli
893	6	1.2	995	1	US-08-162-809-18	Sequence 18, Appli	966	6	1.2	1531	1	US-08-463-092B-4	Sequence 4, Appli
894	6	1.2	995	2	US-08-673-789-5	Sequence 5, Appli	967	6	1.2	1531	2	US-08-462-109A-2	Sequence 2, Appli
895	6	1.2	997	4	US-09-369-364A-7	Sequence 7, Appli	968	6	1.2	1531	2	US-08-462-109A-4	Sequence 4, Appli
896	6	1.2	998	2	US-08-449-645A-20	Sequence 20, Appli	969	6	1.2	1531	2	US-08-460-907B-2	Sequence 2, Appli
897	6	1.2	998	2	US-08-702-367A-20	Sequence 20, Appli	970	6	1.2	1531	2	US-08-460-907B-4	Sequence 4, Appli
898	6	1.2	998	5	PCT-US95-04681-20	Sequence 20, Appli	971	6	1.2	1531	3	US-08-463-179A-2	Sequence 2, Appli
899	6	1.2	999	2	US-08-473-553A-5	Sequence 5, Appli	972	6	1.2	1531	3	US-08-463-179A-4	Sequence 4, Appli
900	6	1.2	1011	1	US-08-162-809-12	Sequence 12, Appli	973	6	1.2	1531	3	US-08-461-384B-2	Sequence 2, Appli
901	6	1.2	1048	3	US-09-356-952-5	Sequence 5, Appli	974	6	1.2	1531	3	US-08-461-384B-4	Sequence 4, Appli
902	6	1.2	1070	4	US-09-091-042A-2	Sequence 2, Appli	975	6	1.2	1531	3	US-08-407-207A-2	Sequence 2, Appli
903	6	1.2	1090	4	US-09-346-237-5	Sequence 5, Appli	976	6	1.2	1544	4	US-09-413-814-46	Sequence 46, Appli

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977 6 1.2 1611 2 US-08-804-227C-5 Sequence 5, Appli
978 6 1.2 1618 4 US-08-462-467B-4 Sequence 4, Appli
979 6 1.2 1622 4 US-08-972-927-6 Sequence 6, Appli
980 6 1.2 1638 4 US-09-071-035-258 Sequence 268, App
981 6 1.2 1638 4 US-09-071-035-262 Sequence 267, App
982 6 1.2 1638 4 US-09-071-035-266 Sequence 266, App
983 6 1.2 1692 4 US-09-263-933-4 Sequence 4, Appli
984 6 1.2 1692 4 US-09-263-933-11 Sequence 11, Appli
985 6 1.2 1692 4 US-09-263-933-18 Sequence 18, Appli
986 6 1.2 1781 2 US-08-477-451-11 Sequence 11, Appli
987 6 1.2 1820 3 US-07-998-289B-8 Sequence 8, Appli
988 6 1.2 1835 4 US-09-404-650-5 Sequence 5, Appli
989 6 1.2 1839 2 US-09-172-977-4 Sequence 4, Appli
990 6 1.2 2013 1 US-08-324-977-12 Sequence 12, Appli
991 6 1.2 2013 2 US-08-324-977-12 Sequence 12, Appli
992 6 1.2 2013 2 US-08-904-686A-12 Sequence 12, Appli
993 6 1.2 2013 4 US-09-315-850-12 Sequence 12, Appli
994 6 1.2 2048 4 US-09-268-347-48 Sequence 48, Appli
995 6 1.2 2071 4 US-09-415-522-6 Sequence 6, Appli
996 6 1.2 2100 2 US-08-808-793-23 Sequence 23, Appli
997 6 1.2 2100 3 US-08-772-512A-19 Sequence 19, Appli
998 6 1.2 2104 2 US-08-808-793-4 Sequence 4, Appli
999 6 1.2 2104 3 US-08-772-512A-4 Sequence 4, Appli
1000 6 1.2 2105 2 US-08-808-793-3 Sequence 3, Appli
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ALIGNMENTS

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RESULT 1
US-08-999-723-2
; Sequence 2, Application US/08999723A
; Patent No. 6025180
; GENERAL INFORMATION:
; APPLICANT: Powell, David J.
; APPLICANT: Southan, Christopher
; APPLICANT: Chapman, Conrad G.
; APPLICANT: Evans, Joanne R.
; TITLE OF INVENTION: ASP1
; FILE REFERENCE: GH70262
; CURRENT APPLICATION NUMBER: US/08/999,723A
; CURRENT FILING DATE: 1997-10-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-999-723-2
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Query Match 100.0%; Score 518; DB 3; Length 518;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MGALRALLLPLLAQMLRAAPELAPAPFTLPLRVAAATNRVVAPTPGGTPAERHADGL 60
DB 1 MGALRALLLPLLAQMLRAAPELAPAPFTLPLRVAAATNRVVAPTPGGTPAERHADGL 60
QY 61 ALALPALASPAGANFLAMVDNLQDSGRGYLEMLIGTPPOKQIIVDTGSSNFAVAG 120
DB 61 ALALPALASPAGANFLAMVDNLQDSGRGYLEMLIGTPPOKQIIVDTGSSNFAVAG 120
QY 121 TPHSYIDYFPDTERSTYRSKGFDTVVKYTOGSGTWGFGVGEDLVTTIPKGFNTSFLVNIATI 180
DB 121 TPHSYIDYFPDTERSTYRSKGFDTVVKYTOGSGTWGFGVGEDLVTTIPKGFNTSFLVNIATI 180
QY 181 FESSENFPLPGIKWNGILGLAVATLAKPSSSLETFPDSLVTOANIPNVFSMOMCGAGLPAVA 240
DB 181 FESSENFPLPGIKWNGILGLAVATLAKPSSSLETFPDSLVTOANIPNVFSMOMCGAGLPAVA 240
QY 241 GSGTNGGSLVIGGIEPSLYKGDITWTPIKEEMWYQIEILKLEIGGOSLNDCREYNADKA 300
DB 241 GSGTNGGSLVIGGIEPSLYKGDITWTPIKEEMWYQIEILKLEIGGOSLNDCREYNADKA 300
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QY 301 IVDGTTLLRLPOKVFDAVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
DB 301 IVDGTTLLRLPOKVFDAVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
QY 361 YLRBENSRSRRTITLLPOLYIQPMKGAGLNECYRFGISPTNALVIGATMBEGFYVFD 420
DB 361 YLRBENSRSRRTITLLPOLYIQPMKGAGLNECYRFGISPTNALVIGATMBEGFYVFD 420
QY 421 RAQRVGAAPCAEIGAAYVEISGPFSTEDVASNCYPAOSLSEPLIMIVSALMSVCG 480
DB 421 RAQRVGAAPCAEIGAAYVEISGPFSTEDVASNCYPAOSLSEPLIMIVSALMSVCG 480
QY 481 ALLVLVLLLPCCQRPRPDEPVNDESSLVHRMK 518
DB 481 ALLVLVLLLPCCQRPRPDEPVNDESSLVHRMK 518
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RESULT 2
US-09-434-427-2
; Sequence 2, Application US/09434427
; Patent No. 6162630
; GENERAL INFORMATION:
; APPLICANT: POWELL, DAVID J.
; APPLICANT: SOUTHAN, CHRISTOPHER
; APPLICANT: CHAPMAN, CONRAD G.
; APPLICANT: EVANS, JOANNE R.
; TITLE OF INVENTION: ASP1
; FILE REFERENCE: GH-70262-D1
; CURRENT APPLICATION NUMBER: US/09/434,427
; CURRENT FILING DATE: 1999-11-04
; EARLIER APPLICATION NUMBER: US 08/999,723
; EARLIER FILING DATE: 1997-10-06
; EARLIER APPLICATION NUMBER: UK 9626022.9
; EARLIER FILING DATE: 1996-12-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-434-427-2
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Query Match 100.0%; Score 518; DB 4; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MGALRALLLPLLAQMLRAAPELAPAPFTLPLRVAAATNRVVAPTPGGTPAERHADGL 60
DB 1 MGALRALLLPLLAQMLRAAPELAPAPFTLPLRVAAATNRVVAPTPGGTPAERHADGL 60
QY 61 ALALPALASPAGANFLAMVDNLQDSGRGYLEMLIGTPPOKQIIVDTGSSNFAVAG 120
DB 61 ALALPALASPAGANFLAMVDNLQDSGRGYLEMLIGTPPOKQIIVDTGSSNFAVAG 120
QY 121 TPHSYIDYFPDTERSTYRSKGFDTVVKYTOGSGTWGFGVGEDLVTTIPKGFNTSFLVNIATI 180
DB 121 TPHSYIDYFPDTERSTYRSKGFDTVVKYTOGSGTWGFGVGEDLVTTIPKGFNTSFLVNIATI 180
QY 181 FESSENFPLPGIKWNGILGLAVATLAKPSSSLETFPDSLVTOANIPNVFSMOMCGAGLPAVA 240
DB 181 FESSENFPLPGIKWNGILGLAVATLAKPSSSLETFPDSLVTOANIPNVFSMOMCGAGLPAVA 240
QY 241 GSGTNGGSLVIGGIEPSLYKGDITWTPIKEEMWYQIEILKLEIGGOSLNDCREYNADKA 300
DB 241 GSGTNGGSLVIGGIEPSLYKGDITWTPIKEEMWYQIEILKLEIGGOSLNDCREYNADKA 300
QY 301 IVDGTTLLRLPOKVFDAVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
DB 301 IVDGTTLLRLPOKVFDAVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
QY 361 YLRBENSRSRRTITLLPOLYIQPMKGAGLNECYRFGISPTNALVIGATMBEGFYVFD 420
DB 361 YLRBENSRSRRTITLLPOLYIQPMKGAGLNECYRFGISPTNALVIGATMBEGFYVFD 420
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Db 361 YLRDENSRSRFRITITLPQLYIQPMGAGLNYECYRFGISPTNALVIGATWMEGFYIFD 420
Qy 421 RAQKRVGFPAASPCAEIAGAASEISGPFSTEDVASCNCPAQSISEPILIMIVSYALMSVCG 480
Db 421 RAQKRVGFPAASPCAEIAGAASEISGPFSTEDVASCNCPAQSISEPILIMIVSYALMSVCG 480
Qy 481 AILVLIVLILLLPFCQRRPRDPEVNDSSLVHRHWK 518
Db 481 AILVLIVLILLLPFCQRRPRDPEVNDSSLVHRHWK 518

RESULT 3
US-09-548-372D-2
; Sequence 2, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-548-372D-2

Query Match 100.0%; Score 518; DB 4; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGALARALLPLLAQWILRAPELAPAPFTLLPLRVAATNRVAVPTPGPTPAERHADGL 60
Db 1 MGALARALLPLLAQWILRAPELAPAPFTLLPLRVAATNRVAVPTPGPTPAERHADGL 60
Qy 61 ALALEPALASPAGANFLAMVDNIQDGSRGYILEMLIGTPPOKQLIIVDTGSSNFAVAG 120
Db 61 ALALEPALASPAGANFLAMVDNIQDGSRGYILEMLIGTPPOKQLIIVDTGSSNFAVAG 120
Qy 121 TPHSYIDTYFPTERSSTYRSKGFDTVTKYTOGSMWTFVGEDELVTIIPKGFNTSFLVNIATI 180
Db 121 TPHSYIDTYFPTERSSTYRSKGFDTVTKYTOGSMWTFVGEDELVTIIPKGFNTSFLVNIATI 180
Qy 181 PFSNFPLPGIKMNGIIGLAVATLAKPSSLETFFDSLVTQANIPIVFSMOMCAGLPVA 240
Db 181 PFSNFPLPGIKMNGIIGLAVATLAKPSSLETFFDSLVTQANIPIVFSMOMCAGLPVA 240
Qy 241 GSGTNGSLVIGIEPSLYKGDIMWTPIKEWYQIEILKLEIGGSLNIDCREYNADKA 300
Db 241 GSGTNGSLVIGIEPSLYKGDIMWTPIKEWYQIEILKLEIGGSLNIDCREYNADKA 300
Qy 301 IVDGTTLLRLPQKVFDAVVAVARASLIPEFSDFMTGSLACWTNSETPMWYFPKISI 360
Db 301 IVDGTTLLRLPQKVFDAVVAVARASLIPEFSDFMTGSLACWTNSETPMWYFPKISI 360
Qy 361 YLRDENSRSRFRITITLPQLYIQPMGAGLNYECYRFGISPTNALVIGATWMEGFYIFD 420
Db 361 YLRDENSRSRFRITITLPQLYIQPMGAGLNYECYRFGISPTNALVIGATWMEGFYIFD 420
Qy 421 RAQKRVGFPAASPCAEIAGAASEISGPFSTEDVASCNCPAQSISEPILIMIVSYALMSVCG 480
Db 421 RAQKRVGFPAASPCAEIAGAASEISGPFSTEDVASCNCPAQSISEPILIMIVSYALMSVCG 480

Qy 481 AILVLIVLILLLPFCQRRPRDPEVNDSSLVHRHWK 518
Db 481 AILVLIVLILLLPFCQRRPRDPEVNDSSLVHRHWK 518

RESULT 4
US-09-548-367D-2
; Sequence 2, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/62808
; CURRENT APPLICATION NUMBER: US/09/548,367D
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-548-367D-2

Query Match 100.0%; Score 518; DB 4; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGALARALLPLLAQWILRAPELAPAPFTLLPLRVAATNRVAVPTPGPTPAERHADGL 60
Db 1 MGALARALLPLLAQWILRAPELAPAPFTLLPLRVAATNRVAVPTPGPTPAERHADGL 60
Qy 61 ALALEPALASPAGANFLAMVDNIQDGSRGYILEMLIGTPPOKQLIIVDTGSSNFAVAG 120
Db 61 ALALEPALASPAGANFLAMVDNIQDGSRGYILEMLIGTPPOKQLIIVDTGSSNFAVAG 120
Qy 121 TPHSYIDTYFPTERSSTYRSKGFDTVTKYTOGSMWTFVGEDELVTIIPKGFNTSFLVNIATI 180
Db 121 TPHSYIDTYFPTERSSTYRSKGFDTVTKYTOGSMWTFVGEDELVTIIPKGFNTSFLVNIATI 180
Qy 181 PFSNFPLPGIKMNGIIGLAVATLAKPSSLETFFDSLVTQANIPIVFSMOMCAGLPVA 240
Db 181 PFSNFPLPGIKMNGIIGLAVATLAKPSSLETFFDSLVTQANIPIVFSMOMCAGLPVA 240
Qy 241 GSGTNGSLVIGIEPSLYKGDIMWTPIKEWYQIEILKLEIGGSLNIDCREYNADKA 300
Db 241 GSGTNGSLVIGIEPSLYKGDIMWTPIKEWYQIEILKLEIGGSLNIDCREYNADKA 300
Qy 301 IVDGTTLLRLPQKVFDAVVAVARASLIPEFSDFMTGSLACWTNSETPMWYFPKISI 360
Db 301 IVDGTTLLRLPQKVFDAVVAVARASLIPEFSDFMTGSLACWTNSETPMWYFPKISI 360
Qy 361 YLRDENSRSRFRITITLPQLYIQPMGAGLNYECYRFGISPTNALVIGATWMEGFYIFD 420
Db 361 YLRDENSRSRFRITITLPQLYIQPMGAGLNYECYRFGISPTNALVIGATWMEGFYIFD 420
Qy 421 RAQKRVGFPAASPCAEIAGAASEISGPFSTEDVASCNCPAQSISEPILIMIVSYALMSVCG 480
Db 421 RAQKRVGFPAASPCAEIAGAASEISGPFSTEDVASCNCPAQSISEPILIMIVSYALMSVCG 480
Qy 481 AILVLIVLILLLPFCQRRPRDPEVNDSSLVHRHWK 518
Db 481 AILVLIVLILLLPFCQRRPRDPEVNDSSLVHRHWK 518

RESULT 5

US-09-717-432-2
; Sequence 2, Application US/09717432
; Patent No. 6291223
; GENERAL INFORMATION:
; APPLICANT: ZHU, YUAN
; APPLICANT: LI, XIAOTONG
; APPLICANT: CHRISTIE, GARY
; APPLICANT: POWELL, DAVID J.
; TITLE OF INVENTION: Mouse Aspartic Secretase-1 (MASP1)
; FILE REFERENCE: GP-70663
; CURRENT APPLICATION NUMBER: US/09/717,432
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/166,974
; PRIOR FILING DATE: 1999-11-23
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 514
; TYPE: PRT
; ORGANISM: MUS MUSCULUS
US-09-717-432-2

Query Match 11.4%; Score 59; DB 4; Length 514;
Best Local Similarity 100.0%; Pred. No. 1.8e-47;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 228 F5M0MCGAGLPVAGSGTNGSLVLGIEP5LYKGD1WYPIKEWYQIEIKLEIGGQ 286

Db 224 F5M0MCGAGLPVAGSGTNGSLVLGIEP5LYKGD1WYPIKEWYQIEIKLEIGGQ 282

RESULT 6

US-09-912-484-2
; Sequence 2, Application US/09912484
; Patent No. 6358725
; GENERAL INFORMATION:
; APPLICANT: Christie, Gary
; APPLICANT: Li, Xiaotong
; APPLICANT: Powell, David J.
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: Mouse Aspartic Secretase-1 (MASP1)
; FILE REFERENCE: GP-70663-D1
; CURRENT APPLICATION NUMBER: US/09/912,484
; CURRENT FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/166,974
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 09/717,432
; PRIOR FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 514
; TYPE: PRT
; ORGANISM: MUS MUSCULUS
US-09-912-484-2

Query Match 11.4%; Score 59; DB 4; Length 514;
Best Local Similarity 100.0%; Pred. No. 1.8e-47;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 228 F5M0MCGAGLPVAGSGTNGSLVLGIEP5LYKGD1WYPIKEWYQIEIKLEIGGQ 286

Db 224 F5M0MCGAGLPVAGSGTNGSLVLGIEP5LYKGD1WYPIKEWYQIEIKLEIGGQ 282

RESULT 7

US-09-548-372D-33
; Sequence 33, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-33

Query Match 4.2%; Score 22; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 497 QRRPRDPEVNDSSLVHRWK 518

Db 4 QRRPRDPEVNDSSLVHRWK 25

RESULT 8

US-09-548-367D-33
; Sequence 33, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-33

Query Match 4.2%; Score 22; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 497 QRRPRDPEVNDSSLVHRWK 518

Db 4 QRRPRDPEVNDSSLVHRWK 25

RESULT 9

US-09-548-372D-28
; Sequence 28, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

```
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-28
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Query Match      2.3%; Score 12; DB 4; Length 425;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 107 ILVDTGSSNFAV 118
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Db 62 ILVDTGSSNFAV 73
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RESULT 10
US-09-548-367D-28
; Sequence 28, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-28
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Query Match      2.3%; Score 12; DB 4; Length 425;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 107 ILVDTGSSNFAV 118
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; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: THEREOF
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; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
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; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
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; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
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; PRIOR FILING DATE: 1998-09-24
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; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
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; PRIOR APPLICATION NUMBER: US 60/101,594
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US-09-548-372D-26
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DB 70 ILVDTGSSNFAV 81
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; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,367D
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
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; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
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; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
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; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
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258	518	100.0	518	9	US-10-205-511-72	Sequence 72, Appl	331	12	2.3	446	10	US-09-794-925-24	Sequence 24, Appl
259	518	100.0	518	9	US-10-205-902-72	Sequence 72, Appl	332	12	2.3	446	10	US-09-794-925-32	Sequence 32, Appl
260	518	100.0	518	9	US-10-205-907-72	Sequence 72, Appl	333	12	2.3	446	10	US-09-681-442-24	Sequence 24, Appl
261	518	100.0	518	9	US-09-918-585A-196	Sequence 196, App	334	12	2.3	446	10	US-09-681-442-32	Sequence 32, Appl
262	518	100.0	518	9	US-10-194-456-72	Sequence 72, Appl	335	12	2.3	446	10	US-09-794-927-6	Sequence 6, Appl
263	518	100.0	518	9	US-10-196-758-72	Sequence 72, Appl	336	12	2.3	446	10	US-09-795-847-6	Sequence 6, Appl
264	518	100.0	518	9	US-10-198-770-72	Sequence 72, Appl	337	12	2.3	446	10	US-09-794-743-6	Sequence 6, Appl
265	518	100.0	518	9	US-10-199-308-72	Sequence 72, Appl	338	12	2.3	446	10	US-09-794-748-6	Sequence 6, Appl
266	518	100.0	518	9	US-10-200-617-72	Sequence 72, Appl	339	12	2.3	446	10	US-09-794-925-6	Sequence 6, Appl
267	518	100.0	518	9	US-10-205-893-72	Sequence 72, Appl	340	12	2.3	446	10	US-09-681-442-6	Sequence 6, Appl
268	518	100.0	518	9	US-10-205-897-72	Sequence 72, Appl	341	12	2.3	446	9	US-09-795-903A-2	Sequence 2, Appl
269	518	100.0	518	10	US-09-794-927-2	Sequence 2, Appl	342	12	2.3	448	10	US-09-796-264-2	Sequence 2, Appl
270	518	100.0	518	10	US-09-795-847-2	Sequence 2, Appl	343	12	2.3	448	10	US-09-845-226-2	Sequence 2, Appl
271	518	100.0	518	10	US-09-794-743-2	Sequence 2, Appl	344	12	2.3	501	9	US-09-969-671A-2	Sequence 2, Appl
272	518	100.0	518	10	US-09-794-748-2	Sequence 2, Appl	345	12	2.3	501	10	US-09-794-927-4	Sequence 4, Appl
273	518	100.0	518	10	US-09-794-925-2	Sequence 2, Appl	346	12	2.3	501	10	US-09-794-927-8	Sequence 8, Appl
274	518	100.0	518	10	US-09-215-450-19	Sequence 19, Appl	347	12	2.3	501	10	US-09-795-847-4	Sequence 4, Appl
275	518	100.0	518	10	US-09-681-442-2	Sequence 2, Appl	348	12	2.3	501	10	US-09-795-847-8	Sequence 8, Appl
276	518	100.0	518	12	US-10-052-586-72	Sequence 72, Appl	349	12	2.3	501	10	US-09-794-743-4	Sequence 4, Appl
277	423	81.7	423	9	US-09-470-954A-46	Sequence 46, Appl	350	12	2.3	501	10	US-09-794-748-4	Sequence 4, Appl
278	50	9.7	50	10	US-09-864-761-49075	Sequence 49075, A	351	12	2.3	501	10	US-09-794-748-8	Sequence 8, Appl
279	287	44	44	10	US-09-864-761-38089	Sequence 38089, A	352	12	2.3	501	10	US-09-794-925-4	Sequence 4, Appl
280	287	4.2	25	10	US-09-794-927-33	Sequence 33, Appl	353	12	2.3	501	10	US-09-794-925-8	Sequence 8, Appl
281	282	4.2	25	10	US-09-795-847-33	Sequence 33, Appl	354	12	2.3	501	10	US-09-794-925-8	Sequence 8, Appl
282	282	4.2	25	10	US-09-794-743-33	Sequence 33, Appl	355	12	2.3	501	10	US-09-681-442-4	Sequence 4, Appl
283	282	4.2	25	10	US-09-794-748-33	Sequence 33, Appl	356	12	2.3	501	10	US-09-681-442-8	Sequence 8, Appl
284	282	4.2	25	10	US-09-794-925-33	Sequence 33, Appl	357	12	2.3	503	9	US-09-795-903A-3	Sequence 3, Appl
285	285	22	25	10	US-09-681-442-33	Sequence 33, Appl	358	12	2.3	503	10	US-09-796-264-3	Sequence 3, Appl
286	16	3.1	16	9	US-09-886-143-6	Sequence 6, Appl	359	12	2.3	503	10	US-09-845-226-3	Sequence 3, Appl
287	12	2.3	425	10	US-09-794-927-28	Sequence 28, Appl	360	12	2.3	774	9	US-09-969-671A-4	Sequence 4, Appl
288	12	2.3	425	10	US-09-795-847-28	Sequence 28, Appl	361	9	1.7	332	9	US-09-470-954A-47	Sequence 47, Appl
289	12	2.3	425	10	US-09-794-743-28	Sequence 28, Appl	362	9	1.7	401	9	US-09-924-340-24	Sequence 24, Appl
290	12	2.3	425	10	US-09-794-748-28	Sequence 28, Appl	363	9	1.7	401	9	US-09-992-600A-24	Sequence 24, Appl
291	12	2.3	425	10	US-09-794-925-28	Sequence 28, Appl	364	8	1.5	448	9	US-09-738-626-3686	Sequence 3686, Ap
292	12	2.3	425	10	US-09-681-442-28	Sequence 28, Appl	365	8	1.5	448	9	US-09-861-400-17	Sequence 17, Appl
293	12	2.3	428	10	US-09-794-927-51	Sequence 51, Appl	366	8	1.5	448	9	US-10-042-431-39	Sequence 39, Appl
294	12	2.3	428	10	US-09-795-847-51	Sequence 51, Appl	367	8	1.5	448	9	US-09-759-1308-409	Sequence 409, App
295	12	2.3	428	10	US-09-794-743-51	Sequence 51, Appl	368	8	1.5	448	10	US-09-731-872-271	Sequence 271, App
296	12	2.3	428	10	US-09-794-748-51	Sequence 51, Appl	369	8	1.5	448	10	US-09-994-185-2	Sequence 2, Appl
297	12	2.3	428	10	US-09-794-925-51	Sequence 51, Appl	370	8	1.5	448	10	US-09-861-400-2	Sequence 2, Appl
298	12	2.3	428	10	US-09-681-442-51	Sequence 51, Appl	371	8	1.5	448	12	US-10-004-139-2	Sequence 2, Appl
299	12	2.3	433	10	US-09-794-927-26	Sequence 26, Appl	372	8	1.5	504	10	US-09-919-497-67	Sequence 67, Appl
300	12	2.3	433	10	US-09-795-847-26	Sequence 26, Appl	373	8	1.5	548	10	US-09-741-669-413	Sequence 413, App
301	12	2.3	433	10	US-09-794-743-26	Sequence 26, Appl	374	8	1.5	632	9	US-09-738-626-6979	Sequence 6979, Ap
302	12	2.3	433	10	US-09-794-748-26	Sequence 26, Appl	375	8	1.5	1246	10	US-09-919-497-85	Sequence 85, Appl
303	12	2.3	433	10	US-09-794-925-26	Sequence 26, Appl	376	7	1.4	13	9	US-10-027-661A-293	Sequence 20, Appl
304	12	2.3	433	10	US-09-681-442-26	Sequence 26, Appl	377	7	1.4	21	9	US-09-974-879-293	Sequence 293, App
305	12	2.3	434	10	US-09-794-927-53	Sequence 53, Appl	378	7	1.4	25	10	US-09-922-199A-19	Sequence 19, Appl
306	12	2.3	434	10	US-09-795-847-53	Sequence 53, Appl	379	7	1.4	25	10	US-09-864-761-45398	Sequence 45398, A
307	12	2.3	434	10	US-09-794-743-53	Sequence 53, Appl	380	7	1.4	38	10	US-09-846-258-8	Sequence 8, Appl
308	12	2.3	434	10	US-09-794-748-53	Sequence 53, Appl	381	7	1.4	30	10	US-09-758-573-3	Sequence 3, Appl
309	12	2.3	434	10	US-09-794-925-53	Sequence 53, Appl	382	7	1.4	34	9	US-09-948-820-94	Sequence 94, Appl
310	12	2.3	434	10	US-09-681-442-53	Sequence 53, Appl	383	7	1.4	50	9	US-09-974-879-291	Sequence 291, App
311	12	2.3	446	10	US-09-794-927-53	Sequence 22, Appl	384	7	1.4	60	8	US-08-914-350-7	Sequence 7, Appl

385	7	1.4	61	9	US-09-852-797-52	Sequence 52, Appl	458	6	1.2	22	10	US-09-847-185-6	Sequence 6, Appl
386	7	1.4	61	10	US-09-853-161-52	Sequence 52, Appl	459	6	1.2	23	9	US-10-057-558-2	Sequence 2, Appl
387	7	1.4	61	10	US-09-852-659A-52	Sequence 52, Appl	460	6	1.2	26	12	US-10-016-481-10	Sequence 10, Appl
388	7	1.4	91	10	US-09-864-761-42428	Sequence 42428, A	461	6	1.2	27	8	US-08-873-601-31	Sequence 81, Appl
389	7	1.4	95	10	US-09-734-569-52	Sequence 52, Appl	462	6	1.2	27	9	US-09-792-630-84	Sequence 84, Appl
390	7	1.4	106	10	US-09-846-258-5	Sequence 5, Appl	463	6	1.2	27	9	US-10-080-376-84	Sequence 84, Appl
391	7	1.4	126	10	US-09-970-518-1	Sequence 1, Appl	464	6	1.2	27	9	US-10-061-995-32	Sequence 32, Appl
392	7	1.4	160	9	US-10-269-781-5	Sequence 5, Appl	465	6	1.2	27	9	US-10-096-339-30	Sequence 30, Appl
393	7	1.4	174	10	US-09-731-872-315	Sequence 315, App	466	6	1.2	27	10	US-09-157-748-35	Sequence 35, Appl
394	7	1.4	175	10	US-09-864-761-46612	Sequence 46612, A	467	6	1.2	27	10	US-09-916-940-35	Sequence 35, Appl
395	7	1.4	185	10	US-09-881-752A-40	Sequence 40, Appl	468	6	1.2	29	9	US-09-832-555A-53	Sequence 53, Appl
396	7	1.4	193	10	US-09-764-898-214	Sequence 214, App	469	6	1.2	31	9	US-09-966-069-12	Sequence 6, Appl
397	7	1.4	194	9	US-09-925-299-1005	Sequence 1005, Ap	470	6	1.2	31	9	US-09-966-069-12	Sequence 12, Appl
398	7	1.4	231	10	US-09-925-299-1005	Sequence 1005, Ap	471	6	1.2	32	9	US-10-057-558-12	Sequence 12, Appl
399	7	1.4	231	10	US-09-768-826-56	Sequence 56, App	472	6	1.2	32	9	US-09-755-109-18	Sequence 18, Appl
400	7	1.4	238	10	US-09-904-954-2	Sequence 2, Appl	473	6	1.2	32	9	US-10-012-542-478	Sequence 478, App
401	7	1.4	262	10	US-09-925-302-522	Sequence 522, App	474	6	1.2	32	10	US-09-864-761-41359	Sequence 41359, A
402	7	1.4	265	9	US-09-866-050A-655	Sequence 655, App	475	6	1.2	33	9	US-10-057-558-4	Sequence 4, Appl
403	7	1.4	270	10	US-09-758-575-2	Sequence 2, Appl	476	6	1.2	34	9	US-09-759-1308-74	Sequence 36036, A
404	7	1.4	273	10	US-09-758-575-2	Sequence 2, Appl	477	6	1.2	35	10	US-09-864-761-36036	Sequence 39580, A
405	7	1.4	273	10	US-09-893-737-228	Sequence 228, App	478	6	1.2	35	10	US-08-873-601-18	Sequence 18, Appl
406	7	1.4	273	10	US-09-820-893-138	Sequence 138, App	479	6	1.2	36	8	US-09-792-630-71	Sequence 71, Appl
407	7	1.4	279	10	US-09-731-872-314	Sequence 314, App	480	6	1.2	36	9	US-10-080-376-71	Sequence 71, Appl
408	7	1.4	280	10	US-09-731-872-314	Sequence 314, App	481	6	1.2	36	9	US-10-061-995-19	Sequence 19, Appl
409	7	1.4	306	10	US-09-741-669-456	Sequence 456, App	482	6	1.2	36	9	US-10-096-339-18	Sequence 18, Appl
410	7	1.4	320	8	US-08-914-350-2	Sequence 2, Appl	483	6	1.2	36	10	US-09-157-748-24	Sequence 24, Appl
411	7	1.4	323	9	US-09-948-820-85	Sequence 85, Appl	484	6	1.2	36	10	US-09-916-940-22	Sequence 22, Appl
412	7	1.4	326	9	US-09-795-903A-31	Sequence 31, Appl	485	6	1.2	36	10	US-09-764-877-1258	Sequence 1258, Ap
413	7	1.4	326	10	US-09-796-264-31	Sequence 31, Appl	486	6	1.2	38	9	US-09-908-1538-51	Sequence 51, Appl
414	7	1.4	326	10	US-09-845-226-31	Sequence 31, Appl	487	6	1.2	38	9	US-09-864-761-40768	Sequence 40768, A
415	7	1.4	327	10	US-09-734-569-156	Sequence 156, App	488	6	1.2	38	10	US-09-873-106B-16	Sequence 16, Appl
416	7	1.4	363	10	US-09-905-173-36	Sequence 36, Appl	489	6	1.2	40	9	US-10-057-558-10	Sequence 10, Appl
417	7	1.4	388	10	US-09-215-450-23	Sequence 23, Appl	490	6	1.2	40	10	US-09-864-761-47336	Sequence 47336, A
418	7	1.4	451	9	US-10-042-431-43	Sequence 43, Appl	491	6	1.2	41	10	US-09-983-802-221	Sequence 221, App
419	7	1.4	451	9	US-09-759-130B-413	Sequence 413, App	492	6	1.2	42	9	US-09-925-299-1537	Sequence 1537, App
420	7	1.4	453	9	US-09-443-745-27	Sequence 27, Appl	493	6	1.2	43	9	US-09-925-299-1538	Sequence 1538, App
421	7	1.4	470	9	US-10-042-431-69	Sequence 69, Appl	494	6	1.2	46	10	US-09-864-761-44970	Sequence 44970, A
422	7	1.4	470	9	US-09-759-130B-439	Sequence 439, App	495	6	1.2	47	10	US-09-864-761-43013	Sequence 43013, A
423	7	1.4	491	9	US-09-712-363-152	Sequence 152, App	496	6	1.2	48	10	US-09-864-761-48227	Sequence 48227, A
424	7	1.4	517	9	US-09-972-268-20	Sequence 20, Appl	497	6	1.2	49	10	US-09-864-761-35522	Sequence 35522, A
425	7	1.4	518	10	US-09-919-172-20	Sequence 20, Appl	498	6	1.2	50	10	US-09-726-624-11	Sequence 1, Appl
426	7	1.4	537	9	US-10-047-542-74	Sequence 74, Appl	499	6	1.2	53	9	US-09-925-299-1537	Sequence 1537, App
427	7	1.4	550	9	US-09-738-626-6950	Sequence 6950, Ap	500	6	1.2	53	9	US-09-925-299-1538	Sequence 1538, App
428	7	1.4	550	9	US-10-226-136-19	Sequence 19, Appl	501	6	1.2	53	9	US-09-925-299-1539	Sequence 1539, App
429	7	1.4	569	10	US-09-815-242-10503	Sequence 10503, A	502	6	1.2	53	10	US-09-925-302-763	Sequence 763, App
430	7	1.4	604	9	US-10-027-961A-18	Sequence 18, Appl	503	6	1.2	53	10	US-09-925-299-1537	Sequence 1537, App
431	7	1.4	615	10	US-09-862-027-49	Sequence 49, Appl	504	6	1.2	53	10	US-09-825-299-1538	Sequence 1538, App
432	7	1.4	638	10	US-09-851-859A-6	Sequence 6, Appl	505	6	1.2	54	10	US-09-825-299-1539	Sequence 1539, App
433	7	1.4	654	10	US-09-969-528-10	Sequence 10, Appl	506	6	1.2	54	10	US-09-764-877-1336	Sequence 1336, App
434	7	1.4	667	9	US-09-874-503-16	Sequence 16, Appl	507	6	1.2	55	10	US-09-908-711-80	Sequence 80, Appl
435	7	1.4	667	9	US-10-000-157-16	Sequence 16, Appl	508	6	1.2	55	10	US-09-864-761-39275	Sequence 39275, A
436	7	1.4	667	9	US-09-816-744-16	Sequence 16, Appl	509	6	1.2	55	10	US-09-864-761-40066	Sequence 40066, A
437	7	1.4	667	9	US-09-747-259-16	Sequence 16, Appl	510	6	1.2	55	10	US-09-800-729-122	Sequence 122, App
438	7	1.4	667	9	US-10-227-884-20	Sequence 20, Appl	511	6	1.2	56	9	US-10-044-359-8	Sequence 8, Appl
439	7	1.4	667	9	US-10-230-163-20	Sequence 20, Appl	512	6	1.2	57	10	US-09-864-761-41100	Sequence 41100, A
440	7	1.4	667	9	US-10-218-631-20	Sequence 20, Appl	513	6	1.2	58	10	US-10-079-954-191	Sequence 191, App
441	7	1.4	667	9	US-10-230-338-20	Sequence 20, Appl	514	6	1.2	58	10	US-09-764-878-191	Sequence 191, App
442	7	1.4	667	9	US-10-230-414-20	Sequence 20, Appl	515	6	1.2	59	9	US-09-848-616-141	Sequence 141, App
443	7	1.4	667	9	US-09-908-827-15	Sequence 16, Appl	516	6	1.2	60	9	US-09-895-913A-342	Sequence 342, App
444	7	1.4	704	10	US-09-912-020-248	Sequence 248, App	517	6	1.2	60	9	US-10-057-558-8	Sequence 8, Appl
445	7	1.4	704	10	US-09-815-242-10363	Sequence 10363, A	518	6	1.2	61	9	US-10-125-258-16	Sequence 16, Appl
446	7	1.4	704	10	US-09-815-242-13965	Sequence 13965, A	519	6	1.2	62	9	US-10-012-542-191	Sequence 191, App
447	7	1.4	760	10	US-09-833-017-26	Sequence 26, Appl	520	6	1.2	66	10	US-09-864-761-33794	Sequence 33794, A
448	7	1.4	862	9	US-09-738-626-3956	Sequence 3956, Ap	521	6	1.2	67	10	US-09-864-761-36500	Sequence 36500, A
449	7	1.4	942	9	US-10-101-464A-911	Sequence 911, App	522	6	1.2	68	10	US-09-796-692-1318	Sequence 1318, App
450	7	1.4	1429	9	US-09-953-407-1	Sequence 1, Appl	523	6	1.2	68	10	US-09-420-920-50	Sequence 50, Appl
451	7	1.4	1520	9	US-09-736-626-4444	Sequence 4444, Ap	524	6	1.2	68	10	US-09-864-761-33739	Sequence 33739, A
452	7	1.4	2047	9	US-09-736-968A-2	Sequence 2, Appl	525	6	1.2	70	9	US-09-925-299-1536	Sequence 1536, App
453	6	1.2	12	8	US-08-424-550B-446	Sequence 446, App	526	6	1.2	70	9	US-10-000-256A-141	Sequence 141, App
454	6	1.2	14	10	US-09-918-171A-28	Sequence 28, Appl	527	6	1.2	70	10	US-09-925-299-1536	Sequence 1536, App
455	6	1.2	19	10	US-09-918-171A-24	Sequence 24, Appl	528	6	1.2	75	9	US-09-272-975-6	Sequence 6, Appl
456	6	1.2	21	12	US-10-096-241-24	Sequence 24, Appl	529	6	1.2	78	10	US-09-881-752A-120	Sequence 120, App
457	6	1.2	22	9	US-09-832-355A-58	Sequence 58, Appl	530	6	1.2	80	9	US-10-114-893-56	Sequence 56, Appl

531	6	1.2	80	10	US-09-867-550-942	Sequence 942, App	604	6	1.2	109	9	US-10-180-549-344	Sequence 344, App
532	6	1.2	82	10	US-09-864-761-37785	Sequence 37785, A	605	6	1.2	109	9	US-10-180-555-344	Sequence 344, App
533	6	1.2	86	10	US-10-092-154-532	Sequence 532, App	606	6	1.2	109	9	US-10-180-559-344	Sequence 344, App
534	6	1.2	86	10	US-09-764-847-532	Sequence 532, App	607	6	1.2	109	9	US-10-181-000-344	Sequence 344, App
535	6	1.2	87	9	US-09-764-872-391	Sequence 391, App	608	6	1.2	109	9	US-10-183-010-344	Sequence 344, App
536	6	1.2	87	9	US-10-083-357-971	Sequence 971, App	609	6	1.2	109	9	US-10-183-012-344	Sequence 344, App
537	6	1.2	87	10	US-09-220-920-115	Sequence 115, App	610	6	1.2	109	9	US-10-184-614-344	Sequence 344, App
538	6	1.2	88	10	US-09-864-761-45546	Sequence 45546, A	611	6	1.2	109	9	US-10-184-623-344	Sequence 344, App
539	6	1.2	91	9	US-09-989-920-205	Sequence 205, App	612	6	1.2	109	9	US-10-184-635-344	Sequence 344, App
540	6	1.2	94	10	US-09-893-737-114	Sequence 114, App	613	6	1.2	109	9	US-10-184-637-344	Sequence 344, App
541	6	1.2	97	9	US-09-925-299-1071	Sequence 1071, App	614	6	1.2	109	9	US-10-184-646-344	Sequence 344, App
542	6	1.2	97	9	US-09-925-299-1195	Sequence 1195, App	615	6	1.2	109	9	US-10-184-647-344	Sequence 344, App
543	6	1.2	97	10	US-09-925-299-1071	Sequence 1071, App	616	6	1.2	109	9	US-10-184-652-344	Sequence 344, App
544	6	1.2	105	9	US-09-925-299-1195	Sequence 1195, App	617	6	1.2	109	9	US-10-187-594-344	Sequence 344, App
545	6	1.2	105	9	US-09-986-480-231	Sequence 231, App	618	6	1.2	109	9	US-10-187-596-344	Sequence 344, App
546	6	1.2	106	10	US-09-864-761-40438	Sequence 40438, A	619	6	1.2	109	9	US-10-187-745-344	Sequence 344, App
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ALIGNMENTS

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US-09-978-295A-196

Sequence 196, Application US/0978295A

Patent No. US20020156006A1

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APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PFC11
CURRENT APPLICATION NUMBER: US/09/978,295A

CURRENT FILING DATE: 2001-10-15
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;; APPLICANT: Quon, Diana Hom
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Best Local Similarity 100.0%; Pred. No. 0;
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QY 301 IVDGTTLLRLPKQKFDVNEAVARASLIPESDGFMTGSOLACTNSETPMSPYPKISI 360
D 301 IVDGTTLLRLPKQKFDVNEAVARASLIPESDGFMTGSOLACTNSETPMSPYPKISI 360
QY 361 YLRDENSRSRFRITLLPOLYIQPMWAGLNYECYRFGISPSSTNALIVATWMEGYVIFD 420
D 361 YLRDENSRSRFRITLLPOLYIQPMWAGLNYECYRFGISPSSTNALIVATWMEGYVIFD 420
QY 421 RAQRVGAAPPCAEIAGAAVSEISGPESTBVSANCYPAQSLSPILIMYSYALMSVCG 480
D 421 RAQRVGAAPPCAEIAGAAVSEISGPESTBVSANCYPAQSLSPILIMYSYALMSVCG 480
QY 481 AILVLIVLILLPFRCORPRDPEVNVDESSLVRRMK 518
D 481 AILVLIVLILLPFRCORPRDPEVNVDESSLVRRMK 518

RESULT 3
US-09-978-697-196
Sequence 196, Application US/0978697
Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
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APPLICANT: Gerber, Hanspeter
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APPLICANT: Goddard, Audrey
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APPLICANT: Grimaldi, J. Christopher
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APPLICANT: Gurney, Austin L.
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APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC27
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 518; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 181 FESENFPLPGIKNNIGILGAYATLAKRSSLETFFPSLVTOANIPIVFSQMOCAGLIPA 240
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QY 301 IVSGTTLRLPKQVPAAVEAVARASLIPESDGFMTGSQLCWNTNSEPMWYFPKIST 360
DB 301 IVSGTTLRLPKQVPAAVEAVARASLIPESDGFMTGSQLCWNTNSEPMWYFPKIST 360

QY 361 YLNDENSSRSFRITILLPOLYIQPMGAGLNYECYRGISBPTNALVIGATVMEGFYIIPD 420
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QY 421 RAQKRVGFASPQAEIAGAAVSEISGPFSTEDVASCNCPQOSISEPILMTVSTALMSVCG 480
DB 421 RAQKRVGFASPQAEIAGAAVSEISGPFSTEDVASCNCPQOSISEPILMTVSTALMSVCG 480

CY 481 ALIVLIVLILPFCORRPRDEPVNDESSIVRRMK 518
Db 481 ALIVLIVLILPFCORRPRDEPVNDESSIVRRMK 518

RESULT 4

US-09-978-192A-196
; Sequence 196, Application US/0978192A
; Patent No. US2002017753A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Bostein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
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; APPLICANT: Kuo, Sophia S.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secretd and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C9
; CURRENT APPLICATION NUMBER: US/09/978,192A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
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Query Match 100.0%; Score 518; DB 9; length 518;
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Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
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; APPLICANT: Shelton, David L.
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; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
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; TITLE OF INVENTION: Acids Encoding the Same
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; PRIOR FILING DATE: 1997-10-17
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3	PRIOR FILING DATE: 1997-11-13
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5	PRIOR FILING DATE: 1997-11-21
6	PRIOR APPLICATION NUMBER: 60/077450
7	PRIOR FILING DATE: 1998-03-10
8	PRIOR APPLICATION NUMBER: 60/077632
9	PRIOR FILING DATE: 1998-03-11
10	PRIOR APPLICATION NUMBER: 60/077641
11	PRIOR FILING DATE: 1998-03-11
12	PRIOR APPLICATION NUMBER: 60/077649
13	PRIOR FILING DATE: 1998-03-11
14	PRIOR APPLICATION NUMBER: 60/078866
15	PRIOR FILING DATE: 1998-03-12
16	PRIOR APPLICATION NUMBER: 60/078804
17	PRIOR FILING DATE: 1998-03-13
18	PRIOR APPLICATION NUMBER: 60/078866
19	PRIOR FILING DATE: 1998-03-20
20	PRIOR APPLICATION NUMBER: 60/078936
21	PRIOR FILING DATE: 1998-03-20
22	PRIOR APPLICATION NUMBER: 60/078910
23	PRIOR FILING DATE: 1998-03-20
24	PRIOR APPLICATION NUMBER: 60/078939
25	PRIOR FILING DATE: 1998-03-20
26	PRIOR APPLICATION NUMBER: 60/079294
27	PRIOR FILING DATE: 1998-03-25
28	PRIOR APPLICATION NUMBER: 60/079656
29	PRIOR FILING DATE: 1998-03-26
30	PRIOR APPLICATION NUMBER: 60/079664
31	PRIOR FILING DATE: 1998-03-27
32	PRIOR APPLICATION NUMBER: 60/079689
33	PRIOR FILING DATE: 1998-03-27
34	PRIOR APPLICATION NUMBER: 60/079683
35	PRIOR FILING DATE: 1998-03-27
36	PRIOR APPLICATION NUMBER: 60/079728
37	PRIOR FILING DATE: 1998-03-27
38	PRIOR APPLICATION NUMBER: 60/079786
39	PRIOR FILING DATE: 1998-03-27
40	PRIOR APPLICATION NUMBER: 60/079920
41	PRIOR FILING DATE: 1998-03-31
42	PRIOR APPLICATION NUMBER: 60/080107
43	PRIOR FILING DATE: 1998-03-31
44	PRIOR APPLICATION NUMBER: 60/079923
45	PRIOR FILING DATE: 1998-03-30
46	PRIOR APPLICATION NUMBER: 60/080105
47	PRIOR FILING DATE: 1998-03-31
48	PRIOR APPLICATION NUMBER: 60/080107
49	PRIOR FILING DATE: 1998-03-31
50	PRIOR APPLICATION NUMBER: 60/080155
51	PRIOR FILING DATE: 1998-03-31
52	PRIOR APPLICATION NUMBER: 60/080194
53	PRIOR FILING DATE: 1998-03-31
54	PRIOR APPLICATION NUMBER: 60/080337
55	PRIOR FILING DATE: 1998-04-01
56	PRIOR APPLICATION NUMBER: 60/080328
57	PRIOR FILING DATE: 1998-04-01
58	PRIOR APPLICATION NUMBER: 60/080333
59	PRIOR FILING DATE: 1998-04-01
60	PRIOR APPLICATION NUMBER: 60/080334
61	PRIOR FILING DATE: 1998-04-01
62	PRIOR APPLICATION NUMBER: 60/081071
63	PRIOR FILING DATE: 1998-04-08
64	PRIOR APPLICATION NUMBER: 60/081049
65	PRIOR FILING DATE: 1998-04-08
66	PRIOR APPLICATION NUMBER: 60/081071
67	PRIOR FILING DATE: 1998-04-08
68	PRIOR APPLICATION NUMBER: 60/081195
69	PRIOR FILING DATE: 1998-04-08
70	PRIOR APPLICATION NUMBER: 60/081203
71	PRIOR FILING DATE: 1998-04-09
72	PRIOR APPLICATION NUMBER: 60/081229
73	PRIOR FILING DATE: 1998-04-09
74	PRIOR APPLICATION NUMBER: 60/081955
75	PRIOR FILING DATE: 1998-04-15

PRIOR APPLICATION NUMBER: 60/081817	PRIOR FILING DATE: 1998-04-15	PRIOR APPLICATION NUMBER: 60/081819	PRIOR FILING DATE: 1998-04-15	PRIOR APPLICATION NUMBER: 60/081952	PRIOR FILING DATE: 1998-04-15	PRIOR APPLICATION NUMBER: 60/081838	PRIOR FILING DATE: 1998-04-15	PRIOR APPLICATION NUMBER: 60/082568	PRIOR FILING DATE: 1998-04-15	PRIOR APPLICATION NUMBER: 60/082569	PRIOR FILING DATE: 1998-04-21	PRIOR APPLICATION NUMBER: 60/082704	PRIOR FILING DATE: 1998-04-22	PRIOR APPLICATION NUMBER: 60/082804	PRIOR FILING DATE: 1998-04-22	PRIOR APPLICATION NUMBER: 60/082700	PRIOR FILING DATE: 1998-04-22	PRIOR APPLICATION NUMBER: 60/082797	PRIOR FILING DATE: 1998-04-22	PRIOR APPLICATION NUMBER: 60/082766	PRIOR FILING DATE: 1998-04-23	PRIOR APPLICATION NUMBER: 60/083336	PRIOR FILING DATE: 1998-04-23	PRIOR APPLICATION NUMBER: 60/083322	PRIOR FILING DATE: 1998-04-28	PRIOR APPLICATION NUMBER: 60/083392	PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083495	PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083496	PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083499	PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083545	PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083554	PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083558	PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083559	PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083500	PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083742	PRIOR FILING DATE: 1998-04-30	PRIOR APPLICATION NUMBER: 60/084411	PRIOR FILING DATE: 1998-05-06	PRIOR APPLICATION NUMBER: 60/084414	PRIOR FILING DATE: 1998-05-06	PRIOR APPLICATION NUMBER: 60/084633	PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/084640	PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/084622	PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/084643	PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/084599	PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/084600	PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/085339	PRIOR FILING DATE: 1998-05-13	PRIOR APPLICATION NUMBER: 60/085388	PRIOR FILING DATE: 1998-05-13	PRIOR APPLICATION NUMBER: 60/085322	PRIOR FILING DATE: 1998-05-13	PRIOR APPLICATION NUMBER: 60/085582	PRIOR FILING DATE: 1998-05-13	PRIOR APPLICATION NUMBER: 60/085582	PRIOR FILING DATE: 1998-05-13
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085700
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085689
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085579
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085580
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 518; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALRALLLPLAQMILRAABELAPAPFTLLPLRVAAATNRVAPTPGPTPAERHADGL 60
DB 1 MGALRALLLPLAQMILRAABELAPAPFTLLPLRVAAATNRVAPTPGPTPAERHADGL 60

QY 61 ALALEPALASPAGANFLAMVDNLQDSDRGYLEMLIGTPQKQLIIVDGGSNFAVAG 120
DB 61 ALALEPALASPAGANFLAMVDNLQDSDRGYLEMLIGTPQKQLIIVDGGSNFAVAG 120

QY 121 TPHSYIDYPTTSSSTYRSKGFDTVTKYQSGWTGFGEDLVITPKGFNTSFLVNIATI 180
DB 121 TPHSYIDYPTTSSSTYRSKGFDTVTKYQSGWTGFGEDLVITPKGFNTSFLVNIATI 180

QY 181 FESENFPLPGIKMNGIILGAYATLAKPSSSETFPDSLVTQANIPIVFSMOCAGLPLVA 240
DB 181 FESENFPLPGIKMNGIILGAYATLAKPSSSETFPDSLVTQANIPIVFSMOCAGLPLVA 240

QY 241 GSGTNGGSLVUGTEPSTLYKGDITWTPIKEEYVQIEILKIEIGQSINLDCRENNAKA 300
DB 241 GSGTNGGSLVUGTEPSTLYKGDITWTPIKEEYVQIEILKIEIGQSINLDCRENNAKA 300

QY 301 IVDGTTLLRLPQKVFDAVNEAVARASLIPERSDGFWTGSOLACTNSETPMSPFKISI 360
DB 301 IVDGTTLLRLPQKVFDAVNEAVARASLIPERSDGFWTGSOLACTNSETPMSPFKISI 360

QY 361 YLRDENSRSRFRITLLPQLYIQPMWAGLNECYRFGISPSFTNALVIGATWMEGYVIFD 420
DB 361 YLRDENSRSRFRITLLPQLYIQPMWAGLNECYRFGISPSFTNALVIGATWMEGYVIFD 420

QY 421 RAQKRVGPAAPCAEIAAGAVSEISGPESTEDVASCNCPAOSLSPEPILMIYSYALMSYCG 480
DB 421 RAQKRVGPAAPCAEIAAGAVSEISGPESTEDVASCNCPAOSLSPEPILMIYSYALMSYCG 480

QY 481 ALLVLVILVLLLPFCORRPRDPEVYNDESSLVRRHK 518
DB 481 ALLVLVILVLLLPFCORRPRDPEVYNDESSLVRRHK 518

RESULT 6
US-09-978-189-196
; Sequence 196, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botsstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gettisen, Mary B.
; APPLICANT: Goddard, Audrey

;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Hillan, Kenneth J.
;; APPLICANT: Kijavlin, Ivar J.
;; APPLICANT: Kuo, Sophia S.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James;
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Shelton, David L.
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumes, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; TITLE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: P2630PIC7
;; CURRENT APPLICATION NUMBER: US/09/978,189
;; CURRENT FILING DATE: 2001-10-15
;; PRIOR APPLICATION NUMBER: 09/918585
;; PRIOR FILING DATE: 2001-07-30
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/064249
;; PRIOR FILING DATE: 1997-11-03
;; PRIOR APPLICATION NUMBER: 60/065311
;; PRIOR FILING DATE: 1997-11-13
;; PRIOR APPLICATION NUMBER: 60/066364
;; PRIOR FILING DATE: 1997-11-21
;; PRIOR APPLICATION NUMBER: 60/07450
;; PRIOR FILING DATE: 1998-03-10
;; PRIOR APPLICATION NUMBER: 60/07632
;; PRIOR FILING DATE: 1998-03-11
;; PRIOR APPLICATION NUMBER: 60/07641
;; PRIOR FILING DATE: 1998-03-11
;; PRIOR APPLICATION NUMBER: 60/07649
;; PRIOR FILING DATE: 1998-03-11
;; PRIOR APPLICATION NUMBER: 60/07791
;; PRIOR FILING DATE: 1998-03-12
;; PRIOR APPLICATION NUMBER: 60/078004
;; PRIOR FILING DATE: 1998-03-13
;; PRIOR APPLICATION NUMBER: 60/07886
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/078936
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;; PRIOR APPLICATION NUMBER: 60/079656
;; PRIOR FILING DATE: 1998-03-26
;; PRIOR APPLICATION NUMBER: 60/079664
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;; PRIOR APPLICATION NUMBER: 60/079689
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;; PRIOR APPLICATION NUMBER: 60/079786
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/079920
;; PRIOR FILING DATE: 1998-03-30
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;; PRIOR APPLICATION NUMBER: 60/080105
;; PRIOR FILING DATE: 1998-03-31
;; PRIOR APPLICATION NUMBER: 60/080107
;; PRIOR FILING DATE: 1998-03-31
;; PRIOR APPLICATION NUMBER: 60/080165

;; PRIOR FILING DATE: 1998-03-31
;; PRIOR APPLICATION NUMBER: 60/080194
;; PRIOR FILING DATE: 1998-03-31
;; PRIOR APPLICATION NUMBER: 60/080327
;; PRIOR FILING DATE: 1998-04-01
;; PRIOR APPLICATION NUMBER: 60/080328
;; PRIOR FILING DATE: 1998-04-01
;; PRIOR APPLICATION NUMBER: 60/080333
;; PRIOR FILING DATE: 1998-04-01
;; PRIOR APPLICATION NUMBER: 60/080334
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;; PRIOR FILING DATE: 1998-04-08
;; PRIOR APPLICATION NUMBER: 60/081071
;; PRIOR FILING DATE: 1998-04-08
;; PRIOR APPLICATION NUMBER: 60/081195
;; PRIOR FILING DATE: 1998-04-08
;; PRIOR APPLICATION NUMBER: 60/081203
;; PRIOR FILING DATE: 1998-04-09
;; PRIOR APPLICATION NUMBER: 60/081229
;; PRIOR FILING DATE: 1998-04-09
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;; PRIOR FILING DATE: 1998-04-15
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;; PRIOR FILING DATE: 1998-04-15
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;; PRIOR APPLICATION NUMBER: 60/082568
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;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/082700
;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/082797
;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/082796
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;; PRIOR APPLICATION NUMBER: 60/083322
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;; PRIOR APPLICATION NUMBER: 60/083392
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;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083496
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083499
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083545
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083554
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083558
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083559
;; PRIOR FILING DATE: 1998-04-29
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;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083742
;; PRIOR FILING DATE: 1998-04-30
;; PRIOR APPLICATION NUMBER: 60/084366
;; PRIOR FILING DATE: 1998-05-05

;; PRIOR APPLICATION NUMBER: 60/084414
;; PRIOR FILING DATE: 1998-05-06
;; PRIOR APPLICATION NUMBER: 60/084441
;; PRIOR FILING DATE: 1998-05-06
;; PRIOR APPLICATION NUMBER: 60/084637
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084639
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084640
;; PRIOR FILING DATE: 1998-05-07
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;; PRIOR APPLICATION NUMBER: 60/084627
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084643
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/085339
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085338
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085323
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085582
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085700
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085689
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085579
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085580
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 518; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MGALRALLLPLLAQWILRALAPELAPAFLLPLVAATNRVVAFTPGPTPARHADGL 60
Db 1 MGALRALLLPLLAQWILRALAPELAPAFLLPLVAATNRVVAFTPGPTPARHADGL 60
Oy 61 ALALEPALASPAGANPLAMVDNIQDSDGRGYYLEMLIGTPPOKLQILVDTGSSNFAVAG 120
Db 61 ALALEPALASPAGANPLAMVDNIQDSDGRGYYLEMLIGTPPOKLQILVDTGSSNFAVAG 120
Oy 121 TPHSVITDVPPTERSSTYRSKGPVTVKYQGSWTGFVGEDLVITIPGFNTSPFVNATI 180
Db 121 TPHSVITDVPPTERSSTYRSKGPVTVKYQGSWTGFVGEDLVITIPGFNTSPFVNATI 180
Oy 181 FESSENFPLPGIKMNGIIGLAATYATLAKPSSSLETFPDSLVTOANI PNVSQMCGAGLPVA 240
Db 181 FESSENFPLPGIKMNGIIGLAATYATLAKPSSSLETFPDSLVTOANI PNVSQMCGAGLPVA 240
Oy 241 GSGTNGGSLVIGIEPSLYKGDWYTPIKEWYQIEILKIEIGQSINLDCREYNADKA 300
Db 241 GSGTNGGSLVIGIEPSLYKGDWYTPIKEWYQIEILKIEIGQSINLDCREYNADKA 300
Oy 301 IVDSGTTLRLPQKVFDAVVAVARASLIPFSGFMTGSLACWTSETWSTYFPKISI 360
Db 301 IVDSGTTLRLPQKVFDAVVAVARASLIPFSGFMTGSLACWTSETWSTYFPKISI 360
Oy 361 YLRDSSRSFRITLIPOLYIQPMMGAGLNEYCRFGISPTNALVIGATMEGFYIFD 420
Db 361 YLRDSSRSFRITLIPOLYIQPMMGAGLNEYCRFGISPTNALVIGATMEGFYIFD 420
Oy 421 RAQKRVGFPAASPCEAIGAAVSEISGPSTEDVANSNCVPAQSLSEPLIMIVSYALMSVCG 480

Db 421 RAQKRVGAAPCAEIAAGAAVSEISGPFSTEDVASCNCPAQSLSSEPIIMIVSYALMSVCG 480
 QY 481 AILLVILVLLLPFCORRRPRDPEVNVDESSLVHRWK 518
 Db 481 AILLVILVLLLPFCORRRPRDPEVNVDESSLVHRWK 518

RESULT 7

US-10-174-590-72

; Sequence 72, Application US/10174590
 ; Publication No. US20030008352A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Matanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3430R1C42
 ; CURRENT APPLICATION NUMBER: US/10/174,590
 ; CURRENT FILING DATE: 2002-06-18
 ; Prior application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 72
 ; LENGTH: 518
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 ; US-10-174-590-72

Query Match 100.0%; Score 518; DB 9; Length 518;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLLAQWILRAAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
 Db 1 MGALARALLPLLAQWILRAAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
 QY 61 ALALEPALASPAGANFLAMVDNIQDGRGYLEMLIGTPPKQLQILVDTGSSNFAVAG 120
 Db 61 ALALEPALASPAGANFLAMVDNIQDGRGYLEMLIGTPPKQLQILVDTGSSNFAVAG 120
 QY 121 TPHSYIDTYPTDTERSSYTRSKGPDVTYKYGSMWTFVGEDLVITIPKGFNTSFLVNIATI 180
 Db 121 TPHSYIDTYPTDTERSSYTRSKGPDVTYKYGSMWTFVGEDLVITIPKGFNTSFLVNIATI 180
 QY 181 FESNPFPLPGIKMNGILGLAVATLAKPSSSLETFPDSLVTOANI PNVSQMCGAGLPVA 240
 Db 181 FESNPFPLPGIKMNGILGLAVATLAKPSSSLETFPDSLVTOANI PNVSQMCGAGLPVA 240
 QY 241 GSGTNGSLVIGIEPSLYKGDIMWTPIKEWYYOIEILKLEIGGOSLNDCREYNADKA 300
 Db 241 GSGTNGSLVIGIEPSLYKGDIMWTPIKEWYYOIEILKLEIGGOSLNDCREYNADKA 300
 QY 301 IVDSGTTLLRLPQKVPDAVVAVARASLIPEFSDGFWTGSOLACWNTSETPMSYFPKISI 360
 Db 301 IVDSGTTLLRLPQKVPDAVVAVARASLIPEFSDGFWTGSOLACWNTSETPMSYFPKISI 360
 QY 361 YLRDENSRSRFRITILPOLYIQPMGAGLNECYRFGISSTNALVIGATVMEGFYIFD 420
 Db 361 YLRDENSRSRFRITILPOLYIQPMGAGLNECYRFGISSTNALVIGATVMEGFYIFD 420
 QY 421 RAQKRVGAAPCAEIAAGAAVSEISGPFSTEDVASCNCPAQSLSSEPIIMIVSYALMSVCG 480
 Db 421 RAQKRVGAAPCAEIAAGAAVSEISGPFSTEDVASCNCPAQSLSSEPIIMIVSYALMSVCG 480

QY 481 AILLVILVLLLPFCORRRPRDPEVNVDESSLVHRWK 518
 Db 481 AILLVILVLLLPFCORRRPRDPEVNVDESSLVHRWK 518

RESULT 8

US-10-176-758-72

; Sequence 72, Application US/10176758
 ; Publication No. US20030008353A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Matanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3430R1C104
 ; CURRENT APPLICATION NUMBER: US/10/176,758
 ; CURRENT FILING DATE: 2002-06-21
 ; Prior application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 72
 ; LENGTH: 518
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 ; US-10-176-758-72

Query Match 100.0%; Score 518; DB 9; Length 518;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLLAQWILRAAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
 Db 1 MGALARALLPLLAQWILRAAPAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
 QY 61 ALALEPALASPAGANFLAMVDNIQDGRGYLEMLIGTPPKQLQILVDTGSSNFAVAG 120
 Db 61 ALALEPALASPAGANFLAMVDNIQDGRGYLEMLIGTPPKQLQILVDTGSSNFAVAG 120
 QY 121 TPHSYIDTYPTDTERSSYTRSKGPDVTYKYGSMWTFVGEDLVITIPKGFNTSFLVNIATI 180
 Db 121 TPHSYIDTYPTDTERSSYTRSKGPDVTYKYGSMWTFVGEDLVITIPKGFNTSFLVNIATI 180
 QY 181 FESNPFPLPGIKMNGILGLAVATLAKPSSSLETFPDSLVTOANI PNVSQMCGAGLPVA 240
 Db 181 FESNPFPLPGIKMNGILGLAVATLAKPSSSLETFPDSLVTOANI PNVSQMCGAGLPVA 240
 QY 241 GSGTNGSLVIGIEPSLYKGDIMWTPIKEWYYOIEILKLEIGGOSLNDCREYNADKA 300
 Db 241 GSGTNGSLVIGIEPSLYKGDIMWTPIKEWYYOIEILKLEIGGOSLNDCREYNADKA 300
 QY 301 IVDSGTTLLRLPQKVPDAVVAVARASLIPEFSDGFWTGSOLACWNTSETPMSYFPKISI 360
 Db 301 IVDSGTTLLRLPQKVPDAVVAVARASLIPEFSDGFWTGSOLACWNTSETPMSYFPKISI 360
 QY 361 YLRDENSRSRFRITILPOLYIQPMGAGLNECYRFGISSTNALVIGATVMEGFYIFD 420
 Db 361 YLRDENSRSRFRITILPOLYIQPMGAGLNECYRFGISSTNALVIGATVMEGFYIFD 420
 QY 421 RAQKRVGAAPCAEIAAGAAVSEISGPFSTEDVASCNCPAQSLSSEPIIMIVSYALMSVCG 480
 Db 421 RAQKRVGAAPCAEIAAGAAVSEISGPFSTEDVASCNCPAQSLSSEPIIMIVSYALMSVCG 480
 QY 481 AILLVILVLLLPFCORRRPRDPEVNVDESSLVHRWK 518
 Db 481 AILLVILVLLLPFCORRRPRDPEVNVDESSLVHRWK 518

RESULT 9

```
US-10-175-737-72
; Sequence 72, Application US/10175737
; Publication No. US2003001353A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C50
; CURRENT APPLICATION NUMBER: US/10/175,737
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-737-72
```

Query Match 100.0%; Score 518; DB 9; Length 518;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MGALARALLPLLAQWLLRAPELAPAPFTLPLRVAATNRVAVPTPGPTPARHADGL 60
DB 1 MGALARALLPLLAQWLLRAPELAPAPFTLPLRVAATNRVAVPTPGPTPARHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLEMLIGTPPOKLQILVDGSSNFAVAG 120
DB 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLEMLIGTPPOKLQILVDGSSNFAVAG 120
QY 121 TPHSYIDTYFPTERSSTYRSKGFDTVKYTOGSMTGFEVGEDLVITPKGFNTSFLVNIATI 180
DB 121 TPHSYIDTYFPTERSSTYRSKGFDTVKYTOGSMTGFEVGEDLVITPKGFNTSFLVNIATI 180
QY 181 FESENFPLPGIKMNGILGLAVATLAKPSSSLFTFDSLVTOANIPNVFSMOMCAGLPVA 240
DB 181 FESENFPLPGIKMNGILGLAVATLAKPSSSLFTFDSLVTOANIPNVFSMOMCAGLPVA 240
QY 241 GSGTNGGSLVIGIEPSLYKGDWYTPPIKEWYQIEILKLEIGGOSLNLDCREYNADKA 300
DB 241 GSGTNGGSLVIGIEPSLYKGDWYTPPIKEWYQIEILKLEIGGOSLNLDCREYNADKA 300
QY 301 IVDGTTLLRLPQKVFDAVVAARASLIPEFSDGFWTGSOLACWTNSETPMSYFPKISI 360
DB 301 IVDGTTLLRLPQKVFDAVVAARASLIPEFSDGFWTGSOLACWTNSETPMSYFPKISI 360
QY 361 YLRDENSRSFRITILLPOLYIQPMGAGLNEYCYRFGISPSNTALVIGATVMEGFYIFD 420
DB 361 YLRDENSRSFRITILLPOLYIQPMGAGLNEYCYRFGISPSNTALVIGATVMEGFYIFD 420
QY 421 RAQKRVGPAASPCAEIAGAASEISGPESTEDVANSNCVPAOSLSEPIILMIVSYALMSVCG 480
DB 421 RAQKRVGPAASPCAEIAGAASEISGPESTEDVANSNCVPAOSLSEPIILMIVSYALMSVCG 480
QY 481 AILLVILVILLPFRCCRRPRDPEVNVDESSLVRRHK 518
DB 481 AILLVILVILLPFRCCRRPRDPEVNVDESSLVRRHK 518
```

RESULT 10

US-10-173-706-72

```
US-10-173-706-72
; Sequence 72, Application US/10173706
; Publication No. US2003002293A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C7
; CURRENT APPLICATION NUMBER: US/10/173,706
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-173-706-72
```

Query Match 100.0%; Score 518; DB 9; Length 518;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MGALARALLPLLAQWLLRAPELAPAPFTLPLRVAATNRVAVPTPGPTPARHADGL 60
DB 1 MGALARALLPLLAQWLLRAPELAPAPFTLPLRVAATNRVAVPTPGPTPARHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLEMLIGTPPOKLQILVDGSSNFAVAG 120
DB 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLEMLIGTPPOKLQILVDGSSNFAVAG 120
QY 121 TPHSYIDTYFPTERSSTYRSKGFDTVKYTOGSMTGFEVGEDLVITPKGFNTSFLVNIATI 180
DB 121 TPHSYIDTYFPTERSSTYRSKGFDTVKYTOGSMTGFEVGEDLVITPKGFNTSFLVNIATI 180
QY 181 FESENFPLPGIKMNGILGLAVATLAKPSSSLFTFDSLVTOANIPNVFSMOMCAGLPVA 240
DB 181 FESENFPLPGIKMNGILGLAVATLAKPSSSLFTFDSLVTOANIPNVFSMOMCAGLPVA 240
QY 241 GSGTNGGSLVIGIEPSLYKGDWYTPPIKEWYQIEILKLEIGGOSLNLDCREYNADKA 300
DB 241 GSGTNGGSLVIGIEPSLYKGDWYTPPIKEWYQIEILKLEIGGOSLNLDCREYNADKA 300
QY 301 IVDGTTLLRLPQKVFDAVVAARASLIPEFSDGFWTGSOLACWTNSETPMSYFPKISI 360
DB 301 IVDGTTLLRLPQKVFDAVVAARASLIPEFSDGFWTGSOLACWTNSETPMSYFPKISI 360
QY 361 YLRDENSRSFRITILLPOLYIQPMGAGLNEYCYRFGISPSNTALVIGATVMEGFYIFD 420
DB 361 YLRDENSRSFRITILLPOLYIQPMGAGLNEYCYRFGISPSNTALVIGATVMEGFYIFD 420
QY 421 RAQKRVGPAASPCAEIAGAASEISGPESTEDVANSNCVPAOSLSEPIILMIVSYALMSVCG 480
DB 421 RAQKRVGPAASPCAEIAGAASEISGPESTEDVANSNCVPAOSLSEPIILMIVSYALMSVCG 480
QY 481 AILLVILVILLPFRCCRRPRDPEVNVDESSLVRRHK 518
DB 481 AILLVILVILLPFRCCRRPRDPEVNVDESSLVRRHK 518
```

RESULT 11

```
US-10-175-738-72
; Sequence 72, Application US/10175738
; Publication No. US20030022294A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC45
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/10/175,738
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-738-72

Query Match          100.0%; Score 518; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLLAQWLRAAPBELAPAPFTPLRVAAATNRVVAPTPGPTPARRHADGL 60
DB 1 MGALARALLPLLAQWLRAAPBELAPAPFTPLRVAAATNRVVAPTPGPTPARRHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYYLEMLIGTPPOKLQILVDTGSSNFAVAG 120
DB 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYYLEMLIGTPPOKLQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYPDTERSSSTYRSKGFVTVKYTGQSWTGFVGBDLVTIIPKGFNTSFLVNIATI 180
DB 121 TPHSYIDTYPDTERSSSTYRSKGFVTVKYTGQSWTGFVGBDLVTIIPKGFNTSFLVNIATI 180
QY 181 PESNFPLPGIKMNGILGLAYATLAKPSSLETFFDSLVTOANI PNVSQMCGAGLPVA 240
DB 181 PESNFPLPGIKMNGILGLAYATLAKPSSLETFFDSLVTOANI PNVSQMCGAGLPVA 240
QY 241 GSGTNGSLVVGIEPSLYKGDIMWTPIKEWYQIEILKLEIGQSLNLDCREYNADKA 300
DB 241 GSGTNGSLVVGIEPSLYKGDIMWTPIKEWYQIEILKLEIGQSLNLDCREYNADKA 300
QY 301 IVDSGTTLLRLPKQVFPDAVVAVARASLIPEFSDGFWTGSQLACTNSETPWSYFPKISI 360
DB 301 IVDSGTTLLRLPKQVFPDAVVAVARASLIPEFSDGFWTGSQLACTNSETPWSYFPKISI 360
QY 361 YLRDENSRSFRITLLPOLYIQPMAGLNECYRFGISPTNALVIGATVMEGFYIFD 420
DB 361 YLRDENSRSFRITLLPOLYIQPMAGLNECYRFGISPTNALVIGATVMEGFYIFD 420
QY 421 RAQKRVGFASPCAEIAGAASEISGPFSTEDVASNCVPAQSISEPIILWISVALMSVCG 480
DB 421 RAQKRVGFASPCAEIAGAASEISGPFSTEDVASNCVPAQSISEPIILWISVALMSVCG 480
QY 481 ALLVLIVLIVLLLPFCORRRPRDPEVVNDDESSLVHRMK 518
DB 481 ALLVLIVLIVLLLPFCORRRPRDPEVVNDDESSLVHRMK 518

RESULT 12
US-10-175-752-72
; Sequence 72, Application US/10175752
; Publication No. US20030022295A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
```

```
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC60
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/10/175,752
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-752-72

Query Match          100.0%; Score 518; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLLAQWLRAAPBELAPAPFTPLRVAAATNRVVAPTPGPTPARRHADGL 60
DB 1 MGALARALLPLLAQWLRAAPBELAPAPFTPLRVAAATNRVVAPTPGPTPARRHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYYLEMLIGTPPOKLQILVDTGSSNFAVAG 120
DB 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYYLEMLIGTPPOKLQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYPDTERSSSTYRSKGFVTVKYTGQSWTGFVGBDLVTIIPKGFNTSFLVNIATI 180
DB 121 TPHSYIDTYPDTERSSSTYRSKGFVTVKYTGQSWTGFVGBDLVTIIPKGFNTSFLVNIATI 180
QY 181 PESNFPLPGIKMNGILGLAYATLAKPSSLETFFDSLVTOANI PNVSQMCGAGLPVA 240
DB 181 PESNFPLPGIKMNGILGLAYATLAKPSSLETFFDSLVTOANI PNVSQMCGAGLPVA 240
QY 241 GSGTNGSLVVGIEPSLYKGDIMWTPIKEWYQIEILKLEIGQSLNLDCREYNADKA 300
DB 241 GSGTNGSLVVGIEPSLYKGDIMWTPIKEWYQIEILKLEIGQSLNLDCREYNADKA 300
QY 301 IVDSGTTLLRLPKQVFPDAVVAVARASLIPEFSDGFWTGSQLACTNSETPWSYFPKISI 360
DB 301 IVDSGTTLLRLPKQVFPDAVVAVARASLIPEFSDGFWTGSQLACTNSETPWSYFPKISI 360
QY 361 YLRDENSRSFRITLLPOLYIQPMAGLNECYRFGISPTNALVIGATVMEGFYIFD 420
DB 361 YLRDENSRSFRITLLPOLYIQPMAGLNECYRFGISPTNALVIGATVMEGFYIFD 420
QY 421 RAQKRVGFASPCAEIAGAASEISGPFSTEDVASNCVPAQSISEPIILWISVALMSVCG 480
DB 421 RAQKRVGFASPCAEIAGAASEISGPFSTEDVASNCVPAQSISEPIILWISVALMSVCG 480
QY 481 ALLVLIVLIVLLLPFCORRRPRDPEVVNDDESSLVHRMK 518
DB 481 ALLVLIVLIVLLLPFCORRRPRDPEVVNDDESSLVHRMK 518

RESULT 13
US-10-176-482-72
; Sequence 72, Application US/10176482
; Publication No. US20030022296A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
```

```

; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Matanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C70
; CURRENT APPLICATION NUMBER: US/10/176,482
; PRIOR APPLICATION removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-482-72

```

Query Match 100.0%; Score 518; DB 9; Length 518;

Best Local Similarity 100.0%; Pred. No. 0; Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MGALRALLLPLAQLRAPELAPAPFTPLRVAATNRVVAFTPGPTPAERHADGL 60
D 1 MGALRALLLPLAQLRAPELAPAPFTPLRVAATNRVVAFTPGPTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLEMLIGTPPKQLIIVDTGSSNFAVAG 120
D 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLEMLIGTPPKQLIIVDTGSSNFAVAG 120
QY 121 TPHSYIDTYPTERSSTYRSKGFDTVTKYQGSWTGFGVGEDLVTTIPKGFNTSFLVNIATI 180
D 121 TPHSYIDTYPTERSSTYRSKGFDTVTKYQGSWTGFGVGEDLVTTIPKGFNTSFLVNIATI 180
QY 181 FESENFPLPGIKMNGILGLAVATLAKPSSSLETFPDSLVTOANIINVFSMOMCAGLPVA 240
D 181 FESENFPLPGIKMNGILGLAVATLAKPSSSLETFPDSLVTOANIINVFSMOMCAGLPVA 240
QY 241 GSGTNGSLVIGIEPSLYKGDWYTPIKEWYQIETLKEIGOSLNDCREYNADKA 300
D 241 GSGTNGSLVIGIEPSLYKGDWYTPIKEWYQIETLKEIGOSLNDCREYNADKA 300
QY 301 IVDGGTTLRLPQKVFDAVEAVARASLIPEFSDGFWTGSOLACWTNSETPWSYEPKISI 360
D 301 IVDGGTTLRLPQKVFDAVEAVARASLIPEFSDGFWTGSOLACWTNSETPWSYEPKISI 360
QY 361 YLRDENSRSFRITITLPOLYIQPMGAGLNECYRFGISPSSTNALVIGATVMEGFYVIFD 420
D 361 YLRDENSRSFRITITLPOLYIQPMGAGLNECYRFGISPSSTNALVIGATVMEGFYVIFD 420
QY 421 RAQKRVGFPAASPCAEIAGAAVSEISGPFSTEDVASCNCPAOSLSEPTLIMIVSYALMSVCG 480
D 421 RAQKRVGFPAASPCAEIAGAAVSEISGPFSTEDVASCNCPAOSLSEPTLIMIVSYALMSVCG 480
QY 481 AILLVLIVLLLPFCQRRPRDPEVNDSSLVHRMK 518
D 481 AILLVLIVLLLPFCQRRPRDPEVNDSSLVHRMK 518

```

RESULT 14
US-10-176-757-72

; Sequence 72, Application US/10176757
; Publication No. US2003002297A1

; GENERAL INFORMATION:

```

; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria

```

```

; APPLICANT: Matanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C86
; CURRENT APPLICATION NUMBER: US/10/176,757
; PRIOR APPLICATION removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-757-72

```

Query Match 100.0%; Score 518; DB 9; Length 518;

Best Local Similarity 100.0%; Pred. No. 0; Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MGALRALLLPLAQLRAPELAPAPFTPLRVAATNRVVAFTPGPTPAERHADGL 60
D 1 MGALRALLLPLAQLRAPELAPAPFTPLRVAATNRVVAFTPGPTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLEMLIGTPPKQLIIVDTGSSNFAVAG 120
D 61 ALALEPALASPAGANFLAMVDNLQDSDGRGYLEMLIGTPPKQLIIVDTGSSNFAVAG 120
QY 121 TPHSYIDTYPTERSSTYRSKGFDTVTKYQGSWTGFGVGEDLVTTIPKGFNTSFLVNIATI 180
D 121 TPHSYIDTYPTERSSTYRSKGFDTVTKYQGSWTGFGVGEDLVTTIPKGFNTSFLVNIATI 180
QY 181 FESENFPLPGIKMNGILGLAVATLAKPSSSLETFPDSLVTOANIINVFSMOMCAGLPVA 240
D 181 FESENFPLPGIKMNGILGLAVATLAKPSSSLETFPDSLVTOANIINVFSMOMCAGLPVA 240
QY 241 GSGTNGSLVIGIEPSLYKGDWYTPIKEWYQIETLKEIGOSLNDCREYNADKA 300
D 241 GSGTNGSLVIGIEPSLYKGDWYTPIKEWYQIETLKEIGOSLNDCREYNADKA 300
QY 301 IVDGGTTLRLPQKVFDAVEAVARASLIPEFSDGFWTGSOLACWTNSETPWSYEPKISI 360
D 301 IVDGGTTLRLPQKVFDAVEAVARASLIPEFSDGFWTGSOLACWTNSETPWSYEPKISI 360
QY 361 YLRDENSRSFRITITLPOLYIQPMGAGLNECYRFGISPSSTNALVIGATVMEGFYVIFD 420
D 361 YLRDENSRSFRITITLPOLYIQPMGAGLNECYRFGISPSSTNALVIGATVMEGFYVIFD 420
QY 421 RAQKRVGFPAASPCAEIAGAAVSEISGPFSTEDVASCNCPAOSLSEPTLIMIVSYALMSVCG 480
D 421 RAQKRVGFPAASPCAEIAGAAVSEISGPFSTEDVASCNCPAOSLSEPTLIMIVSYALMSVCG 480
QY 481 AILLVLIVLLLPFCQRRPRDPEVNDSSLVHRMK 518
D 481 AILLVLIVLLLPFCQRRPRDPEVNDSSLVHRMK 518

```

RESULT 15
US-10-176-913-72

; Sequence 72, Application US/10176913
; Publication No. US2003002298A1

; GENERAL INFORMATION:

```

; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Matanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin

```


TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C66
CURRENT APPLICATION NUMBER: US/10/176,913
CURRENT FILING DATE: 2002-06-20
Prior Application removed - See file wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 72
LENGTH: 518
TYPE: PRT
ORGANISM: Homo Sapien
US-10-176-913-72

Query Match 100.0%; Score 518; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLAOWLIRAPBELAPAPFTPLRYAATNRVVAFTPGGTPAERHADGL 60
DB 1 MGALARALLPLAOWLIRAPBELAPAPFTPLRYAATNRVVAFTPGGTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSDRGVYLEMLIGTPQKQLIVDTGSSNFAVAG 120
DB 61 ALALEPALASPAGANFLAMVDNLQDSDRGVYLEMLIGTPQKQLIVDTGSSNFAVAG 120
QY 121 TPHSYIDTYPPTERSSTYRSKGFDTVVKYTGSGWTFVGEDLVITPKGFNTSFLVNIATI 180
DB 121 TPHSYIDTYPPTERSSTYRSKGFDTVVKYTGSGWTFVGEDLVITPKGFNTSFLVNIATI 180
QY 181 FESSENFELPGIKMNGIIGLAYATLAKPSSLETFFDSLVTOANIPNVFSMOMCGALPVA 240
DB 181 FESSENFELPGIKMNGIIGLAYATLAKPSSLETFFDSLVTOANIPNVFSMOMCGALPVA 240
QY 241 GSGTNGSLVVGIEPSLYKGDIMWTPIKEEMVYQIEILKLEIGGOSLNLDCREYNADKA 300
DB 241 GSGTNGSLVVGIEPSLYKGDIMWTPIKEEMVYQIEILKLEIGGOSLNLDCREYNADKA 300
QY 301 IVDGTTLLRLPQKVFDAVEAVARASLIPEFSDGFWTGSOLACWTNSETPMYSYFPKISI 360
DB 301 IVDGTTLLRLPQKVFDAVEAVARASLIPEFSDGFWTGSOLACWTNSETPMYSYFPKISI 360
QY 361 YLRDENSRSRFRITILLPOLYIQPMAGAGLNECYRFGISBSTNALVIGATMEGFYVIFD 420
DB 361 YLRDENSRSRFRITILLPOLYIQPMAGAGLNECYRFGISBSTNALVIGATMEGFYVIFD 420
QY 421 RAQRVGFPAASPCAIEGAAYSEISGPSTEDVASCNCPAQSLSBPILMTIVSYALMSYCG 480
DB 421 RAQRVGFPAASPCAIEGAAYSEISGPSTEDVASCNCPAQSLSBPILMTIVSYALMSYCG 480
QY 481 AILLVLLVLLLPFCORRRPRDPEVNDSSLVHRMK 518
DB 481 AILLVLLVLLLPFCORRRPRDPEVNDSSLVHRMK 518

Search completed: April 1, 2003, 11:50:44
Job time : 36 secs

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 1, 2003, 11:41:59 ; Search time 46 Seconds
(without alignments)
1082.557 Million cell updates/sec

Title: US-09-668-314C-2
Perfect score: 518
Sequence: 1 MGAARALPLPLAQMQLRA.....RPRDPEVNDSESLVHRHW 518

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR_73:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12	2.3	501	2 A59090	aspartic proteinas
2	9	1.7	319	2 D87087	hypothetical prote
3	9	1.7	863	2 B82654	conserved hypothet
4	8	1.5	166	2 H64131	transcription regu
5	8	1.5	178	2 T09585	high mobility grou
6	8	1.5	202	2 A71935	hypothetical prote
7	8	1.5	205	2 G64646	hypothetical prote
8	8	1.5	237	2 J00729	60K inner-membrane
9	8	1.5	257	2 J02332	ARL protein - cass
10	8	1.5	287	2 G96659	protein F2K11.24 (
11	8	1.5	303	2 H75528	conserved hypothet
12	8	1.5	318	2 B95844	probable sugar ABC
13	8	1.5	319	2 AG0742	high-affinity zinc
14	8	1.5	323	1 PRLJHD	proteinase (EC 3.4
15	8	1.5	327	2 T42999	ethanolamine-phosp
16	8	1.5	340	1 PEIKL	polyporopepsin (EC
17	8	1.5	352	2 C72748	probable sun prote
18	8	1.5	364	2 D96973	spore germination
19	8	1.5	365	2 T37720	ethanolamine-phosp
20	8	1.5	366	2 G65119	hypothetical 40.4
21	8	1.5	393	2 B85992	probable transport
22	8	1.5	399	2 F91146	probable transport
23	8	1.5	449	2 B96676	hypothetical prote
24	8	1.5	472	2 JC7626	amino acid transpo
25	8	1.5	477	2 A35843	lipopolysaccharide
26	8	1.5	478	1 B65173	probable 60K inner
27	8	1.5	548	2 H91208	60 KD inner-membra
28	8	1.5	548	2 B86055	60 KD inner-membra
29	8	1.5	548	2 AF0957	probable membrane

30	8	1.5	580	2 C71182	probable ABC trans
31	8	1.5	637	2 T01961	hypothetical prote
32	8	1.5	904	2 C83030	exoribonuclease RN
33	8	1.5	1247	1 MMHUND	nidogen precursor
34	8	1.5	1622	2 JE0378	DNA (cytosine-5')-
35	7	1.4	88	2 PN0135	pepsin (EC 3.4.23.
36	7	1.4	96	2 D83228	hypothetical prote
37	7	1.4	97	4 S26485	cytochrome P450 21
38	7	1.4	104	2 AH1551	hypothetical prote
39	7	1.4	106	2 H84370	hypothetical prote
40	7	1.4	115	2 T51324	nickel-insertion a
41	7	1.4	119	2 D86800	prophage p13 prote
42	7	1.4	128	1 UQDOR	ubiquitin / riboso
43	7	1.4	131	2 B90553	50S ribosomal prot
44	7	1.4	132	2 AE3445	ATP synthase BME11
45	7	1.4	136	2 E69376	hypothetical prote
46	7	1.4	141	2 D83834	flagellar biosynth
47	7	1.4	149	2 C90885	hypothetical prote
48	7	1.4	149	2 D85733	hypothetical prote
49	7	1.4	150	2 B64897	apoptosis inducer
50	7	1.4	160	2 S58214	probable membrane
51	7	1.4	161	2 D81940	probable membrane
52	7	1.4	161	2 E81166	hypothetical prote
53	7	1.4	168	2 C71828	hypothetical prote
54	7	1.4	168	2 F64689	hypothetical prote
55	7	1.4	170	2 AE1391	H+-transporting AT
56	7	1.4	170	2 AG1766	hypothetical prote
57	7	1.4	180	2 G70912	hypothetical prote
58	7	1.4	185	2 B64615	hypothetical prote
59	7	1.4	186	2 AE1450	hypothetical prote
60	7	1.4	192	2 A10268	anthranilate synth
61	7	1.4	200	2 T36305	probable anthranil
62	7	1.4	203	2 AB2285	hypothetical prote
63	7	1.4	206	2 B97594	50S ribosomal prot
64	7	1.4	206	2 AC2815	50S ribosomal prot
65	7	1.4	212	2 C65165	ctk protein - Esch
66	7	1.4	212	2 D91193	probable transcrip
67	7	1.4	212	2 E86040	probable transcrip
68	7	1.4	219	2 H85358	hypothetical prote
69	7	1.4	222	2 S61241	hypothetical prote
70	7	1.4	227	2 G75269	conserved hypothet
71	7	1.4	235	2 F86598	pseudouridine synt
72	7	1.4	235	2 H72025	probable pseudouri
73	7	1.4	235	2 G81515	ribosomal large ch
74	7	1.4	238	2 I38849	LEER-3 - human
75	7	1.4	241	2 F71478	probable pseudouri
76	7	1.4	241	2 E81741	ribosomal large ch
77	7	1.4	244	2 AD3266	asparagine transpo
78	7	1.4	245	2 E87719	protein R119.3 (im
79	7	1.4	249	2 T35589	probable secreted
80	7	1.4	251	2 A83660	hypothetical prote
81	7	1.4	254	2 B87630	hypothetical prote
82	7	1.4	257	2 T44278	conserved hypothet
83	7	1.4	267	2 T46853	yibQ protein (lipo
84	7	1.4	267	2 T00114	exodeoxyribonuclea
85	7	1.4	267	2 H64044	exodeoxyribonuclea
86	7	1.4	267	2 B83109	probable transcrip
87	7	1.4	268	1 NCECX3	exodeoxyribonuclea
88	7	1.4	268	2 G90935	exonuclease III (l
89	7	1.4	268	2 C85784	exonuclease III (l
90	7	1.4	270	2 H70690	hypothetical prote
91	7	1.4	276	2 G01564	protease chain L
92	7	1.4	276	2 C44324	hypothetical prote
93	7	1.4	276	2 T35483	hypothetical prote
94	7	1.4	284	2 S58650	hypothetical prote
95	7	1.4	289	2 H83433	hypothetical prote
96	7	1.4	289	2 AC0555	probable membrane
97	7	1.4	290	2 AH3448	xhdc protein (assi
98	7	1.4	291	2 D82491	hypothetical prote
99	7	1.4	294	2 S36932	chitinase (EC 3.2.
100	7	1.4	296	2 UC6050	homoserine kinase
101	7	1.4	297	2 F69054	cobalamin biosynth
102	7	1.4	298	2 S53483	probable membrane

103	7	1.4	299	2	AC185	transcription regu
104	7	1.4	302	2	S61836	chr protein - Rhi
105	7	1.4	302	2	G64311	Na+/Ca2+-exchangin
106	7	1.4	306	1	CCECDL	D-alanine-D-alanin
107	7	1.4	306	2	H90640	D-alanine-D-alanin
108	7	1.4	306	2	H85491	D-alanine-D-alanin
109	7	1.4	306	2	AG0518	hypothetical prote
110	7	1.4	314	2	T14739	hypothetical prote
111	7	1.4	314	2	T50871	hypothetical prote
112	7	1.4	316	2	B82485	iron(III) ABC tran
113	7	1.4	319	2	AH3527	D-xylose-binding p
114	7	1.4	320	2	C81972	probable 3-oxoacyl
115	7	1.4	320	2	C81029	3-oxoacyl-(acyl-ca
116	7	1.4	320	2	A40660	outer membrane pro
117	7	1.4	325	2	H96032	probable thiamine
118	7	1.4	326	2	J00855	hypothetical 36.8K
119	7	1.4	326	2	T34594	probable oxidoredu
120	7	1.4	327	1	A41720	acid phosphatase (
121	7	1.4	327	1	HLHUCD	T-cell surface gly
122	7	1.4	327	1	P95889	probable dehydroge
123	7	1.4	328	2	H81996	probable integral
124	7	1.4	328	2	B81225	hypothetical prote
125	7	1.4	331	2	A83534	probable C4-dicarb
126	7	1.4	331	2	F75268	hypothetical prote
127	7	1.4	333	2	D70855	probable ilvC prot
128	7	1.4	333	2	AH0268	anthranilate phosp
129	7	1.4	334	2	JC4870	pepsin A (EC 3.4.2
130	7	1.4	335	2	H81453	probable nucleosid
131	7	1.4	336	2	T19112	aspartic proteinas
132	7	1.4	336	2	T41118	hypothetical prote
133	7	1.4	337	2	G95915	probable sugar ABC
134	7	1.4	337	2	F70071	hypothetical prote
135	7	1.4	339	2	A83358	hypothetical prote
136	7	1.4	341	2	JC5653	major histocompati
137	7	1.4	345	2	AG3186	hypothetical prote
138	7	1.4	345	2	A10926	probable capsid po
139	7	1.4	345	2	B75274	conserved hypotnet
140	7	1.4	346	2	E86715	transcription regu
141	7	1.4	346	2	A83686	hypothetical prote
142	7	1.4	347	2	AG1817	rod shape-determin
143	7	1.4	350	2	B82777	conserved hypotnet
144	7	1.4	354	2	C71368	probable UDP-N-ace
145	7	1.4	354	2	E60967	YGP1 protein precu
146	7	1.4	356	1	S55437	translation releas
147	7	1.4	365	2	T49733	probable homoserin
148	7	1.4	368	2	B97623	cpaA protein (A100
149	7	1.4	368	2	A82846	Ca2+/H+ antiporter
150	7	1.4	372	2	D98164	hypothetical prote
151	7	1.4	372	2	AC3123	sugar acetylase [I
152	7	1.4	373	2	T45747	GDP-D-mannose-4,6-
153	7	1.4	374	2	AB1765	B. subtilis O-succ
154	7	1.4	376	2	E70918	hypothetical prote
155	7	1.4	379	2	B71331	conserved hypotnet
156	7	1.4	380	2	S03433	candidapepsin (EC
157	7	1.4	381	2	JC7247	prochymosin - comm
158	7	1.4	382	1	PECH	pepsin A (EC 3.4.2
159	7	1.4	383	2	JC7573	pepsinogen C - Afr
160	7	1.4	384	2	A39314	gastricsin (EC 3.4
161	7	1.4	385	2	C64251	hypothetical prote
162	7	1.4	386	1	PEPG	pepsin A (EC 3.4.2
163	7	1.4	387	2	D38302	pepsin (EC 3.4.23.
164	7	1.4	387	2	C38302	pepsin (EC 3.4.23.
165	7	1.4	387	2	B38302	pepsin (EC 3.4.23.
166	7	1.4	387	2	E38302	pepsin (EC 3.4.23.
167	7	1.4	387	2	I46617	pepsin (EC 3.4.23.
168	7	1.4	387	2	JC7245	pregnancy-associat
169	7	1.4	388	1	PEHU	pepsinogen A - com
170	7	1.4	388	1	PEMOAR	pepsin A (EC 3.4.2
171	7	1.4	388	1	PEMOAT	pepsin A (EC 3.4.2
172	7	1.4	388	1	S19684	pepsin A (EC 3.4.2
173	7	1.4	388	1	S19682	pepsin A (EC 3.4.2
174	7	1.4	388	2	A30142	pepsin A (EC 3.4.2
175	7	1.4	388	2	B30142	pepsin A (EC 3.4.2
176	7	1.4	392	2	E75042	transporter (major
177	7	1.4	394	2	D82725	nicotinate phospho
178	7	1.4	394	2	S74643	proteinase hbaA (E
179	7	1.4	398	2	I51185	cathepsin D (EC 3.
180	7	1.4	398	2	B75475	glucose-fructose o
181	7	1.4	408	2	A46712	glycoprotein IIA -
182	7	1.4	411	2	S40064	3-deoxy-manno-occu
183	7	1.4	416	2	AG0125	N-acetylmutamoyl-L
184	7	1.4	416	2	F83010	probable oxidoredu
185	7	1.4	428	2	S47096	cynarase (EC 3.4.2
186	7	1.4	428	2	B90636	survival protein (
187	7	1.4	428	2	B85487	survival protein (
188	7	1.4	428	2	E64726	probable peptidylp
189	7	1.4	433	2	E96649	hypothetical prote
190	7	1.4	433	2	B75376	sensor histidine k
191	7	1.4	434	2	AD0061	peptidylprolyl iso
192	7	1.4	436	2	C95236	membrane protein (
193	7	1.4	436	2	G96009	probable cell-surf
194	7	1.4	436	2	D98100	conserved hypotnet
195	7	1.4	444	2	T26229	hypothetical prote
196	7	1.4	444	2	S41717	aspartic hemoglobi
197	7	1.4	453	2	S32817	gastrin receptor -
198	7	1.4	460	2	T43324	hypothetical prote
199	7	1.4	462	2	G70544	probable hemu prot
200	7	1.4	468	2	A69468	ammonium transport
201	7	1.4	468	2	T12049	cypsin (EC 3.4.2
202	7	1.4	474	2	T10011	probable penicillin
203	7	1.4	475	2	T45766	hypothetical prote
204	7	1.4	484	1	B69056	IMP dehydrogenase
205	7	1.4	486	2	F84682	probable protein k
206	7	1.4	488	2	G81213	conserved hypotnet
207	7	1.4	490	2	B81790	conserved hypotnet
208	7	1.4	491	2	C98275	polyketide synthas
209	7	1.4	491	2	AC3009	polyketide synthas
210	7	1.4	491	2	JC6197	seromelysin 3 (EC
211	7	1.4	491	2	H84379	4-hydroxybutyrate
212	7	1.4	491	2	F70699	probable pBPA prot
213	7	1.4	492	1	B86911	probable penicillin
214	7	1.4	494	1	AC4HUC2	steroid 21-monoxy
215	7	1.4	496	2	JS0732	aspartic proteinas
216	7	1.4	496	2	B83160	aspartic prote
217	7	1.4	504	2	F70813	hypothetical prote
218	7	1.4	506	2	T07915	probable aspartic
219	7	1.4	506	2	S71591	aspartic proteinas
220	7	1.4	506	2	F86253	hypothetical prote
221	7	1.4	508	2	D85056	probable aspartic
222	7	1.4	509	2	JC7272	aspartic proteinas
223	7	1.4	510	2	D89786	hypothetical prote
224	7	1.4	511	2	UC7682	spermatogenesis as
225	7	1.4	513	2	T09739	aspartic endopepti
226	7	1.4	517	2	S12227	hypothetical prote
227	7	1.4	518	2	JC4024	poliovirus recepto
228	7	1.4	519	2	T45764	hypothetical prote
229	7	1.4	527	2	H85135	hypothetical prote
230	7	1.4	527	2	G89999	conserved hypotnet
231	7	1.4	541	2	D97930	sensor histidine k
232	7	1.4	547	2	H87679	arginine-tRNA lig
233	7	1.4	550	1	A49936	hypothetical prote
234	7	1.4	551	2	T16426	hypothetical prote
235	7	1.4	551	2	A12964	conserved hypotnet
236	7	1.4	554	2	G82538	unknown protein [I
237	7	1.4	555	2	F86487	potassium channel
238	7	1.4	555	2	T43357	methyl-accepting c
239	7	1.4	556	2	F82342	hypothetical glyci
240	7	1.4	558	2	E70756	hypothetical prote
241	7	1.4	562	2	T05758	aspartyllopepsin I
242	7	1.4	569	2	S64957	probable ATP-bindi
243	7	1.4	570	2	A83118	poly(3-hydroxybuty
244	7	1.4	589	2	A34341	aspartic proteinas
245	7	1.4	596	2	S57971	nodulin-like prote
246	7	1.4	601	2	T02581	prostaglandin-endo
247	7	1.4	603	2	UC5063	prostaglandin-endo
248	7	1.4	604	2	A46150	prostaglandin-endo

249	7	1.4	625	2	E83127	transcription regu	322	7	1.4	1513	2	A70982	probable ATP-depen
250	7	1.4	626	2	H82147	methyl-accepting c	323	7	1.4	1533	2	A46221	abdominal segment
251	7	1.4	638	2	E71018	hypothetical prote	324	7	1.4	1632	2	C70752	probable ctpi prot
252	7	1.4	644	2	T34879	probable integral	325	7	1.4	1690	2	T35694	ATP dependent DNA
253	7	1.4	646	2	T28868	hypothetical prote	326	7	1.4	1875	2	A36429	integrin beta-4 ch
254	7	1.4	646	2	T38171	probable serine/th	327	7	1.4	2014	2	T21560	hypothetical prote
255	7	1.4	660	1	UYVPP	noncapsid protein	328	7	1.4	2055	2	D86201	hypothetical prote
256	7	1.4	662	1	UYVNA	secretion system a	329	7	1.4	2894	2	C64474	hypothetical prote
257	7	1.4	682	2	AE0033	NADH2 dehydrogenas	330	7	1.4	6486	2	T31076	tyrocidine synthet
258	7	1.4	689	2	T11917	alpha-amylase VCA0	331	7	1.4	8243	2	T31307	type I fatty acid
259	7	1.4	690	2	B82409	ABC protein AGR_L	332	6	1.2	9	2	PT0326	Ig heavy chain CRD
260	7	1.4	690	2	D98318	hypothetical prote	333	6	1.2	16	2	A44352	candidaepsin (EC
261	7	1.4	697	2	T37827	hypothetical prote	334	6	1.2	23	2	PH1364	Ig heavy chain DJ
262	7	1.4	699	2	E84565	translational elonga	335	6	1.2	31	2	T46840	gene TAP1 protein
263	7	1.4	704	2	BEFCG	translational elonga	336	6	1.2	33	2	I68894	protein kinase sgg
264	7	1.4	704	2	JC1424	translational elonga	337	6	1.2	39	2	S35325	hypothetical prote
265	7	1.4	704	2	G91152	translational elonga	338	6	1.2	40	2	D64733	endo-beta-1,6-gluc
266	7	1.4	704	2	C85998	translational elonga	339	6	1.2	48	2	JV0019	gene 5.9 protein -
267	7	1.4	704	2	AC1005	elongation factor	340	6	1.2	49	2	S55324	gene 5.9 protein -
268	7	1.4	707	2	F86925	probable acyl-CoA	341	6	1.2	52	1	S07502	cathepsin E (EC 3.
269	7	1.4	709	2	T29692	hypothetical prote	342	6	1.2	52	2	A34657	gene 5.9 protein -
270	7	1.4	715	2	G86634	hypothetical prote	343	6	1.2	52	2	A34657	gene 5.9 protein -
271	7	1.4	715	2	B43943	ATP-dependent memb	344	6	1.2	59	2	B87614	pilus subunit prot
272	7	1.4	717	2	A39203	comA protein - Str	345	6	1.2	64	2	E98056	hypothetical prote
273	7	1.4	717	2	C97877	transport ATP-bind	346	6	1.2	65	2	F81607	hypothetical prote
274	7	1.4	721	2	F95004	hypothetical prote	347	6	1.2	67	2	AB1771	hypothetical prote
275	7	1.4	721	2	F82198	probable toxin sec	348	6	1.2	67	2	AF1487	probable transcrip
276	7	1.4	722	2	T46560	swi2 protein - fis	349	6	1.2	67	2	AI1126	probable transcrip
277	7	1.4	725	2	T03514	probable secretion	350	6	1.2	68	2	E86772	hypothetical prote
278	7	1.4	754	2	S62512	probable cytochrome	351	6	1.2	68	2	B83632	hypothetical prote
279	7	1.4	773	2	JH0609	protein-tyrosine-p	352	6	1.2	71	2	T07731	1-aminocyclopropan
280	7	1.4	775	2	S55345	protein-tyrosine-p	353	6	1.2	71	2	S22905	lysine protein S -
281	7	1.4	784	2	AC1091	5'-nucleotidase, p	354	6	1.2	72	2	S01799	pepsin (EC 3.4.23.
282	7	1.4	788	2	G82764	membrane protein X	355	6	1.2	73	1	F2NR0P	photosystem II pho
283	7	1.4	802	2	D85035	conserved hypochet	356	6	1.2	73	2	S21754	gastricin (EC 3.4
284	7	1.4	830	2	C69011	nitrate reductase	357	6	1.2	73	2	A87686	hypothetical prote
285	7	1.4	831	2	A48489	TS18.5 protein - A	358	6	1.2	74	2	B40020	collagen alpha 1(X
286	7	1.4	832	2	C86431	DNA-directed DNA p	359	6	1.2	79	2	S03266	aspartic proteinas
287	7	1.4	843	1	JDVLR	hypothetical prote	360	6	1.2	79	2	D64596	hypothetical prote
288	7	1.4	843	1	T16906	hypothetical prote	361	6	1.2	81	1	MSWL35	E5 protein - human
289	7	1.4	881	2	F83530	hypothetical prote	362	6	1.2	81	2	A24522	mitochondrial prot
290	7	1.4	887	2	T20866	hypothetical prote	363	6	1.2	81	2	H82515	hypothetical prote
291	7	1.4	899	2	S62428	probable coiled co	364	6	1.2	83	2	C69440	hypothetical prote
292	7	1.4	933	1	BVECC	sensor protein rcs	365	6	1.2	87	2	JQ1135	hypothetical prote
293	7	1.4	933	2	C91017	sensor for ctr cap	366	6	1.2	88	2	A28056	levi tide precursor
294	7	1.4	933	2	B85861	hypothetical prote	367	6	1.2	88	2	D64562	hypothetical prote
295	7	1.4	939	2	AE2275	hypothetical prote	368	6	1.2	88	2	T31230	hypothetical prote
296	7	1.4	958	2	S47179	hypothetical prote	369	6	1.2	89	2	T14135	NADH2 dehydrogenas
297	7	1.4	964	2	JC5545	integrin beta-4 pr	370	6	1.2	89	2	A33542	islet amyloid poly
298	7	1.4	964	2	AG3433	diagnalytic cyclas	371	6	1.2	89	2	F86706	hypothetical prote
299	7	1.4	967	2	S58360	lanthiotic Peps b	372	6	1.2	90	2	S56455	probable ATP-bind
300	7	1.4	971	2	H97454	hypothetical prote	373	6	1.2	90	2	D70678	hypothetical prote
301	7	1.4	971	2	AB2673	conserved hypochet	374	6	1.2	91	1	S00060	phospholipid trans
302	7	1.4	1015	2	T39697	beta-galactosidase	375	6	1.2	91	2	T42907	hypothetical prote
303	7	1.4	1015	2	A42915	type II CAMP-depen	376	6	1.2	92	2	S06034	hypothetical prote
304	7	1.4	1039	2	G83748	alpha-mannosidase	377	6	1.2	92	2	S06033	hypothetical prote
305	7	1.4	1054	2	T18304	acid trehalase hom	378	6	1.2	92	2	AG3634	norf (imported) -
306	7	1.4	1062	2	T46444	hypothetical prote	379	6	1.2	94	2	S03380	major fecal allerg
307	7	1.4	1073	2	S56230	probable membrane	380	6	1.2	96	2	A87110	conserved hypochet
308	7	1.4	1121	2	C87973	protein Y43F8C.12	381	6	1.2	98	2	PQ0496	hypothetical prote
309	7	1.4	1131	2	AD2166	two-component sens	382	6	1.2	99	2	B95393	protein (imported
310	7	1.4	1142	2	C97080	levanase/invertase	383	6	1.2	99	2	AI1907	apolipoprotein C-I
311	7	1.4	1153	2	T26883	hypothetical prote	384	6	1.2	100	2	A38685	hypothetical prote
312	7	1.4	1172	2	T36053	probable ABC-type	385	6	1.2	100	2	P95369	hypothetical prote
313	7	1.4	1194	2	G70837	probable ABC trans	386	6	1.2	100	2	B71410	ABC transporter, t
314	7	1.4	1236	2	T50904	Mg protoporphytrin	387	6	1.2	100	2	D98044	H+-transporting tw
315	7	1.4	1238	2	T03465	probable exonuclea	388	6	1.2	101	2	A33351	hypothetical prote
316	7	1.4	1246	2	G89287	protein H39E23.1 [389	6	1.2	101	2	T17689	hypothetical prote
317	7	1.4	1253	2	F86436	hypothetical prote	390	6	1.2	101	2	G72450	hypothetical prote
318	7	1.4	1269	2	T14476	pela protein - sli	391	6	1.2	101	2	AD3542	hypothetical prote
319	7	1.4	1336	2	T39978	M-factor ABC-type	392	6	1.2	101	2	B83061	conserved hypochet
320	7	1.4	1379	2	T13718	pollux gene protei	393	6	1.2	102	2	B34770	ORF2 protein - sal
321	7	1.4	1433	2	A46053	bullous pemphigoid	394	6	1.2	102	2	AH3257	bola protein (impo

395	6	1.2	102	2	D90915	hypothetical prote
396	6	1.2	102	2	A85764	hypothetical prote
397	6	1.2	102	2	A12693	conserved hypotnet
398	6	1.2	103	2	T03013	hypothetical prote
399	6	1.2	103	2	G75513	conserved hypotnet
400	6	1.2	104	2	G75090	hypothetical prote
401	6	1.2	105	2	S62844	H+-transporting tw
402	6	1.2	105	2	B69857	chaperonin homolog
403	6	1.2	105	2	T94932	hypothetical prote
404	6	1.2	105	2	G90023	hypothetical prote
405	6	1.2	105	2	A03365	hypothetical prote
406	6	1.2	106	2	S72815	hypothetical prote
407	6	1.2	107	2	J02035	hypothetical 11.7K
408	6	1.2	107	2	T25670	hypothetical prote
409	6	1.2	108	2	S09278	insulin precursor
410	6	1.2	108	2	A39883	insulin precursor
411	6	1.2	109	2	A45887	leukocyte differen
412	6	1.2	109	2	S53546	hypothetical prote
413	6	1.2	109	2	H72641	hypothetical prote
414	6	1.2	110	1	PEBO	pepsin A (EC 3.4.2
415	6	1.2	110	1	IPHU	insulin precursor
416	6	1.2	110	1	INRB	insulin precursor
417	6	1.2	110	1	IPDG	insulin precursor
418	6	1.2	110	2	B42179	insulin precursor
419	6	1.2	110	2	J00178	insulin precursor
420	6	1.2	110	2	E69607	protein secretion
421	6	1.2	110	2	D95267	hypothetical prote
422	6	1.2	112	2	T44986	probable sulfate/t
423	6	1.2	112	2	T48324	DNAJ protein-like
424	6	1.2	112	2	G95961	hypothetical membr
425	6	1.2	112	2	A80687	probable membrane
426	6	1.2	113	2	A70553	hypothetical prote
427	6	1.2	113	2	T42985	hypothetical prote
428	6	1.2	113	2	C83893	hypothetical prote
429	6	1.2	114	2	D6516	Ig lambda chain V
430	6	1.2	114	2	F83735	chaperonin BH0686
431	6	1.2	114	2	E72724	hypothetical prote
432	6	1.2	114	2	A82761	hypothetical prote
433	6	1.2	115	1	DNHUN3	NADH2 dehydrogenas
434	6	1.2	115	1	QXBO3M	NADH2 dehydrogenas
435	6	1.2	115	1	QXMS3M	NADH2 dehydrogenas
436	6	1.2	115	2	S04754	NADH2 dehydrogenas
437	6	1.2	115	2	S26158	NADH2 dehydrogenas
438	6	1.2	115	2	A55746	NADH2 dehydrogenas
439	6	1.2	115	2	S41842	NADH2 dehydrogenas
440	6	1.2	115	2	S41827	NADH2 dehydrogenas
441	6	1.2	115	2	C57746	NADH2 dehydrogenas
442	6	1.2	115	2	S65745	NADH2 dehydrogenas
443	6	1.2	115	2	H58850	NADH2 dehydrogenas
444	6	1.2	115	2	T17139	NADH2 dehydrogenas
445	6	1.2	115	2	T17176	NADH2 dehydrogenas
446	6	1.2	115	2	T17182	NADH2 dehydrogenas
447	6	1.2	115	2	T17347	NADH2 dehydrogenas
448	6	1.2	115	2	T17359	NADH2 dehydrogenas
449	6	1.2	115	2	T17362	NADH2 dehydrogenas
450	6	1.2	115	2	T17135	NADH2 dehydrogenas
451	6	1.2	115	2	T17142	NADH2 dehydrogenas
452	6	1.2	115	2	T17173	NADH2 dehydrogenas
453	6	1.2	115	2	T17083	NADH2 dehydrogenas
454	6	1.2	115	2	T17094	NADH2 dehydrogenas
455	6	1.2	115	2	T17082	NADH2 dehydrogenas
456	6	1.2	115	2	T17098	NADH2 dehydrogenas
457	6	1.2	115	2	T17090	NADH2 dehydrogenas
458	6	1.2	115	2	T11448	NADH2 dehydrogenas
459	6	1.2	115	2	T11500	NADH2 dehydrogenas
460	6	1.2	115	2	T11396	NADH2 dehydrogenas
461	6	1.2	115	2	T11461	NADH2 dehydrogenas
462	6	1.2	115	2	T11840	NADH2 dehydrogenas
463	6	1.2	115	2	T11864	NADH2 dehydrogenas
464	6	1.2	115	2	T10979	NADH2 dehydrogenas
465	6	1.2	115	2	T11057	NADH2 dehydrogenas
466	6	1.2	115	2	T11487	NADH2 dehydrogenas
467	6	1.2	115	2	T11147	NADH2 dehydrogenas
468	6	1.2	115	2	T11254	NADH2 dehydrogenas
469	6	1.2	115	2	T11344	NADH2 dehydrogenas
470	6	1.2	115	2	T11370	NADH2 dehydrogenas
471	6	1.2	115	2	T11409	NADH2 dehydrogenas
472	6	1.2	115	2	H59153	NADH2 dehydrogenas
473	6	1.2	115	2	T17350	NADH2 dehydrogenas
474	6	1.2	115	2	D64914	hypothetical prote
475	6	1.2	116	2	S08425	NADH2 dehydrogenas
476	6	1.2	116	2	S10194	NADH2 dehydrogenas
477	6	1.2	116	2	A30401	NADH2 dehydrogenas
478	6	1.2	116	2	B30401	NADH2 dehydrogenas
479	6	1.2	116	2	E30396	NADH2 dehydrogenas
480	6	1.2	116	2	F30396	NADH2 dehydrogenas
481	6	1.2	116	2	G30396	NADH2 dehydrogenas
482	6	1.2	116	2	H30396	NADH2 dehydrogenas
483	6	1.2	116	2	S36004	NADH2 dehydrogenas
484	6	1.2	116	2	H58892	NADH2 dehydrogenas
485	6	1.2	116	2	T11174	NADH2 dehydrogenas
486	6	1.2	116	2	S47877	NADH2 dehydrogenas
487	6	1.2	116	2	H90612	NADH dehydrogenase
488	6	1.2	116	2	H90614	NADH dehydrogenase
489	6	1.2	116	2	H90616	NADH dehydrogenase
490	6	1.2	116	2	H90618	NADH dehydrogenase
491	6	1.2	116	2	H90620	NADH dehydrogenase
492	6	1.2	116	2	H90622	NADH dehydrogenase
493	6	1.2	116	2	H90624	NADH dehydrogenase
494	6	1.2	116	2	H90626	NADH2 dehydrogenas
495	6	1.2	116	2	T10993	NADH2 dehydrogenas
496	6	1.2	116	2	T11200	NADH2 dehydrogenas
497	6	1.2	116	2	T11294	NADH2 dehydrogenas
498	6	1.2	116	2	T11541	NADH2 dehydrogenas
499	6	1.2	116	2	T11082	NADH2 dehydrogenas
500	6	1.2	116	2	T11108	NADH2 dehydrogenas
501	6	1.2	116	2	T11187	NADH2 dehydrogenas
502	6	1.2	116	2	T11331	NADH2 dehydrogenas
503	6	1.2	116	2	T11771	NADH2 dehydrogenas
504	6	1.2	116	2	T09954	NADH2 dehydrogenas
505	6	1.2	116	2	T11029	NADH2 dehydrogenas
506	6	1.2	116	2	T11307	NADH2 dehydrogenas
507	6	1.2	116	2	T11435	NADH2 dehydrogenas
508	6	1.2	117	2	T45557	NADH2 dehydrogenas
509	6	1.2	117	2	T09185	lipid transfer pro
510	6	1.2	119	2	S24294	choiron protein -
511	6	1.2	119	2	S24291	early chorion prot
512	6	1.2	119	2	B45937	hypothetical prote
513	6	1.2	120	2	D95980	choiron class CA p
514	6	1.2	121	2	S24293	hypothetical prote
515	6	1.2	121	2	B97446	ATP synthase, subu
516	6	1.2	121	2	AC2664	hypothetical prote
517	6	1.2	121	2	T18126	hypothetical prote
518	6	1.2	121	2	G90170	hypothetical prote
519	6	1.2	121	2	F72560	hypothetical prote
520	6	1.2	122	1	A55115	uterine plasmin/tr
521	6	1.2	122	2	J00150	hypothetical 13K p
522	6	1.2	123	2	D84383	hypothetical prote
523	6	1.2	124	1	NRCB	pancreatic ribonuc
524	6	1.2	124	1	GCAP	glucagon 1 precurs
525	6	1.2	125	2	JN0470	interferon gamma-i
526	6	1.2	125	2	F84604	hypothetical prote
527	6	1.2	125	2	B97470	hypothetical prote
528	6	1.2	125	2	AG2688	Na+/H+ antiporter
529	6	1.2	125	2	H70101	glpE protein (glpE
530	6	1.2	125	2	F83072	hypothetical prote
531	6	1.2	125	2	F70106	hypothetical prote
532	6	1.2	125	2	S74723	hypothetical prote
533	6	1.2	126	2	B83265	hypothetical prote
534	6	1.2	126	2	H86347	ribosomal protein
535	6	1.2	128	2	H82060	conserved hypotnet
536	6	1.2	128	2	H72500	hypothetical prote
537	6	1.2	128	2	H82267	hypothetical prote
538	6	1.2	128	2	T30714	hypothetical prote
539	6	1.2	129	2	E90535	hypothetical prote
540	6	1.2	129	2	I56195	gene Tap-1 protein

541	6	1.2	129	2	AB3459	hypothetical prote	614	6	1.2	152	2	B75042	aspartate carbamoy
542	6	1.2	130	2	T16788	hypothetical prote	615	6	1.2	152	2	F72702	hypothetical prote
543	6	1.2	130	2	T12478	hypothetical prote	616	6	1.2	152	2	D75367	hypothetical prote
544	6	1.2	131	2	S24285	RNA-directed RNA p	617	6	1.2	152	2	B72754	hypothetical prote
545	6	1.2	131	2	S06479	fatty acid-binding	618	6	1.2	153	2	S12206	hypothetical prote
546	6	1.2	131	2	D90419	transcriptional re	619	6	1.2	153	2	D83012	hypothetical prote
547	6	1.2	131	2	B84598	hypothetical prote	620	6	1.2	153	2	AP3648	hypothetical prote
548	6	1.2	132	2	F70650	hypothetical prote	621	6	1.2	154	2	AB0163	probable membrane
549	6	1.2	132	2	D69520	hypothetical prote	622	6	1.2	155	2	B64105	acetyl-CoA carboxy
550	6	1.2	132	2	T35141	hypothetical prote	623	6	1.2	155	2	AB3512	modulation protein
551	6	1.2	132	2	H75548	hypothetical prote	624	6	1.2	155	2	E72661	hypothetical prote
552	6	1.2	132	2	AB1767	ATP synthase chain	625	6	1.2	155	2	AB1226	hypothetical prote
553	6	1.2	132	2	AH1391	ATP synthase chain	626	6	1.2	155	2	AD1579	hypothetical prote
554	6	1.2	133	2	D87690	hypothetical prote	627	6	1.2	157	2	H83082	probable transcrip
555	6	1.2	133	2	S69803	hypothetical prote	628	6	1.2	157	2	C82121	phosphohistidine p
556	6	1.2	134	2	B72101	ribosomal protein	629	6	1.2	157	2	H72673	hypothetical prote
557	6	1.2	134	2	F86521	ribosomal protein	630	6	1.2	158	2	D72017	conserved hypotet
558	6	1.2	134	2	F72802	gp24 protein - Myc	631	6	1.2	158	2	H86607	CT788 hypothetical
559	6	1.2	134	2	F75543	hypothetical prote	632	6	1.2	158	2	B75141	hypothetical prote
560	6	1.2	134	2	F97475	conserved hypotet	633	6	1.2	158	2	D83382	hypothetical prote
561	6	1.2	135	2	AC3234	hypothetical prote	634	6	1.2	159	2	G70841	hypothetical prote
562	6	1.2	135	2	D71228	hypothetical prote	635	6	1.2	159	2	H86997	conserved hypotet
563	6	1.2	136	2	T07975	probable arabinoga	636	6	1.2	159	2	T35623	probable protein p
564	6	1.2	136	2	T07945	hypothetical prote	637	6	1.2	159	2	B71423	hypothetical prote
565	6	1.2	136	2	H82763	photosystem II pro	638	6	1.2	160	2	B70718	hypothetical prote
566	6	1.2	137	2	S53025	hypothetical prote	639	6	1.2	160	2	C70947	hypothetical prote
567	6	1.2	138	2	G65096	hypothetical prote	640	6	1.2	160	2	H70889	hypothetical prote
568	6	1.2	138	2	D91124	hypothetical prote	641	6	1.2	161	1	VCTMSH	coat protein - cuc
569	6	1.2	138	2	G85969	hypothetical prote	642	6	1.2	161	2	S54434	phosphoribosylamin
570	6	1.2	138	2	H75333	homeotic protein b	643	6	1.2	161	2	S27127	tropomyosin homolo
571	6	1.2	138	2	S20087	hypothetical prote	644	6	1.2	161	2	H69184	conserved hypotet
572	6	1.2	138	2	H83299	hypothetical prote	645	6	1.2	161	2	S52600	probable membrane
573	6	1.2	138	2	D72539	conserved hypotet	646	6	1.2	161	2	S53473	hypothetical prote
574	6	1.2	139	2	G69543	transcription regu	647	6	1.2	161	2	E71099	hypothetical prote
575	6	1.2	139	2	D82296	ribosomal protein	648	6	1.2	161	2	AD2506	hypothetical prote
576	6	1.2	140	2	S75420	probable biopolyme	649	6	1.2	162	1	D71206	hypothetical prote
577	6	1.2	140	2	E75518	hypothetical prote	650	6	1.2	162	2	H75019	conserved hypotet
578	6	1.2	140	2	F69389	probable transcrip	651	6	1.2	162	2	C82765	conserved hypotet
579	6	1.2	141	2	A91249	hypothetical prote	652	6	1.2	162	2	C69495	conserved hypotet
580	6	1.2	141	2	A90130	hypothetical prote	653	6	1.2	162	2	D97467	hypothetical prote
581	6	1.2	141	2	F97978	alanine dehydrogen	654	6	1.2	162	2	AG2685	acetyltransferase
582	6	1.2	141	2	AC3590	3-oxoadipate CoA-t	655	6	1.2	163	2	H72759	probable dCTP deam
583	6	1.2	142	2	T40837	DNA-directed RNA p	656	6	1.2	164	1	RGECLR	leucine-responsive
584	6	1.2	142	2	S27050	hemoglobin alpha-2	657	6	1.2	164	1	S22196	Mu0653 homolog - D
585	6	1.2	142	2	A60514	hemoglobin alpha-2	658	6	1.2	164	2	G64132	phosphoribosylamin
586	6	1.2	142	2	AC3345	LSU ribosomal prot	659	6	1.2	164	2	S59991	transcription regu
587	6	1.2	142	2	T49256	hypothetical prote	660	6	1.2	164	2	S59993	transcription regu
588	6	1.2	143	2	T13214	minor capsid prote	661	6	1.2	164	2	S59992	transcription regu
589	6	1.2	143	2	T41630	very hypothetical	662	6	1.2	164	2	B82142	leucine-responsive
590	6	1.2	143	2	B70010	Na+/H+ antiporter	663	6	1.2	164	2	A10167	leucine-responsive
591	6	1.2	144	2	B82556	c-type cytochrome	664	6	1.2	164	2	F90750	leucine-responsive
592	6	1.2	144	2	C70455	hypothetical prote	665	6	1.2	164	2	D85614	leucine-responsive
593	6	1.2	144	2	T49706	hypothetical prote	666	6	1.2	164	2	AE0611	leucine-responsive
594	6	1.2	145	2	T34303	hypothetical prote	667	6	1.2	165	1	A54184	leucine-responsive
595	6	1.2	145	2	D83424	hypothetical prote	668	6	1.2	165	1	A35179	leucine-responsive
596	6	1.2	146	2	A72115	conserved hypotet	669	6	1.2	165	2	H75284	hypothetical prote
597	6	1.2	146	2	D86508	hypothetical prote	670	6	1.2	165	2	A12904	hypothetical prote
598	6	1.2	147	2	G90337	hypothetical prote	671	6	1.2	165	2	S61602	probable membrane
599	6	1.2	147	2	A26697	echinoidin sea u	672	6	1.2	166	2	D66695	ribosomal protein
600	6	1.2	147	2	S05320	transhyretin prec	673	6	1.2	167	2	H72579	hypothetical prote
601	6	1.2	147	2	G72384	conserved hypotet	674	6	1.2	167	2	C97542	hypothetical prote
602	6	1.2	148	2	C70451	biopolymer transpo	675	6	1.2	168	2	B43755	vasopressin / neur
603	6	1.2	148	2	E75283	conserved hypotet	676	6	1.2	168	2	D29016	cell division inh
604	6	1.2	148	2	F86701	hypothetical prote	677	6	1.2	168	2	AE0175	probable cell divi
605	6	1.2	148	2	C72422	hypothetical prote	678	6	1.2	168	2	D75259	hypothetical prote
606	6	1.2	148	2	H95849	hypothetical prote	679	6	1.2	168	2	A72226	conserved hypotet
607	6	1.2	149	2	D98156	hypothetical prote	680	6	1.2	168	2	G83428	hypothetical prote
608	6	1.2	149	2	AF3090	conserved hypotet	681	6	1.2	169	1	QOBCA1	cell division inh
609	6	1.2	151	2	A86705	transcriptional re	682	6	1.2	169	2	B29016	cell division inh
610	6	1.2	151	2	D87683	conserved hypotet	683	6	1.2	169	2	C29016	cell division inh
611	6	1.2	151	2	A82978	hypothetical prote	684	6	1.2	169	2	B90759	suppressor of lon
612	6	1.2	151	2	G84165	hypothetical prote	685	6	1.2	169	2	H85622	hypothetical prote
613	6	1.2	151	2	T18478	hypothetical prote	686	6	1.2	169	2	AB0627	cell division inh

687	6	1.2	169	2	A86912	hypothetical prote	760	6	1.2	192	2	H70375	conserved hypot
688	6	1.2	169	2	D90857	hypothetical prote	761	6	1.2	192	2	G71089	hypothetical prote
689	6	1.2	169	2	B75490	hypothetical prote	762	6	1.2	194	2	E84097	imidazoleglycerol-
690	6	1.2	169	2	F85762	hypothetical prote	763	6	1.2	194	2	H82520	hypothetical prote
691	6	1.2	170	2	B80214	MAH dehydrogenase	764	6	1.2	194	2	T14746	hypothetical prote
692	6	1.2	171	2	C87418	hypothetical prote	765	6	1.2	195	2	B40535	anthranilate synth
693	6	1.2	171	2	E87459	cytochrome c fam11	766	6	1.2	195	2	A99240	anthranilate synth
694	6	1.2	171	2	G84421	probable auxin-ind	767	6	1.2	195	2	H97288	para-aminobenzoate
695	6	1.2	171	2	A84561	probable bzif tran	768	6	1.2	195	2	G70211	hypothetical prote
696	6	1.2	172	2	A91070	hypothetical prote	769	6	1.2	195	2	A96998	CDP-diacylglycerid sy
697	6	1.2	172	2	D85914	hypothetical prote	770	6	1.2	196	2	D87712	imidazoleglycerol-
698	6	1.2	172	2	T02229	protein BYJ15 - co	771	6	1.2	196	2	A71325	hypothetical prote
699	6	1.2	172	2	B86439	protein T19E23.11	772	6	1.2	196	2	F88382	protein W06F11.2 (
700	6	1.2	173	2	S34767	neuropeptides prec	773	6	1.2	196	2	D81696	hypothetical prote
701	6	1.2	173	2	AF3293	crossover junction	774	6	1.2	196	2	AD2949	acetyltransferase
702	6	1.2	173	2	FA5392	orf6 protein - por	775	6	1.2	197	2	J00638	imidazoleglycerol-
703	6	1.2	173	2	A44281	envelope protein -	776	6	1.2	197	2	S25106	hypothetical prote
704	6	1.2	173	2	A55512	hypothetical prote	777	6	1.2	197	2	S70678	protein W06F11.2 (
705	6	1.2	173	2	D83464	conserved hypotet	778	6	1.2	197	2	S51372	membrane protein L
706	6	1.2	174	2	A47113	glucuronosyltransf	779	6	1.2	198	2	S25656	T-cell surface gly
707	6	1.2	174	2	B65046	hypothetical prote	780	6	1.2	198	2	T29135	hypothetical prote
708	6	1.2	174	2	B72712	hypothetical prote	781	6	1.2	199	2	E95211	N-(5'-phosphoribos
709	6	1.2	174	2	S64440	probable membrane	782	6	1.2	199	2	S41316	coat protein - cuc
710	6	1.2	174	2	S73052	hypothetical prote	783	6	1.2	199	2	AE3509	maf protein [impor
711	6	1.2	174	2	H87617	hypothetical prote	784	6	1.2	199	2	T64125	nucleotide-binding
712	6	1.2	175	2	D86787	hypothetical prote	785	6	1.2	199	2	F86832	hypothetical prote
713	6	1.2	175	2	B44102	di-N-acetylchitobi	786	6	1.2	200	2	T18479	hypothetical prote
714	6	1.2	176	2	T48752	gene RXPbeta1 prot	787	6	1.2	201	1	VCVOGB	coat protein - bee
715	6	1.2	176	2	T18921	hypothetical prote	788	6	1.2	201	1	H90025	molybdenum transpo
716	6	1.2	176	2	B70445	heat shock protein	789	6	1.2	201	2	A87059	lipoprotein signal
717	6	1.2	177	2	I39709	heat shock protein	790	6	1.2	201	2	D70519	probable lipoC prot
718	6	1.2	178	2	D86696	pantothenate metab	791	6	1.2	202	1	VCVOFL	coat protein - bee
719	6	1.2	178	2	I40124	outer surface prot	792	6	1.2	202	2	C72701	probable heme expo
720	6	1.2	178	2	S03629	neurogenic gene co	793	6	1.2	202	2	B83375	hypothetical prote
721	6	1.2	178	2	T08444	hypothetical prote	794	6	1.2	202	2	AC2875	hypothetical prote
722	6	1.2	178	2	E88637	protein W09G12.6 (795	6	1.2	202	2	C70650	probable lipoprote
723	6	1.2	179	2	S39078	auxin-induced prot	796	6	1.2	202	2	H70760	nef protein (C1one
724	6	1.2	179	2	C75469	hypothetical prote	797	6	1.2	204	2	S03246	conserved hypotet
725	6	1.2	180	2	T16445	hypothetical prote	798	6	1.2	204	2	H72256	hypothetical prote
726	6	1.2	180	2	D83254	probable transcrib	799	6	1.2	204	2	C97389	conserved hypotet
727	6	1.2	182	2	S70689	adenine phosphorib	800	6	1.2	204	2	AD2607	nef protein - huma
728	6	1.2	182	2	A71688	heat shock protein	801	6	1.2	205	1	B44963	guanylate kinase (
729	6	1.2	182	2	A97754	heat shock protein	802	6	1.2	205	2	C88662	D-alanine-D-alanin
730	6	1.2	183	2	A72657	VP529-like phospho	803	6	1.2	205	2	FQ0272	heme exporter prot
731	6	1.2	183	2	T22183	hypothetical prote	804	6	1.2	205	2	G64989	heme exporter prot
732	6	1.2	184	2	S10125	alpha-2u-globulin	805	6	1.2	205	2	B91015	ATP binding protei
733	6	1.2	185	2	A80787	thiol, disulfide in	806	6	1.2	205	2	D85859	heme exporter prot
734	6	1.2	185	2	A10960	CD45-associated 30	807	6	1.2	205	2	AC0960	heme exporter prot
735	6	1.2	185	2	A49557	conserved hypotet	808	6	1.2	205	2	AD0788	heme exporter prot
736	6	1.2	185	2	B70072	probable CDP-alcoh	809	6	1.2	205	2	A36377	B61 protein precu
737	6	1.2	186	2	D75005	SSU ribosomal prot	810	6	1.2	205	2	S37804	hypothetical prote
738	6	1.2	186	2	AH3348	hypothetical prote	811	6	1.2	205	2	T34724	probable membrane
739	6	1.2	186	2	AB2408	hypothetical prote	812	6	1.2	206	2	JC4268	fibroblast growth
740	6	1.2	186	2	T32656	hypothetical prote	813	6	1.2	206	2	AF2289	cobalt transport A
741	6	1.2	186	2	AF2556	hypothetical prote	814	6	1.2	206	2	AE0891	probable membrane
742	6	1.2	187	2	S69315	hypothetical prote	815	6	1.2	206	2	T48149	hypothetical prote
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744	6	1.2	187	2	T08912	hypothetical prote	817	6	1.2	206	2	H89828	superoxide dismuta
745	6	1.2	188	2	E71157	probable CDP-alcoh	818	6	1.2	207	2	B86498	superoxide dismuta
746	6	1.2	188	2	F83855	GTP cyclohydrolyase	819	6	1.2	207	2	B72124	imideoleglycerol-
747	6	1.2	188	2	T02781	probable conjuagl	820	6	1.2	207	2	JE0045	hypothetical prote
748	6	1.2	188	2	B84719	hypothetical prote	821	6	1.2	207	2	B84151	hypothetical prote
749	6	1.2	188	2	AF3559	hypothetical prote	822	6	1.2	207	2	T36937	probable transcrip
750	6	1.2	188	2	B70736	hypothetical prote	823	6	1.2	208	2	T09901	hypothetical prote
751	6	1.2	189	2	A71569	hypothetical prote	824	6	1.2	209	1	SS3657	hydrogenase matura
752	6	1.2	189	2	JC7262	receptor activity	825	6	1.2	209	2	G98075	phosphoribosylath
753	6	1.2	189	2	F96333	hypothetical prote	826	6	1.2	209	2	S30541	prolactin precurs
754	6	1.2	189	2	T18480	hypothetical prote	827	6	1.2	209	2	G72528	hypothetical prote
755	6	1.2	190	2	T10740	carbonate dehydrat	828	6	1.2	210	2	F69510	fibrillarlin (fib)
756	6	1.2	191	2	I45716	GTP-binding protei	829	6	1.2	210	2	B71527	probable o-sialogl
757	6	1.2	191	2	C40364	hypothetical prote	830	6	1.2	211	2	D69888	micrococcal nuclea
758	6	1.2	191	2	E75132	molybdopterln-guan	831	6	1.2	211	2	A69619	deoxyribose-phosph
759	6	1.2	192	1	NNSE2	anthranilate synth	832	6	1.2	211	2	A81700	conserved hypotet

833	6	1.2	212	1	BSH5LH	ribosomal protein	906	6	1.2	230	2	H72244	conserved hypochet
834	6	1.2	212	2	T36720	probable glutamine	907	6	1.2	230	2	G83680	ABC transporter (A
835	6	1.2	212	2	H84266	50S ribosomal prot	908	6	1.2	230	2	E87578	hypothetical prote
836	6	1.2	212	2	T05721	germin-like protei	909	6	1.2	231	2	H81698	hypothetical prote
837	6	1.2	212	2	T44970	gas-vesicle operon	910	6	1.2	231	2	G69403	conserved hypochet
838	6	1.2	213	2	P98019	hypothetical prote	911	6	1.2	231	2	S48966	hypothetical prote
839	6	1.2	213	2	B87694	cytidylate kinase	912	6	1.2	232	2	C70699	probable paba prot
840	6	1.2	213	2	T27841	hypothetical prote	913	6	1.2	232	2	T10008	probable p-aminobe
841	6	1.2	214	2	S59149	H+-transporting tw	914	6	1.2	232	2	S58353	Cdb protein - she
842	6	1.2	214	2	B87424	outer membrane pro	915	6	1.2	232	2	T12740	hypothetical prote
843	6	1.2	215	2	B35534	hypothetical 23k p	916	6	1.2	232	2	G87629	hypothetical prote
844	6	1.2	215	2	P97835	50S ribosomal prot	917	6	1.2	232	2	AG1452	hypothetical prote
845	6	1.2	215	2	C72635	triase-phosphate 1	918	6	1.2	232	2	A87504	6-phospho-glucono-
846	6	1.2	215	2	AH3389	transporter BME111	919	6	1.2	232	2	G84382	cobalt transporter A
847	6	1.2	216	2	A71672	ribosomal protein	920	6	1.2	232	2	D70537	hypothetical prote
848	6	1.2	216	2	S09509	outer membrane pro	921	6	1.2	232	2	T49391	hypothetical prote
849	6	1.2	216	2	S40720	hypothetical prote	922	6	1.2	232	2	T79358	IA-alpha polypote
850	6	1.2	216	2	T34527	hypothetical prote	923	6	1.2	233	2	I79357	probable hemolysin
851	6	1.2	217	2	D82407	outer membrane pro	924	6	1.2	233	2	AF0110	hypothetical prote
852	6	1.2	217	2	F83502	hypothetical prote	925	6	1.2	233	2	B84237	hypothetical prote
853	6	1.2	218	2	T50070	superoxide dismuta	926	6	1.2	233	2	AF0419	probable ABC trans
854	6	1.2	218	2	S75100	ABC transport prot	927	6	1.2	234	1	QOBR43	membrane antigen g
855	6	1.2	218	2	S73675	hypothetical prote	928	6	1.2	234	2	AC0431	conserved hypochet
856	6	1.2	218	2	C72747	hypothetical prote	929	6	1.2	234	2	B64331	hypothetical prote
857	6	1.2	218	2	T23318	probable endonucle	930	6	1.2	234	2	AF1863	cobalamn biosynth
858	6	1.2	219	1	A35617	HDEL receptor ERD2	931	6	1.2	235	1	RWHUT8	T-cell surface gly
859	6	1.2	219	1	S75541	hypothetical prote	932	6	1.2	235	2	E86821	glucosamine-6-phos
860	6	1.2	219	2	B71511	probable sugar nuc	933	6	1.2	235	2	C98204	probable permease
861	6	1.2	219	2	T20732	hypothetical prote	934	6	1.2	235	2	AE3082	hypothetical prote
862	6	1.2	219	2	C70855	hypothetical prote	935	6	1.2	235	2	B70530	hypothetical prote
863	6	1.2	219	2	A99194	lton (III) ABC tra	936	6	1.2	235	2	P97391	probable transcrip
864	6	1.2	219	2	G87708	hypothetical prote	937	6	1.2	235	2	AG2609	transcription regu
865	6	1.2	219	2	H81824	hypothetical perip	938	6	1.2	236	2	T07260	sulfate transport
866	6	1.2	220	2	T43857	hypothetical prote	939	6	1.2	236	2	D72729	hypothetical prote
867	6	1.2	220	2	A75362	H-2 class II histo	940	6	1.2	236	2	T50908	hypothetical prote
868	6	1.2	221	1	HUMSA1	ABC transporter, p	941	6	1.2	237	2	E82674	3'-phosphoadenosin
869	6	1.2	222	2	H98178	ABC transporter, p	942	6	1.2	237	2	A36149	spiralin - Spiropl
870	6	1.2	222	2	AD3108	propanediol dehydr	943	6	1.2	237	2	D70463	hypothetical prote
871	6	1.2	223	2	AG3263	hypothetical prote	944	6	1.2	237	2	G87286	conserved hypochet
872	6	1.2	223	2	A86057	hypothetical prote	945	6	1.2	237	2	AG3573	6-phosphogluconola
873	6	1.2	223	2	P91210	hypothetical prote	946	6	1.2	237	2	S45463	probable membrane
874	6	1.2	224	2	AB1377	ABC transporter, p	947	6	1.2	238	1	LNR7MA	mannose-binding le
875	6	1.2	224	2	AD1746	ABC transporter, p	948	6	1.2	238	2	T10771	NADPH-ferrihemopro
876	6	1.2	224	2	B96586	hypothetical prote	949	6	1.2	238	2	C72576	probable glutamine
877	6	1.2	224	2	T35058	hypothetical prote	950	6	1.2	238	2	S67594	hypothetical prote
878	6	1.2	224	2	S69635	hypothetical prote	951	6	1.2	238	2	T51072	RAD59 protein - ye
879	6	1.2	224	2	T32655	hypothetical prote	952	6	1.2	238	2	H87578	hypothetical prote
880	6	1.2	225	1	WZVZC2	G2K protein - Amsa	953	6	1.2	238	2	B97634	transcription regu
881	6	1.2	225	2	AC0587	KOP operon transcr	954	6	1.2	238	2	AD2857	probable transcrip
882	6	1.2	225	2	T29632	hypothetical prote	955	6	1.2	238	2	AG2909	transcription regu
883	6	1.2	225	2	B72587	hypothetical prote	956	6	1.2	239	1	S34193	phosphoadenylyl-su
884	6	1.2	225	2	F72642	probable shikimate	957	6	1.2	239	1	LNMGMA	mannose-binding le
885	6	1.2	226	1	TYMVS	POGF-related trans	958	6	1.2	239	2	AF0261	faty acid metabol
886	6	1.2	226	2	AC0388	probable short-cha	959	6	1.2	239	2	G97425	flagellar L-ring p
887	6	1.2	226	2	S75665	ABC-type transport	960	6	1.2	240	1	QOBRG3	flagellar L-ring p
888	6	1.2	226	2	G75342	hypothetical prote	961	6	1.2	240	1	AG2643	HMLF4 protein - hu
889	6	1.2	226	2	H84213	hypothetical prote	962	6	1.2	240	2	JI0143	antigen BCM1 precu
890	6	1.2	227	2	A75304	ABC transporter, A	963	6	1.2	240	2	D69261	sulfate ABC transp
891	6	1.2	227	2	T34990	hypothetical prote	964	6	1.2	240	2	A97531	branched-chain ami
892	6	1.2	227	2	B84696	probable glutathio	965	6	1.2	240	2	AB2750	hypothetical prote
893	6	1.2	227	2	AG1314	hypothetical prote	966	6	1.2	240	2	A36791	hypothetical prote
894	6	1.2	227	2	AG1686	hypothetical prote	967	6	1.2	240	2	D72415	zinc ABC transport
895	6	1.2	227	2	T45388	hypothetical prote	968	6	1.2	240	2	A39016	T-cell surface gly
896	6	1.2	228	2	T10507	ribulose-phosphate	969	6	1.2	241	1	D71233	probable 3-isoprop
897	6	1.2	228	2	B83583	dehydrobiotin synth	970	6	1.2	241	2	A75200	hypothetical prote
898	6	1.2	228	2	H83639	hypothetical prote	971	6	1.2	241	2	F82620	superoxide dismuta
899	6	1.2	228	2	AG3330	hypothetical prote	972	6	1.2	242	2	S30888	PRP38 protein - ye
900	6	1.2	228	2	C87467	ABC transporter, A	973	6	1.2	243	1	WMVZP2	F2 protein - fowlp
901	6	1.2	229	2	S33182	probable transport	974	6	1.2	243	2	G72482	probable 3-oxoacyl
902	6	1.2	229	2	T34277	hypothetical prote	975	6	1.2	243	2	E72405	ABC transporter, p
903	6	1.2	229	2	F75482	transcription regu	976	6	1.2	243	2	T39002	26S proteasome reg
904	6	1.2	230	2	H83001	probable permease	977	6	1.2	243	2	T18851	hypothetical prote
905	6	1.2	230	2	F71122	hypothetical prote	978	6	1.2	244	2	G98320	fixr protein homol

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979 6 1.2 244 2 AG2962 short-chain alchoh
980 6 1.2 244 2 G83953 ribosomal protein
981 6 1.2 244 2 A88330 sporulation transc
982 6 1.2 244 2 AD2953 transcription regu
983 6 1.2 244 2 A59365 cyanamide hydratase
984 6 1.2 244 2 B83630 hypotrichal prote
985 6 1.2 244 2 T39507 probable ATP synth
986 6 1.2 245 2 S43293 PLT3/PLK2 ligand (
987 6 1.2 245 2 T47501 do66 zinc finger p
988 6 1.2 245 2 A70777 hypotrichal prote
989 6 1.2 245 2 G90282 hypotrichal prote
990 6 1.2 245 2 A97381 hypotrichal trans
991 6 1.2 245 2 G98182 hypotrichal prote
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993 6 1.2 245 2 AD3104 conserved hypotrich
994 6 1.2 245 2 AC2203 glucose inhibited
995 6 1.2 246 2 T37021 probable methyltra
996 6 1.2 246 2 E75481 RNA methyltransfer
997 6 1.2 246 2 B87482 conserved hypotrich
998 6 1.2 247 2 C98340 2-deoxy-D-gluconat
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ALIGNMENTS

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RESULT 1
A59090 aspartic proteinase (BC 3.4.23.-) BACE precursor - human
N:Alternate names: beta-secretase; beta-site APP cleaving enzyme
C:Species: Homo sapiens (man)
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 11-May-2000
C:Accession: A59090
R:Vassar, R.; Bennett, B.D.; Babu-Khan, S.; Kahn, S.; Mendiaz, E.A.; Denis, P.; Teplow,
M.A.; Biere, A.L.; Curran, E.; Burgess, T.; Louis, J.C.; Collins, F.; Treanor, J.; Rogers
Science 286, 735-741, 1999
A:Title: beta-secretase cleavage of Alzheimer's amyloid precursor protein by the transme
A:Reference number: A59090; MUID:20002972; PMID:10531052
A>Note: submitted to Genbank, September 1999
A:Accession: A59090
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-501 <VAS>
A:Cross-references: GB:AF190725; NID:G6118538; PIDN:AAFO4142.1; PID:G6118539
C:Genetics:
A:Gene: BACE
C:Superfamily: beta-secretase
C:Keywords: Alzheimer's disease; aspartic proteinase; brain; glycoprotein; hydrolase; pr
F:1-21/Domains: signal sequence #status predicted <SIG>
F:1-21/Domains: propeptide #status predicted <PRO>
F:46-501/Product: acid proteinase BACE #status predicted <MAT>
F:461-477/Domains: transmembrane #status predicted <TRN>
F:93,289/Active site: Asp #status predicted
F:153,172,223,354/Binding site: carboxylate (Asn) (covalent) #status predicted
F:330-380/Disulfide bonds: #status predicted

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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 107 ILVDGSSNFAY 118
DB 90 ILVDGSSNFAY 101

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RESULT 2

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D87087 hypothetical protein ML1426 [imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C:Accession: D87087
R:Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho

```

```

R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Felwell, T.; Fraser, A.; Hamlin, N.; Holroyd
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A:Authors: Ruter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S.
A:Title: Massive gene decay in the leprosy bacillus.
A:Reference number: A86909; MUID:21128732; PMID:11234002
A:Accession: D87087
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-319 <SNO>
A:Cross-references: GB:AL450380; NID:G13093303; PIDN:CAC30377.1; GSPDB:GN00147
C:Genetics:
A:Gene: ML1426
C:Superfamily: inner membrane protein ugpA

Query Match 1.7%; Score 9; DB 2; Length 319;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 481 AILVLIVL 489
DB 294 AILVLIVL 302

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RESULT 3

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E82654 conserved hypothetical protein XF1641 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: E82654
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A>Note: for a complete list of authors see reference number A59328 below
A:Accession: E82654
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-863 <STM>
A:Cross-references: GB:AE003991; GB:AE003849; NID:G9106696; PIDN:AAF84450.1; GSPDB:GN00
A:Experimental source: strain 9a5c
R:Simpson, A.D.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carer,
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to Genbank, June 2000
A:Authors: Ferreira, V.C.A.; Perro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Froh
J.D.; Jungueira, M.L.; Kemper, E.L.; Klitajima, U.P.; Krieger, J.E.; Kurame, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins,
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasat
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silve
M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF1641

Query Match 1.7%; Score 9; DB 2; Length 863;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 59 GIALALEPA 67
DB 153 GIALALEPA 161

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RESULT 4

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H64131 transcription regulator H11596, leucine-responsive - Haemophilus influenzae (strain Rd
N:Alternate names: leucine-responsive regulatory protein
C:Species: Haemophilus influenzae
C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 26-Aug-1999

```

C/Accession: H64131
 R.Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Goceayme, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
 A/Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A./Title: Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd.
 A/Reference number: A64000; MUID:95350630; PMID:7542800
 A/Accession: H64131
 A/Status: nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-166 <TIGR>
 A/Cross-references: GB:U32833; GB:I42023; NID:g1574432; PIDN:AA023241.1; PID:g1574439; T C/Function:
 A/Description: activates a number of operons in response to the presence of exogenous le C/Superfamily: regulatory protein ascC
 C/Keywords: DNA binding; transcription regulation
 F:34-60/Region: helix-turn-helix motif

Query Match 1.5%; Score 8; DB 2; Length 166;
 Best Local Similarity 100.0%; Pred. No. 9.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 305 GTTLRLP 312
 Db 136 GTTLRLP 143

RESULT 5
 T09585
 high mobility group protein HMG1/Y-2 - sword bean
 C/Species: Canavalia gladiata (sword bean)
 C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
 C/Accession: T09585
 R.Yamamoto, S.; Minamikawa, T.
 Plant Mol. Biol. 33, 537-544, 1997
 A/Title: Two genes for the high mobility group protein HMG-Y are present in the genome C A/Reference number: Z16751; MUID:97201487; PMID:9049273
 A/Accession: T09585
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-178 <YAM>
 A/Cross-references: EMBL:D86595
 C/Genetics:
 A/Intons: 17/3
 C/Superfamily: histone H1

Query Match 1.5%; Score 8; DB 2; Length 178;
 Best Local Similarity 100.0%; Pred. No. 9.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 VVAPTPGP 49
 Db 149 VVAPTPGP 156

RESULT 6
 A71935
 hypothetical protein jhp0408 - *Helicobacter pylori* (strain J99)
 C/Species: *Helicobacter pylori*
 A/Variety: strain J99
 C/Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
 C/Accession: A71935
 R.Alm, R.A.; Ling, L.S.L.; Molt, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Meberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
 A/Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A/Reference number: A71800; MUID:99120557; PMID:9923682
 A/Accession: A71935
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-202 <ARN>
 A/Cross-references: GB:AE001475; GB:AE001439; NID:g4154939; PIDN:AA05989.1; PID:g415494

A/Experimental source: strain J99
 C/Genetics:
 A/Gene: jhp0408

Query Match 1.5%; Score 8; DB 2; Length 202;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 479 CGATLVL 486
 Db 29 CGATLVL 36

RESULT 7
 G64646
 hypothetical protein HPI015 - *Helicobacter pylori* (strain 26695)
 C/Species: *Helicobacter pylori*
 C/Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Aug-1997
 C/Accession: G64646
 R/Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKen son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Wathey, L Nature 388, 539-547, 1997
 A/Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C A/Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.
 A/Reference number: A64520; MUID:97394467; PMID:9252185
 A/Accession: G64646
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-205 <TOM>
 A/Cross-references: GB:AE000511; TIGR:HPI015

Query Match 1.5%; Score 8; DB 2; Length 205;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 479 CGATLVL 486
 Db 32 CGATLVL 39

RESULT 8
 JQ0729
 60K inner-membrane protein - *Proteus mirabilis* (fragment)
 C/Species: *Proteus mirabilis*
 C/Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 08-Oct-1999
 C/Accession: JQ0729
 R.Skovgaard, O.
 Gene 93, 27-34, 1990
 A/Title: Nucleotide sequence of a *Proteus mirabilis* DNA fragment homologous to the 60K- A/Reference number: JQ0729; MUID:91033012; PMID:2172087
 A/Accession: JQ0729
 A/Molecule type: DNA
 A/Residues: 1-237 <SKO>
 A/Cross-references: GB:M58352; GB:M31295; NID:g150873; PIDN:AAA83954.1; PID:g150874
 A/Experimental source: strain LM1509
 C/Keywords: DNA replication; membrane protein

Query Match 1.5%; Score 8; DB 2; Length 237;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 DTGSSNPA 117
 Db 206 DTGSSNPA 213

RESULT 9
 JQ2332
 ARI protein - cassava latent virus
 C/Species: cassava latent virus
 C/Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 07-May-1999
 C/Accession: JQ2332

R;Hong, Y.G.; Robinson, D.U.; Harrison, B.D.
J. Gen. Virol. 74, 2437-2443, 1993
A;Title: Nucleotide sequence evidence for the occurrence of three distinct whitefly-tran
A;Reference number: JQ2326; MUID:94065670; PMID:8245859
A;Accession: JQ2326
A;Molecule type: DNA
A;Residues: 1-257 <HON>
C;Superfamily: cassava latent virus coat protein
C;Keywords: coat protein

Query Match 1.5%; Score 8; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 39 TNRVAPT 46
Db 28 TNRVAPT 35

RESULT 10

G96659
Protein F2K11.24 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: G96659
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salbeck, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,
ker M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: G96659
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-287 <STO>
A;Cross-references: GB:AE005173; NID:g6633844; PIDN:AAFI9703.1; GSPDB:GN00141
C;Genetics:
A;Gene: F2K11.24
A;Map position: 1
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 1.5%; Score 8; DB 2; Length 287;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 301 IYDSGTTL 308
Db 269 IYDSGTTL 276

RESULT 11

H75528
Conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: H75528
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
S.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: H75528
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-303 <WHI>
A;Cross-references: GB:AE00196; GB:AE000513; NID:g6458032; PIDN:AAFO9938.1; PID:g645803
A;Experimental source: strain R1

C;Genetics:
A;Gene: DR0358
A;Map position: 1

Query Match 1.5%; Score 8; DB 2; Length 303;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 246 GGSIVLGG 253
Db 137 GGSIVLGG 144

RESULT 12

B95844
probable sugar ABC transporter permease protein ABC transporter SMB20015 [imported] - S
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: B95844
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhmester, J.; Chain, P.; Vorholter, F.J.; Herna
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing end
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: B95844
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-318 <KUR>
A;Cross-references: GB:AL591965; PIDN:CAC48418.1; PID:G1513890; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kise, E.; Komp, C.; Lelaure
heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: SMB20015
C;Superfamily: l-arabinose transport system permease arah

Query Match 1.5%; Score 8; DB 2; Length 318;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 484 LVLIVLL 491
Db 16 LVLIVLL 23

RESULT 13

AG0742
high-affinity zinc uptake system periplasmic binding protein [imported] - Salmonella en
C;Species: Salmonella enterica subsp. enterica serovar Typh
A;Note: this species has also been called Salmonella typh
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
C;Accession: AG0742
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar
S.; Moule, S.; O'Gaora, P.
Nature 413, 846-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero
A;Reference number: AB0502; PMID:11677608
A;Accession: AG0742
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-319 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD05642.1; PID:G16503138; GSPDB:GN00176
C;Genetics:
A;Gene: STY2099

C:Superfamily: hypothetical protein HI0119

Query Match 1.5%; Score 8; DB 2; Length 319;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 318 AVEAVAR 325
 |||||
 Db 271 AVEAVAR 278

RESULT 14

PRLIHD

Proteinase (EC 3.4.23.-) - squirrel monkey retrovirus SMRV-H

C:Species: squirrel monkey retrovirus SMRV-H

C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 23-Feb-1997

C:Accession: B31827

R:Oda, T.; Ikeda, S.; Watanabe, S.; Hatsushika, M.; Akiyama, K.; Mitsunobu, F.

Virology 167, 468-476, 1988

A:Title: Molecular cloning, complete nucleotide sequence, and gene structure of the prov

A:Reference number: A31827; MUID:89073750; PMID:3201749

A:Accession: B31827

A:Molecule type: DNA

A:Residues: 1-323 <ODA>

C:Genetics:

A:Gene: prt

C:Complex: homodimer

C:Superfamily: retroviral proteinase

C:Keywords: aspartic proteinase; homodimer; hydrolase

F:193/Active site: Asp (shared with dimeric partner) #status predicted

Query Match

1.5%; Score 8; DB 1; Length 323;

Best Local Similarity 100.0%; Pred. No. 17;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 161 DLVTIPKG 168
 |||||
 Db 126 DLVTIPKG 133

RESULT 15

T4299

ethanolamine-phosphate cytidyltransferase homolog - fission yeast (Schizosaccharomyces

C:Species: Schizosaccharomyces pombe

C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000

C:Accession: T42999

R:Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.

DNA Res. 4, 363-369, 1997

A:Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.

A:Reference number: 217323; MUID:98162722; PMID:9501991

A:Accession: T42999

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-327 <YOS>

A:Cross-references: EMBL:D89199; NID:G1749605; PIDN:BA013860.1; PID:G1749606

A:Experimental source: strain PR745

Query Match

1.5%; Score 8; DB 2; Length 327;

Best Local Similarity 100.0%; Pred. No. 17;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 304 SGTLLRL 311
 |||||
 Db 153 SGTLLRL 160

Search completed: April 1, 2003, 11:46:40
 Job time : 75 secs

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OM protein - protein search, using sw model

Run on: April 1, 2003, 11:35:19 ; Search time 27 Seconds
(without alignments)
795.731 Million cell updates/sec

Title: US-09-668-314C-2

Perfect score: 518
Sequence: 1 MGLARALLPLLAQMLRA.....RPDPEVNDSSLVRRHWK 518

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	518	100.0	518	1	BAC2_HUMAN
2	112	2.3	501	1	BACE_HUMAN
3	12	2.3	501	1	BACE_MOUSE
4	12	2.3	501	1	BACE_RAT
5	8	1.5	166	1	LRP_HAEM
6	8	1.5	237	1	60IM_PROMI
7	8	1.5	323	1	VPRT_SMRVH
8	8	1.5	340	1	CARP_POLTU
9	8	1.5	362	1	YHDX_ECOLI
10	8	1.5	365	1	ECTI_SCHPO
11	8	1.5	481	1	LBP_HUMAN
12	8	1.5	548	1	60IM_ECOLI
13	8	1.5	692	1	GLND_CORGL
14	8	1.5	1247	1	NIDO_HUMAN
15	8	1.5	1620	1	DNM1_MOUSE
16	8	1.5	1622	1	DNM1_RAT
17	7	1.4	126	1	DOCR_HUMAN
18	7	1.4	126	1	GA_HUMAN
19	7	1.4	136	1	VAI3_ARCFU
20	7	1.4	149	1	YDCZ_ECOLI
21	7	1.4	160	1	BIK_HUMAN
22	7	1.4	198	1	TTK_ECOLI
23	7	1.4	238	1	EPF3_HUMAN
24	7	1.4	249	1	YBGO_STRCO
25	7	1.4	267	1	EX3_HAEM
26	7	1.4	268	1	EX3_ECOLI
27	7	1.4	276	1	PSB8_HUMAN
28	7	1.4	296	1	KHSE_LACIC
29	7	1.4	297	1	COBD_MERTH
30	7	1.4	298	1	CHIA_PHANA
31	7	1.4	298	1	YAKI_YEAST
32	7	1.4	302	1	PPT2_HUMAN
33	7	1.4	302	1	Y091_MERUA

34	7	1.4	305	1	DDLB_ECO57
35	7	1.4	305	1	DDLB_ECOLI
36	7	1.4	305	1	DDLB_SALTI
37	7	1.4	305	1	DDLB_SALTY
38	7	1.4	324	1	PEPI_GADMO
39	7	1.4	325	1	DLP3_HUMAN
40	7	1.4	326	1	YR75_ECOLI
41	7	1.4	327	1	CD1A_HUMAN
42	7	1.4	337	1	PPAS_RAT
43	7	1.4	333	1	ILVC_MYCTU
44	7	1.4	337	1	YXAG_BACSU
45	7	1.4	334	1	MYRB_TREPA
46	7	1.4	354	1	YGP1_YEAST
47	7	1.4	356	1	RF1_BACSU
48	7	1.4	367	1	PEPA_CHICK
49	7	1.4	379	1	MRAM_TREPA
50	7	1.4	381	1	CHWV_CALJA
51	7	1.4	385	1	Y464_MYCGE
52	7	1.4	386	1	CYB_SARGL
53	7	1.4	386	1	PEPA_PIG
54	7	1.4	387	1	PEPI_RABIT
55	7	1.4	387	1	PEPI_RABIT
56	7	1.4	387	1	PEP3_RABIT
57	7	1.4	387	1	PEP4_RABIT
58	7	1.4	387	1	PEP4_RABIT
59	7	1.4	388	1	PEPI_MACFU
60	7	1.4	388	1	PEP2_MACFU
61	7	1.4	388	1	PEP4_MACFU
62	7	1.4	388	1	PEPA_HUMAN
63	7	1.4	388	1	PEPA_MACMU
64	7	1.4	388	1	PNCB_XYLFA
65	7	1.4	394	1	CATD_CHICK
66	7	1.4	408	1	LMP1_BOVIN
67	7	1.4	416	1	DAD2_PSEAE
68	7	1.4	419	1	CARY_CANAL
69	7	1.4	420	1	PAG2_PIG
70	7	1.4	428	1	SURA_ECOLI
71	7	1.4	452	1	MTN3_CHICK
72	7	1.4	452	1	PLM1_PLAFA
73	7	1.4	453	1	GASR_CANPA
74	7	1.4	454	1	GASR_BOVIN
75	7	1.4	460	1	VATB_TREVO
76	7	1.4	462	1	GSA_MYCTU
77	7	1.4	473	1	CYPI_CYNCA
78	7	1.4	494	1	CPS1_HUMAN
79	7	1.4	496	1	ASPR_ORYSA
80	7	1.4	513	1	ASPR_CUCPRE
81	7	1.4	517	1	PVRI_HUMAN
82	7	1.4	550	1	SYR_CORGL
83	7	1.4	558	1	YJ83_MYCTU
84	7	1.4	560	1	Y663_HAEM
85	7	1.4	569	1	YAP3_YEAST
86	7	1.4	589	1	PHBC_ALCEU
87	7	1.4	596	1	MKC7_YEAST
88	7	1.4	602	1	VE1_MNPV
89	7	1.4	603	1	PGH2_SHEEP
90	7	1.4	604	1	PGH2_BOVIN
91	7	1.4	604	1	PGH2_CAVPO
92	7	1.4	604	1	PGH2_HORSE
93	7	1.4	604	1	PGH2_HUMAN
94	7	1.4	604	1	PGH2_RABIT
95	7	1.4	646	1	KDBE_SCHPO
96	7	1.4	660	1	VNCS_PAVPN
97	7	1.4	662	1	BGL1_CANPA
98	7	1.4	662	1	VNCS_PAVPO
99	7	1.4	697	1	YE9C_SCHPO
100	7	1.4	703	1	EPG_ECOLI
101	7	1.4	703	1	EPG_SALTY
102	7	1.4	715	1	LCCT_LACLA
103	7	1.4	715	1	LCNC_LACLA
104	7	1.4	716	1	E2BE_RAT
105	7	1.4	717	1	COWA_STREN
106	7	1.4	721	1	E2BE_HUMAN

08x96	escherichia
P07862	escherichia
Q82967	salmonella
08x971	salmonella
P56272	gadis morhu
095866	homo sapien
P21314	escherichia
P06126	homo sapien
P29288	rattus norv
053248	mycobacteri
P42106	bacillus su
083128	treponema p
P38616	saccharomyc
P45872	bacillus su
P00793	gallus gall
083399	treponema p
09n242	callithrix
P47702	mycoplasma
063848	sarcophyton
P00791	sus scrofa
P28712	oryctolagus
P27821	oryctolagus
P28713	oryctolagus
Q9n264	callithrix
P03994	macaca fusc
P27677	macaca fusc
P27678	macaca fusc
P00790	homo sapien
P11489	macaca mula
Q9ped1	xyella fas
005744	gallus gall
005204	bos taurus
09n099	pseudomonas
P10977	candida alb
Q29079	sus scrofa
P21202	escherichia
Q42401	gallus gall
P38898	plasmidium
P79266	cantis fami
P92652	bos taurus
Q97c99	thermoplas
006390	mycobacteri
P40782	cygnata card
P08266	homo sapien
P42211	oryza sativ
004057	cucurbita p
Q15223	homo sapien
P35868	corynebacte
Q10873	mycobacteri
P71355	haemophilus
P23229	saccharomyc
P23608	a poly-beta
P53379	saccharomyc
Q84356	mascomys na
P79240	ovis aries
062658	bos taurus
P70682	cavia porce
Q19183	equus cabal
P35354	homo sapien
002768	oryctolagus
Q10364	schizosacch
P18547	porcine par
Q97y99	cantis fami
P52502	porcine par
Q13773	schizosacch
P02996	escherichia
P26229	salmonella
Q9c348	lactococcus
000564	lactococcus
064350	rattus norv
Q03727	streptococc
Q13144	homo sapien

107	7	1.4	721	1	E2B8_RABT	P47823	oryctolagus	180	6	1.2	115	1	NUM_FELCA	P48912	felis silve
108	7	1.4	733	1	YACK_RHIME	Q94447	rhizobium m	181	6	1.2	115	1	NUM_HALGR	P38600	hallicotamus
109	7	1.4	754	1	YAF6_SCHPO	O09860	schizosacch	182	6	1.2	115	1	NUM_HIPAM	Q92474	hippocretarus
110	7	1.4	775	1	PTNC_MOUSE	P35881	mus muscullu	183	6	1.2	115	1	NUM_HORSE	P48654	equus caball
111	7	1.4	797	1	SHK3_HUMAN	O98y80	homo sapien	184	6	1.2	115	1	NUM_HUMAN	O95708	homo sapien
112	7	1.4	831	1	NAPA_ALCBU	P31885	alcaligenes	185	6	1.2	115	1	NUM_HYLLA	O21519	hylobates l
113	7	1.4	841	1	RELA_STRAT	O85709	streptomyce	186	6	1.2	115	1	NUM_MICPE	P03899	mus muscullu
114	7	1.4	843	1	AD17_DROME	O94y65	drosophila b	187	6	1.2	115	1	NUM_PERGO	O95881	peromyscus
115	7	1.4	863	1	YABD_SCHPO	O09778	schizosacch	188	6	1.2	115	1	NUM_PERMA	O95897	peromyscus
116	7	1.4	899	1	RSCC_ECOLI	P14373	eschericchia	189	6	1.2	115	1	NUM_PERME	O95921	peromyscus
117	7	1.4	949	1	IF3A_TOBAC	Q40554	nicotiana t	190	6	1.2	115	1	NUM_PERPL	O21513	photopus su
118	7	1.4	958	1	EPB2_MOUSE	P54763	mus muscullu	191	6	1.2	115	1	NUM_PHOSU	Q00541	phoca vitul
119	7	1.4	993	1	BSG14_CAEEL	P41846	caenorhabdi	192	6	1.2	115	1	NUM_PHOVI	O79880	sus scrofa
120	7	1.4	1009	1	BGAL_ARTSP	O59140	actinobacte	193	6	1.2	115	1	NUM_PIG	O95915	polyporus
121	7	1.4	1015	1	TREA_EMENT	P78617	emericella	194	6	1.2	115	1	NUM_POLOR	P92697	pongo pygma
122	7	1.4	1054	1	EPB2_HUMAN	P29323	homo sapien	195	6	1.2	115	1	NUM_PONPA	O79444	oryctolagus
123	7	1.4	1055	1	YFPD4_YEAST	P43564	saccharomyc	196	6	1.2	115	1	NUM_RABIT	P05506	rattus norv
124	7	1.4	1073	1	CARB_RHIME	Q92p24	rhizobium m	197	6	1.2	115	1	NUM_RAT	O96066	rhinoceros
125	7	1.4	1163	1	SBCC_RHOCA	O68032	rhodobacter	198	6	1.2	115	1	NUM_RHITUN	O78753	ovis aries
126	7	1.4	1238	1	MAML_SCHPO	O08775	rattus norv	199	6	1.2	115	1	NUM_SHEEP	O21566	sigmodon hi
127	7	1.4	1336	1	VGR2_RAT	P25822	drosophila	200	6	1.2	115	1	NUM_SIGHT	P76172	eschericchia
128	7	1.4	1343	1	PIM_DROME	Q10900	mycobacteri	201	6	1.2	115	1	NUM_BRARE	O9m473	brechydanio
129	7	1.4	1533	1	CTPI_MYCTU	P16144	homo sapien	202	6	1.2	116	1	NUM_CARAU	O78686	carassius a
130	7	1.4	1625	1	ITB4_HUMAN	O36144	b tyrocidin	203	6	1.2	116	1	NUM_CHICK	P18938	gallus gall
131	7	1.4	1822	1	TYCC_BACBR	O70174	mus muscullu	204	6	1.2	116	1	NUM_CYPCA	P24974	cyprinus ca
132	7	1.4	6486	1	ACH4_MOUSE	P20440	thunmus thy	205	6	1.2	116	1	NUM_DIDMA	P41306	didelphis m
133	6	1.2	27	1	V59_BPT3	P20406	bacterioph	206	6	1.2	116	1	NUM_GADMO	P15957	gadus morhu
134	6	1.2	52	1	V59_BPT7	P20406	bacterioph	207	6	1.2	116	1	NUM_LATCH	O03171	latimeria c
135	6	1.2	52	1	SCP2_MESMA	Q9m473	mesobutius	208	6	1.2	116	1	NUM_MACRO	P92666	macroptus ro
136	6	1.2	56	1	SCP3_MESMA	Q9u8d1	mesobutius	209	6	1.2	116	1	NUM_ONCRO	P20666	oncothychnu
137	6	1.2	56	1	Y06H_BPT4	P13315	bacterioph	210	6	1.2	116	1	NUM_ONCKE	Q32567	oncothychnu
138	6	1.2	58	1	VLYS_BP21	P27360	bacterioph	211	6	1.2	116	1	NUM_ONCKI	P20687	oncothychnu
139	6	1.2	71	1	PEP2_THRUO	P20140	thunmus thy	212	6	1.2	116	1	NUM_ONCMA	P31629	oncothychnu
140	6	1.2	72	1	PEP2_THRUO	P20140	thunmus thy	213	6	1.2	116	1	NUM_ONCMA	P31629	oncothychnu
141	6	1.2	72	1	PEP2_THRUO	P20140	thunmus thy	214	6	1.2	116	1	NUM_ONCMA	P31629	oncothychnu
142	6	1.2	73	1	PEP2_THRUO	P20140	thunmus thy	215	6	1.2	116	1	NUM_ONCMA	P31629	oncothychnu
143	6	1.2	80	1	Y6A9_YEREN	O85269	yersinia en	216	6	1.2	116	1	NUM_ONCNE	P20688	oncothychnu
144	6	1.2	80	1	Y6A9_YERPE	Q9g9g3	yersinia pe	217	6	1.2	116	1	NUM_ONCTS	P25707	oncothychnu
145	6	1.2	81	1	VES_HPV35	P27226	human papil	218	6	1.2	116	1	NUM_PAROL	P92817	paralichthy
146	6	1.2	83	1	YF24_ARCFU	O28748	archaeoglob	219	6	1.2	116	1	NUM_SALSA	Q35929	salmo salar
147	6	1.2	87	1	Y123_BURCE	P24538	burkholderi	220	6	1.2	116	1	NUM_SALT	O03252	salmo trutt
148	6	1.2	88	1	LEVI_XENIA	P13684	xenopus lae	221	6	1.2	116	1	NUM_SCYCA	O79448	scylliorhinu
149	6	1.2	89	1	IAPF_FELCA	P12967	felis silve	222	6	1.2	116	1	NUM_SQUAC	O92477	squalus aca
150	6	1.2	96	1	Y698_MYCLE	O33024	mycobacteri	223	6	1.2	117	1	NUM_STRCA	O79102	struthio ca
151	6	1.2	100	1	APC2_CAVPO	P27916	cavia porce	224	6	1.2	117	1	NUM_PRUDU	Q9m558	prunus avic
152	6	1.2	100	1	PINL_HUMAN	O15428	homo sapien	225	6	1.2	117	1	NUM_SPIOL	O95776	spiniacia ol
153	6	1.2	101	1	ATPL_SULTO	P23040	sulfolobus	226	6	1.2	117	1	NUM_SPTOL	P13531	bombyx mori
154	6	1.2	101	1	PIPI1_PIG	P83106	sus scrofa	227	6	1.2	119	1	CHC2_BOMMO	Q17212	bombyx mori
155	6	1.2	102	1	COLL_HSVSC	P25576	herpesvirus	228	6	1.2	119	1	CHC3_BOMMO	Q17212	bombyx mori
156	6	1.2	105	1	ATPL_MYCPN	O59550	mycoplasma	229	6	1.2	119	1	CHC4_BOMMO	Q29100	sus scrofa
157	6	1.2	105	1	YKRD_BACSU	P49857	bacillus su	230	6	1.2	121	1	UPTI_PIG	Q29100	sus scrofa
158	6	1.2	106	1	Y0B5_MYCLE	O49723	mycobacteri	231	6	1.2	122	1	GLU1_LOBAM	Q9x3w1	zymomonas m
159	6	1.2	107	1	PKR2_RAT	O84613	rattus norv	232	6	1.2	124	1	HIS3_ZYMO	P00675	chinchilla
160	6	1.2	108	1	INS_AOTTR	P10604	aotus civivi	233	6	1.2	124	1	RNP_CHIR	P50509	homo sapien
161	6	1.2	108	1	INS_PIG	P01315	sus scrofa	234	6	1.2	124	1	SECG_BOREU	O51083	boirelia bu
162	6	1.2	108	1	INS_RODSP	P21563	rodentia sp	235	6	1.2	125	1	SZ09_HUMAN	O07325	homo sapien
163	6	1.2	109	1	RSBV_BACLI	O50230	bacillus li	236	6	1.2	125	1	CART_MOUSE	O95776	crotalus vi
164	6	1.2	109	1	CD1B_RABIT	P23042	oryctolagus	237	6	1.2	125	1	PRK2_MOUSE	O95776	crotalus vi
165	6	1.2	110	1	CSNA_BACSU	P37584	bacillus su	238	6	1.2	128	1	CVB_CROVY	O95776	crotalus vi
166	6	1.2	110	1	INS_CANFA	P01321	canis famli	239	6	1.2	128	1	PRK2_MOUSE	O95776	crotalus vi
167	6	1.2	110	1	INS_CERAE	P30407	cercopithec	240	6	1.2	129	1	CART_MOUSE	O95776	crotalus vi
168	6	1.2	110	1	INS_HACPA	P30406	macaca fasc	241	6	1.2	131	1	FABB_BOVIN	O04158	porcine res
169	6	1.2	110	1	INS_PSAOB	O65587	psammomy o	242	6	1.2	131	1	CRB1_MYCTU	O28118	archaeoglob
170	6	1.2	110	1	INS_PSAOB	O65587	psammomy o	243	6	1.2	132	1	Y164_ARCFU	Q81998	fusobacteri
171	6	1.2	110	1	INS_PSAOB	O65587	psammomy o	244	6	1.2	132	1	RS9_FUSUN	Q71912	anopheles g
172	6	1.2	110	1	PEPA_BOVIN	P00792	bos taurus	245	6	1.2	133	1	CC42_ANGGA	O92818	chlamydia p
173	6	1.2	113	1	TYBP_HUMAN	O43914	homo sapien	246	6	1.2	134	1	RS9_CHLPN	O64248	mycobacteri
174	6	1.2	115	1	NUM_BALPH	P24974	baiaenopter	247	6	1.2	134	1	VG24_BPMD2	O41387	spiniacia ol
175	6	1.2	115	1	NUM_BOVIN	O92898	bos taurus	248	6	1.2	137	1	PSBW_SPTOL	P95992	sulfolobus
176	6	1.2	115	1	NUM_CANFA	O03202	ceratotheri	249	6	1.2	137	1	RS9_SULTO	Q96y43	sulfolobus
177	6	1.2	115	1	NUM_CERSI	O03202	ceratotheri	250	6	1.2	137	1	RS9_SULTO	Q96y43	sulfolobus
178	6	1.2	115	1	NUM_DASNO	O03202	daeypus nov	251	6	1.2	137	1	RS9_SULTO	Q96y43	sulfolobus
179	6	1.2	115	1	NUM_EQUAS	P92482	equus asinu	252	6	1.2	137	1	RS9_SULTO	Q96y43	sulfolobus

253	6	1.2	138	1	YGM_ECOLI	P42554 escherichia	326	6	1.2	195	1	TRPG_SULSO	Q06129 sulfobus
254	6	1.2	140	1	RS12_CABEL	P49156 caenorhabdi	327	6	1.2	196	1	HIS7_CAUCR	Q94332 caulobacter
255	6	1.2	140	1	YB19_ARCFU	Q29162 archaeoglob	328	6	1.2	196	1	Y449_TREPA	Q83463 treponema p
256	6	1.2	141	1	HBA2_NOTCO	P16308 notochenia	329	6	1.2	197	1	HIS7_STRCO	P16247 streptomyc
257	6	1.2	141	1	TNG1_HUMAN	P56846 homo sapien	330	6	1.2	197	1	PTCA_MOUSE	Q64657 mus musculu
258	6	1.2	142	1	RPB6_SCHPO	P36595 schizosacch	331	6	1.2	198	1	CD8A_PONPY	P30433 pongo pygma
259	6	1.2	144	1	YI00_AQUAE	Q87669 aquiflex aeo	332	6	1.2	198	1	RL19_CABEL	Q02639 caenorhabdi
260	6	1.2	146	1	RBFA_RHIL0	Q98517 rhizobium 1	333	6	1.2	199	1	YB01_RHIL0	Q98474 rhizobium 1
261	6	1.2	147	1	LECE_ANTCR	P06027 anthocidari	334	6	1.2	199	1	YET4_HAEIN	Q57213 haemophilus
262	6	1.2	147	1	TTHY_SHEEP	P12303 ovis aries	335	6	1.2	202	1	COAT_BMYVG	P09528 beet wester
263	6	1.2	148	1	EXBB_AQUAE	Q67637 aquiflex aeo	336	6	1.2	202	1	COAT_BMYVG	Q00259 beet wester
264	6	1.2	148	1	RNP_GERNI	Q9482 gerbillus n	337	6	1.2	202	1	CUT1_BOTCI	Q0278 botrytis ci
265	6	1.2	152	1	PYR1_PYRAB	P77919 pyrococcus	338	6	1.2	202	1	LSFA_MYCTU	Q10764 mycobacteri
266	6	1.2	153	1	YEH3_PSEAE	Q9hub0 pseudomonas	339	6	1.2	205	1	DDL_ANACE	P35660 anaplasma c
267	6	1.2	155	1	BCCP_HAEIN	P43874 haemophilus	340	6	1.2	205	1	EFAL_HUMAN	P20827 homo sapien
268	6	1.2	156	1	RIB2_PHOLE	Q9392 phorbacter	341	6	1.2	205	1	EFAL_MOUSE	P52793 mus musculu
269	6	1.2	160	1	COAT_CGMVS	P19521 cucumber gr	342	6	1.2	205	1	EFAL_RAT	P97553 rattus norv
270	6	1.2	160	1	Y964_MYCTU	P71546 mycobacteri	343	6	1.2	205	1	KGUA_LACLA	Q9ceeb3 lactococcus
271	6	1.2	161	1	TPW_SCHPO	Q02088 schizosacch	344	6	1.2	205	1	NEP_HVIZH	P05859 human immun
272	6	1.2	161	1	YANB_YEAST	P39564 saccharomyc	345	6	1.2	205	1	YU11_MYCTU	Q07722 mycobacteri
273	6	1.2	163	1	LRP_ECOLI	P19494 escherichia	346	6	1.2	206	1	YK07_YEAST	P36061 saccharomyc
274	6	1.2	163	1	LRP_KLEPN	P37424 klebsiella	347	6	1.2	206	1	FGF4_BOVIN	P48803 bos taurus
275	6	1.2	163	1	LRP_SALTY	P37403 salmonella	348	6	1.2	207	1	CCMA_ECOLI	P33931 escherichia
276	6	1.2	163	1	LRP_SERMA	P37425 serratia ma	349	6	1.2	207	1	HIS7_AZOB	P18787 azospirillum
277	6	1.2	164	1	PUR6_HAEIN	P43849 haemophilus	350	6	1.2	207	1	SODM_CHLPP	Q92924 chlamydia p
278	6	1.2	164	1	YBP3_ACIAM	P32987 acidianus a	351	6	1.2	208	1	NEP_HVILH	Q05858 human immun
279	6	1.2	165	1	DEST_HUMAN	P18282 homo sapien	352	6	1.2	209	1	HUPM_AZOC	Q43954 azotobacter
280	6	1.2	165	1	RL10_BACSU	P42923 bacillus su	353	6	1.2	209	1	PRL_ANGAN	P33096 anguilla an
281	6	1.2	165	1	YGZD_YEAST	P51057 saccharomyc	354	6	1.2	210	1	FGFL_MOUSE	Q9j1n1 mus musculu
282	6	1.2	165	1	YREP_BUCTS	Q12128 buchiera ap	355	6	1.2	210	1	FLPA_ARCFU	Q28192 archaeoglob
283	6	1.2	167	1	YREP_BUCPE	Q39e4 buchiera ap	356	6	1.2	211	1	DEOC_BACSU	P39121 bacillus su
284	6	1.2	168	1	NEU2_MOUSE	P35455 mus musculu	357	6	1.2	211	1	RL1_HALCU	P05966 halobacteri
285	6	1.2	168	1	SULA_SERMA	P08445 serratia ma	358	6	1.2	211	1	RL1_HALCU	P13375 halobacteri
286	6	1.2	169	1	MSA1_STEAM	Q99qds staphylococ	359	6	1.2	213	1	PYRE_METJA	Q57700 methanococc
287	6	1.2	169	1	SULA_ECOLI	P08446 escherichia	360	6	1.2	214	1	ATPE_ALBCO	P48693 albinaria c
288	6	1.2	169	1	SULA_ENTAE	P08447 enterobacte	361	6	1.2	214	1	CYB_AGRKA	P92845 agkistrodon
289	6	1.2	169	1	SULA_SALTY	P08447 salmonella	362	6	1.2	214	1	CYB_AGRKA	P92852 agkistrodon
290	6	1.2	170	1	HPAC_KLEPN	Q48441 klebsiella	363	6	1.2	214	1	CYB_BOTAT	P92846 botriops at
291	6	1.2	173	1	PACA_ONCNE	P41585 oncohychnu	364	6	1.2	214	1	CYB_BOTBI	P92847 botriops at
292	6	1.2	173	1	RUVG_BRUME	Q8Yiv7 bruceella me	365	6	1.2	214	1	CYB_BORSC	P92849 botriochis
293	6	1.2	173	1	VENV_TELV	Q04565 lelyetia vi	366	6	1.2	214	1	CYB_CERCE	P87419 cerastes ce
294	6	1.2	174	1	CUL1_TENMO	P80681 tenebrio mo	367	6	1.2	214	1	CYB_CROAT	P92850 crocalus at
295	6	1.2	174	1	YGAB_YEAST	P53279 saccharomyc	368	6	1.2	214	1	CYB_LACMU	P92853 lachesis mu
296	6	1.2	174	1	YGAB_ECOLI	P55774 escherichia	369	6	1.2	214	1	CYB_TRIST	P92857 timeresuru
297	6	1.2	175	1	DIAC_BOVIN	Q01458 bos taurus	370	6	1.2	215	1	YFG6_LACCA	P93924 lactobacill
298	6	1.2	176	1	HSIV_AQUAE	Q67587 aquiflex aeo	371	6	1.2	215	1	RL3_RICPR	P48952 rickettsia
299	6	1.2	178	1	ESMS_DROME	P13086 diosophila	372	6	1.2	216	1	YLM3_CABEL	P34357 caenorhabdi
300	6	1.2	179	1	AX16_PEA	P49680 plism sativ	373	6	1.2	217	1	OMPW_VIBCH	P17466 vibrio chol
301	6	1.2	179	1	OPA3_HUMAN	Q9h6k4 homo sapien	374	6	1.2	218	1	SGAH_MYCPN	P75293 mycoplasma
302	6	1.2	180	1	CFTR_CAVPO	Q00552 cavia porce	375	6	1.2	218	1	SODM_SCHPO	Q9ux40 schizosacch
303	6	1.2	182	1	APT_STRCO	P52561 streptomyc	376	6	1.2	219	1	ERD2_YEAST	P18414 saccharomyc
304	6	1.2	182	1	HSIV_RICCN	Q92i17 rickettsia	377	6	1.2	219	1	ISPD_CHLTR	Q84468 chlamydia t
305	6	1.2	182	1	HSIV_RICPR	Q92dk9 rickettsia	378	6	1.2	220	1	TRBF_RHISN	P55403 rhizobium s
306	6	1.2	184	1	MOP3_MOUSE	P04939 mus musculu	379	6	1.2	221	1	HA2Q_MOUSE	P04227 mus musculu
307	6	1.2	185	1	DSBE_SALTY	Q8xf6 salmonella	380	6	1.2	223	1	TPIS_AERPE	Q9lyr1 aeropyrum p
308	6	1.2	185	1	YXAK_BACSU	P42110 bacillus su	381	6	1.2	225	1	GIDB_THETH	Q9lyv2 thermus the
309	6	1.2	188	1	GCHI_BACHD	Q9Kcc7 bacillus ha	382	6	1.2	225	1	VGZB_AMEPV	P29818 amesacta moo
310	6	1.2	188	1	TRAF_RHISN	P55417 rhizobium s	383	6	1.2	225	1	Y574_AERPE	Q9y4k4 aeropyrum p
311	6	1.2	188	1	Y460_PYRHO	Q58215 pyrococcus	384	6	1.2	225	1	YB67_AERPE	Q9yus5 aeropyrum p
312	6	1.2	188	1	Y460_PYRHO	Q58215 pyrococcus	385	6	1.2	226	1	TSIS_SMSAV	P01128 simian sarc
313	6	1.2	189	1	PUR2_CHRVI	Q46482 chromatiu	386	6	1.2	228	1	BID0_PSEAE	Q9i614 pseudomonas
314	6	1.2	189	1	Y006_CHLTR	Q84009 chlamydia t	387	6	1.2	229	1	RPE_RHOCA	P51012 rhodobacter
315	6	1.2	190	1	CAH2_FLALI	P40793 flaveria ji	388	6	1.2	230	1	Y0E1_STRAT	Q53683 streptomyc
316	6	1.2	191	1	CC42_DROME	P40793 flaveria ji	389	6	1.2	230	1	Y128_AQUAE	Q67688 aquiflex aeo
317	6	1.2	191	1	MOBA_PYRAB	Q9V0d0 pyrococcus	390	6	1.2	231	1	YH62_YEAST	P38829 saccharomyc
318	6	1.2	191	1	PIC2_AGRTH	P29113 agrobacteri	391	6	1.2	232	1	6PGL_CAUCR	Q9aen1 caulobacter
319	6	1.2	191	1	RUV2_THETH	Q9f1q3 thermus the	392	6	1.2	233	1	CI83_SHEEP	P80943 ovis aries
320	6	1.2	192	1	MOBA_PYRHO	Q58708 pyrococcus	393	6	1.2	233	1	HA2F_MOUSE	P14435 mus musculu
321	6	1.2	192	1	TRPG_SERMA	P00900 serratia ma	394	6	1.2	233	1	HA2R_MOUSE	P14436 mus musculu
322	6	1.2	192	1	TRPG_SERMA	P71381 haemophilus	395	6	1.2	233	1	HA2S_MOUSE	P14437 mus musculu
323	6	1.2	194	1	HIS7_BACHD	Q9K6z3 bacillus ha	396	6	1.2	234	1	VG8_EBV	P03224 epstein-bar
324	6	1.2	194	1	HIS7_BACHD	Q9K6z3 bacillus ha	397	6	1.2	235	1	CD8A_HUMAN	P01732 homo sapien
325	6	1.2	195	1	CSF3_PIG	Q02837 sus scrofa	398	6	1.2	236	1	CYSA_CHLVU	P56344 chlorella v

399	6	1.2	237	1	CYSH_XYLFA	Q9pda2 xylella fas	472	6	1.2	268	1	CH14_BRANA	Q06209 braesia na
400	6	1.2	237	1	YBSO_YEAST	P38242 saccharomyc	473	6	1.2	268	1	EX3_SALTY	Q92612 salmonella
401	6	1.2	237	1	Y194_AOUAE	O67734 aquifex aeo	474	6	1.2	268	1	MIND_BACSU	Q01464 bacillus su
402	6	1.2	238	1	MABA_RAT	P19999 retius norv	475	6	1.2	268	1	Y489_METUA	O57993 methanococ
403	6	1.2	239	1	CD8A_CANPA	P33706 canis famli	476	6	1.2	269	1	IGT_BACSU	O34752 bacillus su
404	6	1.2	239	1	CYSH_THIRO	P52672 thlocapsa r	477	6	1.2	269	1	SAPF_HAEIN	P45289 haemophilus
405	6	1.2	239	1	FLGH_AGRIS	Q44342 agrobacteri	478	6	1.2	269	1	TRPA_BACST	P19867 bacillus st
406	6	1.2	239	1	MABA_MOUSE	P39039 mus musculu	479	6	1.2	269	1	YRBF_ECOLI	P45393 escherichia
407	6	1.2	240	1	CD48_MOUSE	P18181 mus musculu	480	6	1.2	270	1	TONB_HAEIN	P42872 haemophilus
408	6	1.2	240	1	CD7_HUMAN	P09564 homo sapien	481	6	1.2	271	1	CRK_DROME	O9xymo drosophila
409	6	1.2	240	1	TPMT_MOUSE	O55060 mus musculu	482	6	1.2	271	1	PDX4_HUMAN	O13162 homo sapien
410	6	1.2	240	1	TPMT_MOUSE	Q9gx22 mus spretus	483	6	1.2	271	1	YM34_MYCTU	O05879 mycobacteri
411	6	1.2	240	1	US19_HCVWA	P09722 human cytom	484	6	1.2	271	1	Y233_AOUAE	O66144 aquifex aeo
412	6	1.2	240	1	VG45_HSV11	Q00111 ictaluriid h	485	6	1.2	273	1	RFAP_YEAST	P26754 saccharomyc
413	6	1.2	240	1	Y124_THEMA	O70601 rattus norv	486	6	1.2	273	1	YF45_SCHPO	O10475 schizosacch
414	6	1.2	241	1	LAT_RAT	P21625 spiroplasma	487	6	1.2	273	1	YKAK_CABEL	P34224 caenorhabdi
415	6	1.2	241	1	SPIR_SPIME	O54957 mus musculu	488	6	1.2	274	1	PDX4_BOVIN	P41217 homo sapien
416	6	1.2	242	1	PR38_YEAST	Q00723 saccharomyc	489	6	1.2	274	1	POR4_ARATH	O9b912 bos taurus
417	6	1.2	242	1	RPNA_SCHPO	O94444 schizosacch	490	6	1.2	275	1	POR4_SOLTU	Q9stf5 arabidopsis
418	6	1.2	243	1	Y128_FOMPV	P15910 fowlpox vir	491	6	1.2	275	1	TF2D_ARTSF	P42055 solanum tub
419	6	1.2	243	1	CYAH_MYRYE	P22143 myrothecium	492	6	1.2	275	1	MOX2_PARDE	O17488 artemia san
420	6	1.2	244	1	NGN1_MOUSE	P70660 mus musculu	493	6	1.2	276	1	PLPB_PASHA	P29900 patrococcus
421	6	1.2	244	1	NGN1_MOUSE	P70595 rattus norv	494	6	1.2	276	1	TNR5_HUMAN	O08869 pasteurella
422	6	1.2	244	1	RS2_BACHD	Q9ka63 bacillus ha	495	6	1.2	277	1	CEMA_CYACA	P25942 homo sapien
423	6	1.2	244	1	GIDB_ANASP	O8ysa7 anabeena sp	496	6	1.2	278	1	OX2G_RAT	O9tm16 cyatidulm c
424	6	1.2	245	1	YM29_MYCTU	O10513 mycobacteri	497	6	1.2	279	1	PSA1_DROME	P04218 rattus norv
425	6	1.2	245	1	YOR4_ANATH	O44408 anaerocellu	498	6	1.2	279	1	CEBE_DROME	P12881 drosophila
426	6	1.2	246	1	LPXH_XANCP	P58976 xanthomonas	499	6	1.2	281	1	P2C1_YEAST	O15774 homo sapien
427	6	1.2	247	1	SLTI_CABEL	Q9u3n5 caenorhabdi	500	6	1.2	281	1	Y1YF_PSEPU	P35182 saccharomyc
428	6	1.2	247	1	YFBB_HAEIN	O28641 haemophilus	501	6	1.2	281	1	PANC_PSEAE	P23106 pseudomonas
429	6	1.2	247	1	Y629_ARCFU	O28641 archaeoglob	502	6	1.2	283	1	FRI1_MAIZE	Q9h9vc pseudomonas
430	6	1.2	247	1	HMXI_CHICK	P28361 gallus gall	503	6	1.2	285	1	BLAI_ENTCT	P29036 zea mays (m
431	6	1.2	249	1	PSM2_HAIYO	O9v235 halobacteri	504	6	1.2	286	1	RER2_YEAST	P18215 enterobacte
432	6	1.2	249	1	PYR2_FREDI	P18543 fremyella d	505	6	1.2	287	1	SMN_BOVIN	P31516 saccharomyc
433	6	1.2	249	1	YK73_MYCTU	Q10681 mycobacteri	506	6	1.2	287	1	SMN_CANPA	O02771 canis famli
434	6	1.2	251	1	E1A_ADE41	P10542 human adeno	507	6	1.2	287	1	STX4_CABEL	P91409 caenorhabdi
435	6	1.2	251	1	GLI2_BUCAI	P57336 buchiera ap	508	6	1.2	288	1	AOX4_AERPE	Q9ydx4 aeropyrum p
436	6	1.2	251	1	TRPC_HALVO	P18304 halobacteri	509	6	1.2	288	1	HME2_CHICK	Q05917 gallus gall
437	6	1.2	251	1	Y484_MYCTU	O11150 mycobacteri	510	6	1.2	288	1	HMXX_CHICK	P50223 gallus gall
438	6	1.2	251	1	ZNUC_ECOLI	P52648 escherichia	511	6	1.2	288	1	IPYR_SCHPO	P19117 schizosacch
439	6	1.2	252	1	KDSB_VIBCH	Q9qgx2 vibrio chol	512	6	1.2	288	1	SDC_CABEL	P50605 caenorhabdi
440	6	1.2	252	1	RL2_YEAST	P05736 saccharomyc	513	6	1.2	289	1	CRTB_THETH	P37270 thermus the
441	6	1.2	253	1	HA2J_MOUSE	P23150 mus musculu	514	6	1.2	289	1	DLX5_MOUSE	P70356 mus musculu
442	6	1.2	253	1	ST19_MOUSE	O9jhn8 mus musculu	515	6	1.2	289	1	DLX5_RAT	P50575 rattus norv
443	6	1.2	254	1	GLI2_MOUSE	P05446 rhodopsedu	516	6	1.2	290	1	RASI_CANAL	P90x77 candida alb
444	6	1.2	255	1	SSUB_ECOLI	P38053 escherichia	517	6	1.2	292	1	Y240_MYCBE	P47482 mycoplasma
445	6	1.2	255	1	HA2D_MOUSE	P04228 mus musculu	518	6	1.2	293	1	BLAC_RHOCA	P14171 rhodobacter
446	6	1.2	256	1	MYF5_NOTVI	Q91154 notophthalm	519	6	1.2	293	1	CWFL_SCHPO	O14161 schizosacch
447	6	1.2	256	1	Y929_TREPA	O83899 treponema p	520	6	1.2	294	1	DPM1_USYMA	P54856 usiliago ma
448	6	1.2	256	1	BAC2_HALS2	P29563 halobacteri	521	6	1.2	294	1	MENA_MYCLE	O07134 mycobacteri
449	6	1.2	259	1	EXB4_ARATH	O9bjd1 arabidopsis	522	6	1.2	295	1	Y005_RICPR	O92637 rickettsia
450	6	1.2	259	1	MURB_HELPY	O25963 helicobacte	523	6	1.2	295	1	Y234_METUA	O60258 methanococ
451	6	1.2	259	1	SSAT_SALTY	P96068 salmonella	524	6	1.2	297	1	Y103_HUMAN	O15006 homo sapien
452	6	1.2	259	1	T10C_HUMAN	O14798 h tumor nec	525	6	1.2	297	1	YD67_METUA	O88762 methanococ
453	6	1.2	259	1	SSAT_SALTY	O57993 methanococ	526	6	1.2	299	1	DAPA_STRCO	O68481 streptomyce
454	6	1.2	259	1	Y500_METUA	P73369 synectocyst	527	6	1.2	299	1	SPY4_HUMAN	O9C004 homo sapien
455	6	1.2	260	1	YSAI_CHICK	O42265 gallus gall	528	6	1.2	300	1	COX2_YEAST	P19516 saccharomyc
456	6	1.2	260	1	PSAI_CHICK	O42265 gallus gall	529	6	1.2	302	1	CH14_SOLTU	P52406 solanum tub
457	6	1.2	261	1	DER3_DERPT	P33675 dermatophag	530	6	1.2	302	1	HTPX_AOUAE	O6779X aquifex aeo
458	6	1.2	261	1	YHEB_CHLVI	P56160 chlorobium	531	6	1.2	302	1	PP13_DROME	P12962 drosophila
459	6	1.2	261	1	SUMT_SYNY3	O55749 mycobocyst	532	6	1.2	302	1	PP13_DROME	O05547 drosophila
460	6	1.2	263	1	YD56_MYCTU	O11026 mycobacteri	533	6	1.2	302	1	PPT2_MOUSE	O35448 mus musculu
461	6	1.2	263	1	YHCK_ECOLI	P45427 escherichia	534	6	1.2	302	1	PPT2_MOUSE	O70489 rattus norv
462	6	1.2	264	1	VALI_MDV	P06847 wheat dwarf	535	6	1.2	302	1	SPAO_SALDU	O53968 salmonella
463	6	1.2	264	1	MYO2_LYCES	P54927 lycopersico	536	6	1.2	303	1	SPAO_SALTI	O56022 salmonella
464	6	1.2	266	1	ETFB_MYCTU	O53075 mycobacteri	537	6	1.2	303	1	ISPE_MYCTU	P40699 salmonella
465	6	1.2	266	1	TRP1_CYACA	O9t1w8 cyatidium c	538	6	1.2	306	1	YHBE_HAEIN	P13360 haemophilus
466	6	1.2	267	1	PM27_STRPU	Q26x16 strongyloce	539	6	1.2	309	1	GLU1_ECOLI	P43387 haemophilus
467	6	1.2	267	1	Y123_THEMA	O9wxxt thermotoga	540	6	1.2	310	1	TUS_KLEPO	P77454 escherichia
468	6	1.2	267	1	Y441_METUA	O57883 methanococ	541	6	1.2	311	1	HEM3_NEIMA	O52715 klebsiella
469	6	1.2	267	1	YSR4_CABEL	O09952 caenorhabdi	542	6	1.2	311	1		O9jve4 neisseria m
470	6	1.2	267	1			543	6	1.2				
471	6	1.2	267	1			544	6	1.2				

545	6	1.2	311	1	HEM3_NEIME	Q9K0p6 neisseries m	618	6	1.2	351	1	COLF_ARATH	Q9fhn8 arabidopsis
546	6	1.2	312	1	FMT_MYCTU	P71674 mycobacteri	619	6	1.2	351	1	KLIF2_RAT	Q9et58 rattus norv
547	6	1.2	312	1	MEM_EBV	P03208 epstein-bar	620	6	1.2	351	1	ROM1_BOVIN	P52205 bos taurus
548	6	1.2	312	1	YC39_CVACA	O19883 cyanidium c	621	6	1.2	351	1	ROM1_HUMAN	O03395 homo sapien
549	6	1.2	313	1	LDH_CLOAB	O97md1 clostridium	622	6	1.2	351	1	ROM1_MOUSE	K32958 mus musculu
550	6	1.2	314	1	YC35_GUITH	O78472 guillardia	623	6	1.2	352	1	CLTI_MOUSE	O99344 mus musculu
551	6	1.2	317	1	KDT2_SALT	O88h3 salmonella	624	6	1.2	353	1	Y634_CHLMU	O9pk39 chlamydia m
552	6	1.2	317	1	KDT2_SALT	O88q24 salmonella	625	6	1.2	353	1	YNCB_ECOLI	P76113 escherichia
553	6	1.2	317	1	MTX1_HUMAN	O13505 homo sapien	626	6	1.2	354	1	AC14_HUMAN	P35250 homo sapien
554	6	1.2	317	1	MTX1_MOUSE	P47802 mus musculu	627	6	1.2	354	1	KLIF2_MOUSE	O60843 mus musculu
555	6	1.2	317	1	Y196_MYCTU	O10862 mycobacteri	628	6	1.2	355	1	CYSA_SYNY3	P74548 synechocyst
556	6	1.2	318	1	Y196_MYCTU	O9X081 thermocoga	629	6	1.2	355	1	DEGS_ECOLI	P31137 escherichia
557	6	1.2	319	1	YC39_PORPU	P51238 porphyra pu	630	6	1.2	355	1	KLIF2_HUMAN	O9Y5v3 homo sapien
558	6	1.2	319	1	YF18_MYCTU	O05090 mycobacteri	631	6	1.2	355	1	Y121_TREPA	O83358 treponema p
559	6	1.2	320	1	RLPA_RICPR	O94ed2 rickettsia	632	6	1.2	356	1	HITC_HAEIN	P44513 haemophilus
560	6	1.2	321	1	YC39_CVAPA	P48279 cyanophora	633	6	1.2	356	1	SPAS_SALT	P40702 salmonella
561	6	1.2	322	1	ARG1_HUMAN	P05089 homo sapien	634	6	1.2	357	1	AMRP_RAT	O99068 rattus norv
562	6	1.2	323	1	CMGB_BACHD	O9K920 bacillus ha	635	6	1.2	358	1	VCOK_ADB40	P48753 human adeno
563	6	1.2	323	1	VANH_ENTFA	O47748 enterococcu	636	6	1.2	358	1	Y4E8_RHISN	P55428 rhizobium s
564	6	1.2	325	1	LXBI_PHOLE	P09141 photobacter	637	6	1.2	359	1	AC14_CHICK	P53033 gallus gall
565	6	1.2	326	1	GGH_ARATH	O65355 arabidopsis	638	6	1.2	359	1	WECP_ECO57	O8xax8 escherichia
566	6	1.2	326	1	PHP_MYCTU	P96413 mycobacteri	639	6	1.2	359	1	WECP_ECOLI	P56258 escherichia
567	6	1.2	327	1	XYNA_ASAPC	O59859 aspergillus	640	6	1.2	360	1	AMRP_MOUSE	P55302 mus musculu
568	6	1.2	327	1	YBC5_CHLYT	O50310 chlorobium	641	6	1.2	360	1	MANB_BACSU	P55278 bacillus su
569	6	1.2	328	1	AFUC_HAEIN	P45231 haemophilus	642	6	1.2	362	1	ILVE_STRCO	O86505 streptomyce
570	6	1.2	328	1	GRHR_BOVIN	P32236 bos taurus	643	6	1.2	363	1	BASS_ECOLI	P20844 escherichia
571	6	1.2	328	1	GRHR_SHEEP	P32237 ovis aries	644	6	1.2	364	1	CD13_HUMAN	P20148 homo sapien
572	6	1.2	329	1	COT4_HUMAN	O9bix3 homo sapien	645	6	1.2	364	1	RECE_AZOVI	P49977 azobacter
573	6	1.2	329	1	CTAO_BACSU	O31652 bacillus su	646	6	1.2	365	1	CATD_SHEEP	O9mz88 ovis aries
574	6	1.2	329	1	IPNS_STRCL	P10621 streptomyce	647	6	1.2	365	1	CYSA_ECOLI	P16676 escherichia
575	6	1.2	330	1	GP43_HUMAN	O15552 homo sapien	648	6	1.2	365	1	CYSA_SALT	P40860 salmonella
576	6	1.2	330	1	YH75_ARCFU	O28499 archaeoglob	649	6	1.2	365	1	YI13_YEAST	P40506 saccharomyc
577	6	1.2	332	1	TRPD_VIBPA	P22096 vibrio para	650	6	1.2	366	1	PMEA_ERWCH	P07683 erwinia chr
578	6	1.2	333	1	CIB1_SHEEP	O28565 ovis aries	651	6	1.2	366	1	YCHO_ECOLI	O46840 escherichia
579	6	1.2	333	1	CIB2_SHEEP	O29422 ovis aries	652	6	1.2	367	1	DCUP_HUMAN	P06132 homo sapien
580	6	1.2	333	1	HK32_HUMAN	P78367 homo sapien	653	6	1.2	367	1	DIAC_RAT	Q01460 rattus norv
581	6	1.2	334	1	MRPL_CAEEL	O30459 caenorhabdi	654	6	1.2	368	1	ILVE_MYCTU	Q01039 mycobacteri
582	6	1.2	334	1	PIT_RHIME	O30459 rhizobium m	655	6	1.2	368	1	ST19_HUMAN	P49842 homo sapien
583	6	1.2	334	1	UNG_HSV11	P10166 herpes simp	656	6	1.2	369	1	MURR_MYCTU	O11448 mycobacteri
584	6	1.2	334	1	YCL1_MERTH	O27279 methanobact	657	6	1.2	370	1	CYB_COREN	O48039 corallus en
585	6	1.2	335	1	YDS9_SCHRO	O10312 eschiosacch	658	6	1.2	370	1	CYB_EPIAN	O48041 epirates a
586	6	1.2	335	1	YB81_MYCTU	P71762 mycobacteri	659	6	1.2	370	1	CYB_EPICE	O48043 epirates c
587	6	1.2	337	1	CLT1_HUMAN	O9Y271 homo sapien	660	6	1.2	370	1	CYB_EPIEX	O48047 epirates e
588	6	1.2	337	1	PXA2_PSEAE	O31495 pseudomonas	661	6	1.2	370	1	CYB_EPIFO	O48050 epirates f
589	6	1.2	337	1	SYM_TREPA	O83640 treponema p	662	6	1.2	370	1	CYB_EPISF	O48052 epirates s
590	6	1.2	338	1	KHSE_SCHRO	O43056 schizosacch	663	6	1.2	370	1	CYB_EPISM	O48053 epirates s
591	6	1.2	338	1	YFVJ_ECOLI	P52137 escherichia	664	6	1.2	370	1	CYB_EPISG	O48057 epirates s
592	6	1.2	339	1	CLT1_RAT	O92418 rattus norv	665	6	1.2	370	1	CYB_EPIST	O48053 epirates s
593	6	1.2	339	1	ILVC_CAUCR	O28781 archaeglob	666	6	1.2	370	1	CYB_EPIST	O48053 epirates s
594	6	1.2	339	1	RLAO_ARCFU	P46564 caenorhabdi	667	6	1.2	370	1	CYB_EUNNO	O48065 eunectes no
595	6	1.2	339	1	SG12_CAEEL	O95n02 sus scrofa	668	6	1.2	370	1	GP10_RAT	O64121 rattus norv
596	6	1.2	340	1	CLT1_PIG	O95n02 sus scrofa	669	6	1.2	370	1	H2AY_RAT	O02874 rattus norv
597	6	1.2	340	1	YMDA_CAEEL	P34486 caenorhabdi	670	6	1.2	370	1	ODPA_BACSU	P21881 bacillus su
598	6	1.2	341	1	ACBB_ACTIS	O9aeb4 actinoplanes	671	6	1.2	371	1	AM1B_PSEAE	O51416 pseudomonas
599	6	1.2	341	1	CATL_DROME	O95023 drosophila	672	6	1.2	371	1	CYB_BOACO	P92248 boa constricti
600	6	1.2	341	1	CREM_MOUSE	P27639 mus musculu	673	6	1.2	371	1	CYB_CALKE	O9mld7 calliphoris
601	6	1.2	341	1	CREM_RAT	O03061 rattus norv	674	6	1.2	371	1	CYB_CALMC	O9mld7 calliphoris
602	6	1.2	341	1	TRPD_LACCA	P17170 lactobacilli	675	6	1.2	371	1	CYB_CANAS	O48023 candida asp
603	6	1.2	342	1	YR9A_YEAST	P53757 saccharomyc	676	6	1.2	371	1	CYB_CANCA	O48025 candida car
604	6	1.2	344	1	CREM_CANPA	P79145 canis famli	677	6	1.2	371	1	CYB_CASDU	O48027 casarea dus
605	6	1.2	344	1	CYSA_SYNP7	P14788 synechococc	678	6	1.2	371	1	CYB_COLCO	O9m110 coluber con
606	6	1.2	345	1	CATD_PIG	P00795 sus scrofa	679	6	1.2	371	1	CYB_EPIMO	O48052 epirates m
607	6	1.2	345	1	SPUC_SERMA	P21410 serratia ma	680	6	1.2	371	1	CYB_EPRYC	O48066 eryx colubr
608	6	1.2	345	1	YAT2_SCHRO	O10149 schizosacch	681	6	1.2	371	1	CYB_ERYCL	O48067 eryx colubr
609	6	1.2	346	1	MRBW_BRUME	O8Y174 bruceella me	682	6	1.2	371	1	CYB_ERYEL	O48073 eryx elegans
610	6	1.2	347	1	MRWB_ECOLI	P13519 escherichia	683	6	1.2	371	1	CYB_ERYJA	O48076 eryx jaculu
611	6	1.2	348	1	ADH1_PICST	O00093 pichia stip	684	6	1.2	371	1	CYB_ERYMI	O48079 eryx miliar
612	6	1.2	348	1	AFUC_ACTPL	O57293 actinobacill	685	6	1.2	371	1	CYB_ERYMN	O48080 eryx miliar
613	6	1.2	348	1	AFUC_ECOLI	P37009 escherichia	686	6	1.2	371	1	CYB_ERYTA	O48085 eryx tatar
614	6	1.2	348	1	CYSA_MESVI	O9mmu1 mesostigma	687	6	1.2	371	1	CYB_MICEU	O9m1k5 micurotoides
615	6	1.2	348	1	NRI3_HUMAN	Q14594 homo sapien	688	6	1.2	371	1	CYB_TOXPR	O9m1k3 toxicoalam
616	6	1.2	350	1	ADH1_CANAL	P43067 candida alb	689	6	1.2	371	1	DUT_HSV11	P10234 herpes simp
617	6	1.2	350	1	Y170_METVA	O57634 methanococc	690	6	1.2	371	1	H2AY_HUMAN	O75367 homo sapien

691	1.2	371	1	TGT CAUCR	Q9a7y1 caulobacter	764	6	1.2	390	1	TGFI_HUMAN	P01137 homo sapien
692	1.2	371	1	Y816_SYNX3	P74041 synechocyst	765	6	1.2	390	1	TGFI_PIG	P07200 sus scrofa
693	1.2	372	1	CD14_RABIT	Q28680 cryocolagus	766	6	1.2	390	1	TGFI_SHEEP	P50410 ovis aries
694	1.2	372	1	CYB_ACRDU	O48010 acrantophis	767	6	1.2	391	1	CAR1_CANAL	P28872 candida alb
695	1.2	372	1	CYB_ACRMA	O48012 acrantophis	768	6	1.2	391	1	CATE_CANAL	P25796 cavia porce
696	1.2	372	1	CYB_ASpsc	Q9m1k0 aspidelaps	769	6	1.2	392	1	PEPC_RAT	P04073 rattus norv
697	1.2	372	1	CYB_ELABA	O9g250 elaphe bair	770	6	1.2	393	1	ILIS_HUMAN	Q29612 cercopithec
698	1.2	372	1	CYB_ELAOB	O9g210 elaphe obs	771	6	1.2	393	1	IRK9_HUMAN	Q92806 homo sapien
699	1.2	372	1	CYB_ELAVU	O9g964 elaphe vulp	772	6	1.2	393	1	IRK9_MOUSE	P48543 mus musculu
700	1.2	372	1	CYB_HETSI	Q9m1k0 heterodon s	773	6	1.2	393	1	IRK9_RAT	O63511 rattus norv
701	1.2	372	1	CYB_PARMU	Q9m1j1 paranaia mu	774	6	1.2	394	1	PEPC_CAVPO	O64411 cavia porce
702	1.2	372	1	CYB_SANME	O48114 sanzania ma	775	6	1.2	394	1	SUC1_STRCO	O9k756 streptomyce
703	1.2	372	1	CYB_WALAE	Q9m1j0 walterimnes	776	6	1.2	395	1	IFS_SCHPO	Q09689 schizosacch
704	1.2	373	1	UL16_HSV1	P10200 herpes simp	777	6	1.2	395	1	LIFP_RAT	P04634 rattus norv
705	1.2	375	1	DNBI_HSV1	O03444 equine herd	778	6	1.2	396	1	ARRS_RANCA	P51478 rana catesb
706	1.2	375	1	EFTU_SPIRU	P42478 spirochaeta	779	6	1.2	396	1	ARRS_RANPI	P51477 xenopus lae
707	1.2	375	1	HIS7_XANCP	P58881 xanthomonas	780	6	1.2	396	1	ARRS_XENLA	O01294 neotropora
708	1.2	375	1	HIS7_XANCP	P58882 xanthomonas	781	6	1.2	396	1	CARP_NEUCR	P14031 homo sapien
709	1.2	375	1	HIS7_XYLPA	O9pbct7 xyliella fas	782	6	1.2	396	1	CATE_HUMAN	P21182 saccharomyc
710	1.2	376	1	ACT1_PLAFA	P10988 plasmodium	783	6	1.2	396	1	DCAM_YEAST	P21182 pseudomonas
711	1.2	376	1	PAG2_BOVIN	Q28057 bos taurus	784	6	1.2	396	1	SOTE_PSEAE	O9hw77 mus musculu
712	1.2	377	1	PEPC_MACTU	P03955 macaca fusc	785	6	1.2	397	1	CATE_MOUSE	P70269 mus musculu
713	1.2	377	1	TTL_BOVIN	P38584 bos taurus	786	6	1.2	398	1	APL1_HUMAN	O14791 homo sapien
714	1.2	378	1	CKD6_MOUSE	O08707 mus musculu	787	6	1.2	398	1	ASPI_CAREL	P55956 caenorhabdi
715	1.2	379	1	CYB_PHOGR	Q35457 phoca grien	788	6	1.2	398	1	CAR2_CANAL	P28871 candida alb
716	1.2	379	1	TTL_PIG	P38160 sus scrofa	789	6	1.2	398	1	CATE_RAT	P16288 rattus norv
717	1.2	379	1	VPP_BPMU	P08558 bacterioph	790	6	1.2	398	1	ILIS_HUMAN	P27930 homo sapien
718	1.2	380	1	AROC_AERPE	O9ye14 aeropyrum p	791	6	1.2	398	1	TRFR_BOVIN	P34981 homo sapien
719	1.2	380	1	CYB_FALCA	O79204 halobaena c	792	6	1.2	398	1	TRFR_SHEEP	O28566 ovis aries
720	1.2	380	1	PAG1_BOVIN	Q29432 bos taurus	793	6	1.2	398	1	TRFR_HUMAN	P22811 homo sapien
721	1.2	380	1	SELFP_MOUSE	P70274 mus musculu	794	6	1.2	400	1	PRIZ_HUMAN	P52115 ovis aries
722	1.2	381	1	CYB_THYCY	Q36012 thylacinus	795	6	1.2	400	1	RENT_SHEEP	O19978 mycobacteri
723	1.2	381	1	SELFP_CHICK	O90907 gallus gall	796	6	1.2	401	1	AV6L_CAEEL	P95013 mycobacteri
724	1.2	381	1	YEG12_YEAST	P49908 homo sapien	797	6	1.2	401	1	RENS_MOUSE	P00796 mus musculu
725	1.2	381	1	CARA_ECOLI	P53155 saccharomyc	798	6	1.2	402	1	C123_MYCTU	P77922 mycobacteri
726	1.2	382	1	CARA_ECOLI	P00907 escherichia	799	6	1.2	402	1	CAR1_CANPA	P32951 candida par
727	1.2	382	1	CARA_SALTI	Q82918 salmonella	800	6	1.2	402	1	CN7B_SCHPO	O09727 schizosacch
728	1.2	382	1	CARA_SALTY	P14845 salmonella	801	6	1.2	402	1	DG11_BRUME	O8ygr78 bruceia me
729	1.2	382	1	EDG1_MOUSE	O08530 mus musculu	802	6	1.2	402	1	DG11_BRHME	P22777 mus musculu
730	1.2	382	1	LPXB_BCOI7	O848x7 escherichia	803	6	1.2	402	1	PALI_MOUSE	P06281 mus musculu
731	1.2	382	1	LPXB_ECOLI	P10441 escherichia	804	6	1.2	402	1	RENT_MOUSE	P17560 sus scrofa
732	1.2	382	1	LPXB_SALTI	Q829a1 salmonella	805	6	1.2	402	1	RNBP_PIG	P49507 bos taurus
733	1.2	382	1	LPXB_SALTY	Q82rnm salmonella	806	6	1.2	402	1	CINA_DEIRA	O32508 deinococcus
734	1.2	382	1	PAG1_SHEEP	Q28755 ovis aries	807	6	1.2	404	1	PRSB_XENLA	P26461 xenopus lae
735	1.2	382	1	RS1H_BACCE	O06000 bacillus ce	808	6	1.2	404	1	REFL_SALTY	P10523 homo sapien
736	1.2	382	1	VER2_HFV61	P49539 odontella s	809	6	1.2	405	1	ARRS_HUMAN	O30752 gallus gall
737	1.2	382	1	YQ44_ODOSI	P27940 oryza sativ	810	6	1.2	405	1	BMF4_CHICK	O42727 candida alb
738	1.2	383	1	AMC1_ORYSA	P46303 rattus norv	811	6	1.2	405	1	CAR8_CANAL	P07267 saccharomyc
739	1.2	383	1	EDG1_RAT	P16476 gallus gall	812	6	1.2	405	1	CARP_YEAST	O8uep3 agrobacteri
740	1.2	383	1	PEPE_CHICK	O00590 homo sapien	813	6	1.2	405	1	DG11_AGR75	O92q32 rhizobium m
741	1.2	384	1	YAGA_ECOLI	P37007 escherichia	814	6	1.2	405	1	PRSA_XENLA	O42587 xenopus lae
742	1.2	384	1	Y243_METTA	O60298 methanococc	815	6	1.2	405	1	DXR_MYCIE	Q9cbu3 mycobacteri
743	1.2	385	1	NR21_CHICK	Q91379 gallus gall	816	6	1.2	406	1	LMPI_MOUSE	P11438 mus sapien
744	1.2	385	1	SELFP_RAT	O9wx20 acetobacter	817	6	1.2	406	1	RENT_HUMAN	P00797 homo sapien
745	1.2	385	1	BCSY_ACEXY	P58335 homo sapien	818	6	1.2	406	1	CATD_RAT	P24268 rattus norv
746	1.2	386	1	ASPP_AEDAE	O03168 aedes aegypt	819	6	1.2	407	1	LMPI_CRIGR	P49129 cricetus
747	1.2	387	1	CYB_SCHPO	P05501 schizosacch	820	6	1.2	407	1	BMF4_RAT	P14562 rattus norv
748	1.2	387	1	GLUC_BACST	O08326 bacillus st	821	6	1.2	407	1	BMF4_DAMDA	Q29667 dama dama
749	1.2	387	1	MSOX_DEIRA	P23342 bacillus sp	822	6	1.2	408	1	BMF4_MOUSE	P12664 mus sapien
750	1.2	387	1	SAT_DEIRA	P56864 deinococcus	823	6	1.2	408	1	BMF4_RAT	O06826 rattus norv
751	1.2	387	1	YHFX_ECOLI	P45550 escherichia	824	6	1.2	408	1	BMF4_MOUSE	O06826 rattus norv
752	1.2	387	1	YHFX_ECOLI	O9a2d3 callithrix	825	6	1.2	409	1	BMF4_RAT	O46576 coxylobacte
753	1.2	388	1	PEPC_CALJA	P20142 homo sapien	826	6	1.2	410	1	AROC_CONGL	P18242 mus musculu
754	1.2	388	1	PEPC_HUMAN	P27823 oryctolagus	827	6	1.2	410	1	EFTU_CODFR	P50732 codium itag
755	1.2	388	1	PEPC_HUMAN	Q23078 sus scrofa	828	6	1.2	410	1	VE47_IAMBD	P03752 bacterioph
756	1.2	389	1	PAG1_PIG	P22929 saccharomyc	829	6	1.2	410	1	AATC_CHICK	P00504 gallus gall
757	1.2	390	1	CATD_BOVIN	P80209 bos taurus	830	6	1.2	411	1	BCAT_RAT	P54690 rattus norv
758	1.2	390	1	TGFI_CANPA	P54831 canis famli	831	6	1.2	411	1	CAR2_CANPA	P32950 candida par
759	1.2	390	1	TGFI_CANPA	O9a1y6 cavia porce	832	6	1.2	412	1	CATD_HUMAN	P07319 homo sapien
760	1.2	390	1	TGFI_CERAE	P09533 cercopithec	833	6	1.2	412	1	PUR2_LACIA	Q9z144 lactococcus
761	1.2	390	1	TGFI_HORSE	O19011 equus cabal	834	6	1.2	412	1		
762	1.2	390	1			835	6	1.2	412	1		
763	1.2	390	1			836	6	1.2	412	1		

837	6	1.2	413	1	DXR_MYCTU	Q10798 mycobacteri	910	6	1.2	440	1	BIR1_YEAST	P11709 saccharomyc
838	6	1.2	413	1	NODC_RHISN	P50357 rhizobium s	911	6	1.2	440	1	HIP1_ECOLI	P23874 escherichia
839	6	1.2	414	1	GLTP_BACSU	P39817 bacillus su	912	6	1.2	441	1	FLID_AQUAE	O67805 aquifex aeo
840	6	1.2	414	1	LMPI_CHICK	P05300 gallus galli	913	6	1.2	441	1	HISX_STRCO	P16245 streptomyce
841	6	1.2	414	1	MTR_ECOLI	P22306 escherichia	914	6	1.2	441	1	SYS_THENC	O9hkx5 thermoplasm
842	6	1.2	414	1	P2C3_SCHRO	Q09173 schizosacch	915	6	1.2	442	1	PRSA_MOUSE	O8865 mus musculu
843	6	1.2	415	1	Y232_RICPR	Q9242 rickettsia	916	6	1.2	442	1	UHPG_SALTY	P27659 salmonella
844	6	1.2	416	1	LMPI_HUMAN	P11279 homo sapien	917	6	1.2	443	1	FTSA_AGR75	O10991 agrobacteri
845	6	1.2	416	1	PGK2_RAT	P16617 rattus norv	918	6	1.2	444	1	C120_SYNY3	O59930 synechocyst
846	6	1.2	416	1	PGK_CRIGR	P50310 cricetus	919	6	1.2	444	1	CDT1_SCHPO	P51811 schizosacch
847	6	1.2	416	1	PGK_HORSE	P00559 equus cabal	920	6	1.2	444	1	XK_HUMAN	P51811 homo sapien
848	6	1.2	417	1	CAR4_CANAL	P43093 candida alb	921	6	1.2	445	1	OST4_CANFA	O05052 canis famli
849	6	1.2	418	1	CAR5_CANAL	P43094 candida alb	922	6	1.2	445	1	YGCS_ECOLI	O46909 escherichia
850	6	1.2	418	1	CAR6_CANAL	P43095 candida alb	923	6	1.2	447	1	VANS_ENTFA	O47745 enterococcu
851	6	1.2	418	1	LEU2_THETN	O8rdx2 thermoaer	924	6	1.2	449	1	G64F_DROME	P83297 drosophilla
852	6	1.2	418	1	RHAA_BACGD	O9Kc19 bacillus ha	925	6	1.2	449	1	GAD_MOUSE	P22933 mus musculu
853	6	1.2	419	1	GSC_DROME	P54366 drosophila	926	6	1.2	449	1	GAD_RAT	P18506 rattus norv
854	6	1.2	419	1	KAS2_STRCN	Q02579 streptomyce	927	6	1.2	449	1	XYLA_LACBR	P29443 lactobacill
855	6	1.2	419	1	KDAP_MOUSE	O09043 mus musculu	928	6	1.2	450	1	ACHX_HUMAN	O9g226 homo sapien
856	6	1.2	419	1	NOEE_RHISN	P5472 rhizobium s	929	6	1.2	450	1	GASR_PRANA	P30796 praeomys nat
857	6	1.2	419	1	RHO_BUCAL	P57652 buchnera ap	930	6	1.2	450	1	MOO_HELPJ	O9zwm5 helicobacte
858	6	1.2	420	1	NAPI_HUMAN	O96009 homo sapien	931	6	1.2	450	1	MOO_HELPJ	O24913 helicobacte
859	6	1.2	420	1	PGK_TETTH	P50313 tetrahymena	932	6	1.2	451	1	SYS_ARATH	O39220 arabidopsis
860	6	1.2	420	1	PUR2_STEPP	Q97C36 streptococc	933	6	1.2	453	1	HRA3_HUMAN	P83110 homo sapien
861	6	1.2	420	1	RHO_HAEIN	P44619 haemophilus	934	6	1.2	453	1	OP2_MAIZE	P12959 zea mays (m
862	6	1.2	420	1	VIT3_DROME	P06607 drosophila	935	6	1.2	453	1	PLM2_PLAFA	O26366 drosophilla
863	6	1.2	421	1	ACRO_HUMAN	P10323 homo sapien	936	6	1.2	453	1	VG_DROME	O98159 rhizobium 1
864	6	1.2	421	1	PUR2_MOUSE	O9a17 streptococc	937	6	1.2	454	1	YGBN_RHITO	O46892 escherichia
865	6	1.2	421	1	TRAB_AGR75	Q44351 agrobacteri	938	6	1.2	454	1	YGBN_ECOLI	O8y176 bruceila me
866	6	1.2	421	1	PPAL_HUMAN	P1117 homo sapien	939	6	1.2	456	1	NTH_BROME	O39656 homo sapien
867	6	1.2	423	1	PPAL_RAT	P20611 rattus norv	940	6	1.2	458	1	ACHO_HUMAN	O05901 homo sapien
868	6	1.2	424	1	KAS2_STRCO	P3156 streptomyce	941	6	1.2	458	1	YGBH_ECOLI	P76639 escherichia
869	6	1.2	426	1	NMTH_MYCLE	O50103 mycobacteri	942	6	1.2	459	1	EXTL_PSEAE	O9h189 pseudomona
870	6	1.2	426	1	SGAA_HUMAN	P53796 homo sapien	943	6	1.2	459	1	EP1A_ORYLA	O9y1c0 oryzias lat
871	6	1.2	426	1	VA20_VACC	P20995 vaccinia vi	944	6	1.2	461	1	NCB1_HUMAN	O02818 homo sapien
872	6	1.2	426	1	VA20_VAVV	P33849 variola vir	945	6	1.2	461	1	NIFN_SYNP8	O07356 synechococc
873	6	1.2	427	1	DSLI_CHICK	P34822 gallus galli	946	6	1.2	462	1	EF10_XENLA	P13549 xenopus lae
874	6	1.2	427	1	RHO_BACSU	Q03222 bacillus su	947	6	1.2	462	1	EF11_CRIGR	P20001 cricetus
875	6	1.2	428	1	AMY1_ORYSA	P17654 oryza sativ	948	6	1.2	462	1	EF11_HUMAN	P104270 homo sapien
876	6	1.2	428	1	DCTA_ECO57	O8x5m2 escherichia	949	6	1.2	462	1	EF11_MOUSE	P10126 mus musculu
877	6	1.2	428	1	DCTA_ECOLI	P37312 escherichia	950	6	1.2	462	1	EF1A_BRARE	O92005 brachydanio
878	6	1.2	428	1	GLYA_AQUAE	O66776 aquifex aeo	951	6	1.2	462	1	EF1A_CHICK	O90815 gallus galli
879	6	1.2	428	1	ZFZ6_MOUSE	P10076 mus musculu	952	6	1.2	462	1	OCT2_MOUSE	O00196 mus musculu
880	6	1.2	429	1	PUR2_ECOLI	P15640 escherichia	953	6	1.2	463	1	COAT_FRG3V	O67473 frog virus
881	6	1.2	429	1	PUR2_SALTI	O82334 salmonella	954	6	1.2	463	1	MURD_RHIME	O91qz8 rana tigrin
882	6	1.2	429	1	PUR2_SALTY	P26977 salmonella	955	6	1.2	463	1	Y096_MYCTU	O52953 rhizobium m
883	6	1.2	429	1	URAA_ECOLI	P33780 escherichia	956	6	1.2	463	1	CASB_XLEOX	O10892 mycobacteri
884	6	1.2	430	1	GLGC_ECOLI	P00584 escherichia	957	6	1.2	464	1	DLDH_ZYMO	O48409 klebsiella
885	6	1.2	431	1	NOOE_THETH	O56229 thermus the	958	6	1.2	466	1	CYSP_TRYCR	P50970 zymomonas m
886	6	1.2	432	1	ENV2_MOUSE	P11370 mus musculu	959	6	1.2	467	1	EUTR_SALTY	P25779 trypanosoma
887	6	1.2	432	1	ENV2_MOUSE	P55495 rhizobium s	960	6	1.2	467	1	SYFA_SULISO	O9zfx2 salmonella
888	6	1.2	433	1	RHO_CHRYV	P27527 caenorhabdi	961	6	1.2	468	1	LMRB_LISIN	P95961 sulfolobus
889	6	1.2	433	1	HPED_HOKVU	O48604 hordeum vul	962	6	1.2	471	1	YEGB_ECOLI	O92e61 listeria in
890	6	1.2	434	1	PRSA_YEAST	P33297 saccharomyc	963	6	1.2	471	1	YHBE_YEAST	O8y9x8 escherichia
891	6	1.2	434	1	FIXC_BRAJA	P10331 bradyrhizob	964	6	1.2	471	1	RUMA_RHOGE	P38770 saccharomyc
892	6	1.2	435	1	NHGS2_PSEPU	O53552 pseudomonas	965	6	1.2	471	1	CREC_ECOLI	O93p88 rhodocyclu
893	6	1.2	435	1	OADB_HARDU	O9rfe8 haemophilus	966	6	1.2	473	1	DLDR_ALCEU	P08401 escherichia
894	6	1.2	435	1	YOD7_CAREL	O09267 caenorhabdi	967	6	1.2	474	1	MOTD_RHIME	P26292 alcaligenes
895	6	1.2	435	1	COAT_CHVE1	Q45411 ralsconia s	968	6	1.2	475	1	S611_CANFA	O52964 rhizobium m
896	6	1.2	436	1	NMTH_DEIRA	O9rte8 deinooccus	969	6	1.2	475	1	S611_HUMAN	P38378 homo sapien
897	6	1.2	436	1	NEOR_STRCY	P14501 streptomyce	970	6	1.2	475	1	S612_MOUSE	O9y223 homo sapien
898	6	1.2	437	1	YOE2_BACSU	P54465 bacillus su	971	6	1.2	475	1	BAIG_EUBSP	O9j1l1 mus musculu
899	6	1.2	437	1	PRSA_SCHPO	O14126 schizosacch	972	6	1.2	477	1	FIIB_PETMA	O25147 halocynthia
900	6	1.2	438	1	SYS_HELAN	O81993 helianthus	973	6	1.2	477	1	NOMI_PSEAE	P32369 eubacterium
901	6	1.2	438	1	Y16R_MYCIO	O49573 mycoplasma	974	6	1.2	477	1	ALDA_ECOLI	O913k3 pseudomona
902	6	1.2	439	1	IDNT_ECOLI	P39344 escherichia	975	6	1.2	478	1	CARL_HUMAN	P25553 escherichia
903	6	1.2	439	1	PRSA_HUMAN	O63569 rattus norv	976	6	1.2	478	1	EGR4_RAT	O9un66 homo sapien
904	6	1.2	439	1	UHPG_ECOLI	P09836 escherichia	977	6	1.2	478	1	OCT2_HUMAN	Q00911 rattus norv
905	6	1.2	439	1	UHPG_ECOLI	P09836 escherichia	978	6	1.2	478	1	OCT2_HUMAN	P09086 homo sapien
906	6	1.2	439	1	UHPG_ECOLI	P09836 escherichia	979	6	1.2	478	1	OCT2_HUMAN	P09086 homo sapien
907	6	1.2	439	1	UHPG_ECOLI	P09836 escherichia	980	6	1.2	478	1	OCT2_HUMAN	P09086 homo sapien
908	6	1.2	439	1	UHPG_ECOLI	P09836 escherichia	981	6	1.2	478	1	OCT2_HUMAN	P09086 homo sapien
909	6	1.2	439	1	UHPG_ECOLI	P09836 escherichia	982	6	1.2	478	1	OCT2_HUMAN	P09086 homo sapien

SQ SEQUENCE 518 AA; 56180 MM; 2E903150823760D3 CXC64;
 Query Match 100.0%; Score 518; DB 1; Length 518;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGALARAALLPLLAQWLRLAARAPLPAFTLLPLRVAATAATRVAAATPPGPGTAAERHADGL 60
 DB 1 MGALARAALLPLLAQWLRLAARAPLPAFTLLPLRVAATAATRVAAATPPGPGTAAERHADGL 60
 QY 61 ALALEPALASPGANFLAMVDNLQDGRGYLLEMLIGTPPOKIOIIVDTSSNPAVAG 120
 DB 61 ALALEPALASPGANFLAMVDNLQDGRGYLLEMLIGTPPOKIOIIVDTSSNPAVAG 120
 QY 121 TPHSYIDYFPTERSSTYRSKGFDTVVKYXGSGMTGFVGEDLVITPKGFNTSFLVNIAT 180
 DB 121 TPHSYIDYFPTERSSTYRSKGFDTVVKYXGSGMTGFVGEDLVITPKGFNTSFLVNIAT 180
 QY 181 FESENFELPGIKMNGILGLAVTTLAKPSSSLETFPDSLVTOANTINVPVSMQCGAGLPVA 240
 DB 181 FESENFELPGIKMNGILGLAVTTLAKPSSSLETFPDSLVTOANTINVPVSMQCGAGLPVA 240
 QY 241 GSGTNGSLVGGTBPSTLYKGIWYTPIKEMVYQIEILKIEIGGOSINTLDREYNADKA 300
 DB 241 GSGTNGSLVGGTBPSTLYKGIWYTPIKEMVYQIEILKIEIGGOSINTLDREYNADKA 300
 QY 301 IVDSGTTLLRLPOKVFDAVVEAVASASLIPERSDGFMTGSOLACWTNSETPMSPYFKISI 360
 DB 301 IVDSGTTLLRLPOKVFDAVVEAVASASLIPERSDGFMTGSOLACWTNSETPMSPYFKISI 360
 QY 361 YLRDSSRSRFRITTLPOLYIOPMMGAGLNECYRFGISPSSTNALVIGATWEGFYVIFD 420
 DB 361 YLRDSSRSRFRITTLPOLYIOPMMGAGLNECYRFGISPSSTNALVIGATWEGFYVIFD 420
 QY 421 RAOKRVGAASPCAEIAAASEISGSPSTEDVANSNCVPAOSLSPIITMYSYALMSVCG 480
 DB 421 RAOKRVGAASPCAEIAAASEISGSPSTEDVANSNCVPAOSLSPIITMYSYALMSVCG 480
 QY 481 ALLVLVLTLLPFCQRRPRDEPVNDESSIVRHRMK 518
 DB 481 ALLVLVLTLLPFCQRRPRDEPVNDESSIVRHRMK 518
 RESULT 2
 ID BACE HUMAN STANDARD; PRT; 501 AA.
 AC P56817; Q9HUT5; Q9HYC1; Q9BYC0; Q9BYB9;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Beta-secretase precursor (EC 3.4.23.-) (Beta-site APP cleaving enzyme)
 DE (beta-site amyloid precursor protein cleaving enzyme) (aspartyl
 DE protease 2) (Asp 2) (ASPT) (membrane-associated aspartic protease 2)
 DE (memasin-2).
 GN BACE OR BACE1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM A).
 RC TISSUE=Brain;
 RX MEDLINE=20002972; PubMed=10531052;
 RA Vassar R., Bennett B.D., Babu-Khan S., Kahn S., Mendiaz E.A.,
 RA Denis P., Teplow D.B., Ross S., Amarante P., Loeloff R., Luo Y.,
 RA Fisher S., Fuller J., Edenson S., Lile J., Jarosinski M.A.,
 RA Biere A.L., Curran E., Burgess T., Louis J.-C., Collins F.,
 RA Treanor J., Rogers G., Citron M.;
 RT "beta-secretase cleavage of Alzheimer's amyloid precursor protein by
 RT the transmembrane aspartic protease BACE.";
 RL Science 286:735-741(1999).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM A), SEQUENCE OF 46-68, AND

RP CHARACTERIZATION.
 RC TISSUE=Brain;
 RX MEDLINE=20057171; PubMed=10591214;
 RA Sinha S., Anderson J.P., Barbour R., Basl G.S., Caccavello R.,
 RA Davis D., Doan M., Dovey H.F., Frigon N., Hong J., Jacobson-Croak K.,
 RA Jewett N., Keim P., Knops J., Lieberburg I., Power M., Tan H.,
 RA Tatsuno G., Tung J., Schenk D., Seubert P., Slemmons S.M., Wang S.,
 RA Walker D., Zhao J., McConlogue L., Varghese J.;
 RT "Purification and cloning of amyloid precursor protein beta-secretase
 RT from human brain.";
 RL Nature 402:537-540(1999).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM A).
 RX MEDLINE=20057170; PubMed=10591213;
 RA Yan R., Bienkowski M.J., Shuck M.E., Miao H., Torry M.C., Pauley A.M.,
 RA Brashler J.R., Strittman N.C., Mathews W.R., Buhl A.E., Carter D.B.,
 RA Tomasselli A.G., Parodi L.A., Heinrichson R.L., Gurney M.B.;
 RT "Membrane-anchored aspartyl protease with Alzheimer's disease beta-
 RT secretase activity.";
 RL Nature 402:533-537(1999).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM A).
 RX MEDLINE=20120043; PubMed=10656250;
 RA Hussain I., Powell D.J., Howlett D.R., Tew D.G., Week T.D.,
 RA Chapman C., Glover I.S., Murphy K.E., Southern C.D., Ryan D.M.,
 RA Smith T.S., Simmons D.L., Walsh F.S., Dingwall C., Christie G.;
 RT "Identification of a novel aspartic proteinase (Asp 2) as beta-
 RT secretase.";
 RL Mol. Cell. Neurosci. 14:419-427(1999).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM B).
 RC TISSUE=Brain, and Pancreas;
 RA Michel B., De Pietri Tonelli D., Zaccchetti D., Keller P.;
 RT "New beta-site APP cleaving enzyme isoform (BACE-1B) obtained from
 RT human brain and pancreas.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM C).
 RC TISSUE=Pancreas;
 RA Zaccchetti D., De Pietri Tonelli D., Schnubus R.;
 RT "New beta-site APP cleaving enzyme isoform (BACE-1C) obtained from
 RT human pancreas.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORMS B; C AND D).
 RC TISSUE=Brain;
 RX MEDLINE=21408467; PubMed=11516562;
 RA Tanahashi H., Tabira T.;
 RT "Three novel alternatively spliced isoforms of the human beta-site
 RT amyloid precursor protein cleaving enzyme (BACE) and their effect on
 RT amyloid beta-peptide production.";
 RL Neurosci. Lett. 307:9-12(2001).
 RN [8]
 RP SEQUENCE OF 14-501 FROM N.A. (ISOFORM A), AND CHARACTERIZATION.
 RX MEDLINE=20144060; PubMed=10677483;
 RA Lin X., Koelsch G., Wu S., Downs D., Dashti A., Tang J.;
 RT "Human aspartic protease memapsin 2 cleaves the beta-secretase site of
 RT beta-amyloid precursor protein.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1456-1460(2000).
 RN [9]
 RP DISULFIDE BONDS.
 RX MEDLINE=21950860; PubMed=11953458;
 RA Fischer F., Molinari M., Bodendorf U., Paganetti P.;
 RT "The disulfide bonds in the catalytic domain of BACE are critical but
 RT not essential for amyloid precursor protein processing activity.";
 RL J. Neurochem. 80:1079-1088(2002).
 CC -1- FUNCTION: RESPONSIBLE FOR THE PROTEOLYTIC PROCESSING OF THE
 CC AMYLOID PRECURSOR PROTEIN (APP). CLEAVES AT THE AMINO TERMINUS OF
 CC THE A-BETA PEPTIDE SEQUENCE. BETWEEN RESIDUES 671 AND 672 OF APP,
 CC SOLUBLE APP, AND A CORRESPONDING CELL-ASSOCIATED CARBOXY-TERMINAL
 CC FRAGMENT WHICH IS LATER RELEASED BY GAMMA-SECRETASE.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

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CC -1- ALTERNATIVE PRODUCTS: 4 isoforms; A/BACE-1A/BAC-501 (shown here),
CC B/BACE-1B/BACE-1-476; C/BACE-1C/BACE-1-457 and D/BACE-1D/BACE-1-
CC 432; are produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: BRAIN
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF190725; AAF04142.1; -
DR EMBL: AF201468; AAF18982.1; -
DR EMBL: AF200343; AAF17079.1; -
DR EMBL: AF2004943; AAF26367.1; -
DR EMBL: AF338816; AAK38374.1; -
DR EMBL: AF338817; AAK38375.1; -
DR EMBL: AB050436; BAB40931.1; -
DR EMBL: AB050437; BAB40932.1; -
DR EMBL: AB050438; BAB40933.1; -
DR EMBL: AF200193; AAF13715.1; -
DR HSSP: P33329; 1YPS.
DR MEROPS: A01.004; -.
DR Genes: HGNC:933; BACE.
DR MIM: 604252; -.
DR InterPro: IPR001461; AsproteaseA1.
DR InterPro: IPR001969; Asprotease_site.
DR Pfam: PF00026; asp.1.
DR PRINTS: PR00792; PEPsin.
DR PROSITE: PS00141; ASP_PROTEASE; 1.
KW Hydrolyase; Aspartyl protease; Glycoprotein; Zymogen; Transmembrane;
KW Signal; Alternative splicing.
FT SIGNAL 1 21 POTENTIAL.
FT PROPEP 22 45
FT CHAIN 46 501 BETA-SECRETASE.
FT DOMAIN 22 457 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 458 478 POTENTIAL.
FT DOMAIN 479 501 CYTOPLASMIC (POTENTIAL).
FT ACT_SITE 93 93 BY SIMILARITY.
FT ACT_SITE 289 289 BY SIMILARITY.
FT DISULFID 216 420
FT DISULFID 278 443
FT DISULFID 330 380
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPPLIC 146 189 MISSING (IN ISOFORM C AND ISOFORM D).
FT VARSPPLIC 190 214 MISSING (IN ISOFORM B AND ISOFORM D).
SQ SEQUENCE 501 AA; 55763 MW; 377CEFC824ACEF05 CRC64;
Query Match 2.3%; Score 12; DB 1; Length 501;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 107 ILVTGSSNFAV 118
Db 90 ILVTGSSNFAV 101

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DE (Memapsin-2).
GN BACE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20002972; PubMed=10531052;
RA Vassar R., Bennett B.D., Babu-Khan S., Kahn S., Mendiaz E.A.,
RA Denis P., Teplow D.B., Ross S., Amarante P., Loebloff R., Luo Y.,
RA Fisher S., Fuller J., Edenson S., Lile J., Jarosinski M.A.,
RA Biere A.V., Curran E., Burgess T., Louis J.C., Collins F.,
RA Teanor J., Rogers G., Citron M.;
RA "beta-secretase cleavage of Alzheimer's amyloid precursor protein by
RT the transmembrane aspartic protease BACE.";
RL Science 286:735-741(1999).
RN [2]
RP REVISIONS TO 6 AND 81-87.
RA Bennett B.D., Vassar R., Citron M.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20057170; PubMed=10591213;
RA Yan R., Bienkowski M.J., Shuck M.E., Miao H., Torry M.C., Pauley A.M.,
RA Brashers J.R., Stratton N.C., Mathews W.R., Buhl A.B., Carter D.B.,
RA Tomasselli A.G., Parodi L.A., Heinrichson R.L., Gurney M.E.;
RT "Membrane-anchored aspartyl protease with Alzheimer's disease
RT beta-secretase activity.";
RL Nature 402:533-537(1999).
CC -1- FUNCTION: RESPONSIBLE FOR THE PROTEOLYTIC PROCESSING OF THE
CC AMYLOID PRECURSOR PROTEIN (APP). CLEAVES AT THE AMINO TERMINUS OF
CC THE A-BETA PEPTIDE SEQUENCE, BETWEEN RESIDUES 671 AND 672 OF APP,
CC LEADS TO THE GENERATION AND EXTRACELLULAR RELEASE OF BETA-CLEAVED
CC SOLUBLE APP. AND A CORRESPONDING CELL-ASSOCIATED CARBOXY-TERMINAL
CC FRAGMENT WHICH IS LATER RELEASED BY GAMMA-SECRETASE (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: BRAIN.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
CC -----
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CC -----
DR EMBL: AF190726; AAF04143.2; -.
DR EMBL: AF200346; AAF17082.1; -.
DR HSSP: P56272; 1AMS.
DR MEROPS: A01.004; -.
DR MGD: MGI:1346542; Bace.
DR InterPro: IPR001461; AsproteaseA1.
DR InterPro: IPR001969; Asprotease_site.
DR Pfam: PF00026; asp.1.
DR PRINTS: PR00792; PEPsin.
DR PROSITE: PS00141; ASP_PROTEASE; 1.
KW Hydrolyase; Aspartyl protease; Glycoprotein; Zymogen; Transmembrane;
KW Signal.
FT SIGNAL 1 21 POTENTIAL.
FT PROPEP 22 45
FT CHAIN 46 501 BETA-SECRETASE.
FT DOMAIN 22 457 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 458 478 POTENTIAL.
FT DOMAIN 479 501 CYTOPLASMIC (POTENTIAL).
FT ACT_SITE 93 93 BY SIMILARITY.
FT ACT_SITE 289 289 BY SIMILARITY.
FT DISULFID 216 420
FT DISULFID 278 443
FT DISULFID 330 380
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 501 AA; 55747 MW; C085A013145E474E CRC64;

Query Match 2.3%; Score 12; DB 1; Length 501;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 ILVDTGSSNFAV 118
Db 90 ILVDTGSSNFAV 101

RESULT 4
BACE_RAT STANDARD; PRT; 501 AA.
AC P56813;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Beta-secretase precursor (EC 3.4.23.-) (Beta-site APP cleaving enzyme)
DE (Beta-site amyloid precursor protein cleaving enzyme) (aspartyl
DE protease 2) (ASP 2) (ASBP2) (Membrane-associated aspartic protease 2)
DE (Memapsin-2).
GN BACE.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20002972; PubMed=10531052;
RA Vassar R., Bennett B.D., Babu-Khan S., Kahn S., Mendiaz E.A.,
RA Denis P., Teplow D.B., Ross S., Amarante P., Loeloff R., Luo Y.,
RA Fisher S., Fuller J., Edenson S., Lile J., Jarosinski W.A.,
RA Biere A.L., Curran E., Burgess T., Louis J.-C., Collins F.,
RA Treanor J., Rogers G., Citron M.;
RT "beta-secretase cleavage of Alzheimer's amyloid precursor protein by
RT the transmembrane aspartic protease BACE.";
RL Science 266:735-741(1999).
CC -1- FUNCTION: RESPONSIBLE FOR THE PROTEOLYTIC PROCESSING OF THE
CC AMYLOID PRECURSOR PROTEIN (APP). CLEAVES AT THE AMINO TERMINUS OF
CC THE A-BETA PEPTIDE SEQUENCE, BETWEEN RESIDUES 671 AND 672 OF APP,
CC LEADS TO THE GENERATION AND EXTRACELLULAR RELEASE OF BETA-CLEAVED
CC SOLUBLE APP, AND A CORRESPONDING CELL-ASSOCIATED CARBOXY-TERMINAL
CC FRAGMENT WHICH IS LATER RELEASED BY GAMMA-SECRETASE (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF190727; AA04144.1; -
DR HSBP; P32329; IYPS.
DR MEROPS; A01.004; -
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF000026; asp.1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; 1.
KW Hydroxylase; Aspartyl protease; Glycoprotein; Zymogen; Transmembrane;
KW signal.
FT SIGNAL 1 21 POTENTIAL.
FT PROPEP 22 45 POTENTIAL.
FT CHAIN 46 501 BETA-SECRETASE.
FT DOMAIN 22 457 EXTRACELLULAR (POTENTIAL).

```

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FT TRANSMEM 458 478 POTENTIAL.
FT DOMAIN 479 501 CYTOPLASMIC (POTENTIAL).
FT ACT_SITE 93 93 BY SIMILARITY.
FT ACT_SITE 289 289 BY SIMILARITY.
FT DISULFID 216 420 BY SIMILARITY.
FT DISULFID 278 443 BY SIMILARITY.
FT DISULFID 330 380 BY SIMILARITY.
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 501 AA; 55806 MW; 24B445B08B87DE3 CRC64;

Query Match 2.3%; Score 12; DB 1; Length 501;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 ILVDTGSSNFAV 118
Db 90 ILVDTGSSNFAV 101

RESULT 5
LRP_HAETN STANDARD; PRT; 166 AA.
ID LRP_HAETN
AC P45265;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Leucine-responsive regulatory protein.
DE LRP OR H11596.
GN LRP OR H11596.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellales;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Rd / KM20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Knelavan A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Frichman J.L., Fuhrmann J.L., Geoghegan N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
CC -1- FUNCTION: MEDIATES A GLOBAL RESPONSE TO LEUCINE. EXOGENOUS LEUCINE
CC AFFECTS THE EXPRESSION OF A NUMBER OF DIFFERENT OPERONS; LRP
CC MEDIATES THIS EFFECT FOR AT LEAST SOME OF THESE OPERONS
CC (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ASNC FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U32833; AAC23241.1; -
DR TIGR; H11596; -
DR InterPro; IPR000485; ASNC_trans_reg.
DR Pfam; PF01037; ASNC_trans_reg; 1.
DR PRINTS; PR00033; HTHASNC.
DR SMART; SM00344; HTH_ASNC; 1.

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DR PROSITE, PS00519; HTH_ASNF_FAMILY; 1.
KW DNA-binding; Transcription regulation; Activator; Complete proteome.
FT DNA BIND 35 54 H-T-H MOTIF (POTENTIAL).
SQ SEQUENCE 166 AA; 18910 MW; 22C0F1B7B8110CEB CRC64;

Query Match 1.5%; Score 8; DB 1; Length 166;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 305 GTTLRLP 312
    |||||
Db 136 GTTLRLP 143

RESULT 6
601M PROMI STANDARD; PRT; 237 AA.
AC P22833.
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 60 kDa inner-membrane protein homolog (Fragment).
OS Proteus mirabilis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
CC Proteus.
CX NCBI_TaxID=584;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=LM1509.
RX MEDLINE=91033012; PubMed=2172087;
RA Skovgaard O.;
RT "Nucleotide sequence of a Proteus mirabilis DNA fragment homologous
RT to the 60K-rmpA-pmpA-dnaA-dnaN-recF-gyrB region of Escherichia
RT coli."
RL Gene 93:27-34(1990).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Probable).
CC -1- SIMILARITY: BELONGS TO THE OXA1 / 60 KDA IMP FAMILY.
CC -----
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CC -----
DR EMBL; M58352; AAA83954.1; -.
DR PIR; JQ0729; JQ0729.
KW Transmembrane; Inner membrane.
FT TRANSMEM 7 23 POTENTIAL.
FT NON TER 237 237
SQ SEQUENCE 237 AA; 26664 MW; 07FCC405B9DB3F36 CRC64;

Query Match 1.5%; Score 8; DB 1; Length 237;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 110 DTGSSNFA 117
    |||||
Db 206 DTGSSNFA 213

RESULT 7
VPRT SMRVH STANDARD; PRT; 323 AA.
ID VPRT_SMRVH
AC P21407.
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protease (EC 3.4.23.-).
PRT.
SQ Squirrel monkey retrovirus (SMRV-HLB).

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OC Viruses; Retroid viruses; Retroviridae; Betaretrovirus.
CX NCBI_TaxID=11856;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89073750; PubMed=3201749;
RA Oda T., Ikeda S., Watanabe S., Hatausnika M., Akiyama K.,
RA Mitsuoka F.;
RT "Molecular cloning, complete nucleotide sequence, and gene structure
RT of the provirus genome of a retrovirus produced in a human
RT lymphoblastoid cell line."
RL Virology 167:468-476(1988).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A2.
CC -1- SIMILARITY: CONTAINS 1 G-PATCH DOMAIN.
CC -----
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CC -----
DR EMBL; M23385; AAA66452.1; ALT_INIT.
DR PIR; B31827; PRLJHD.
DR HSSP; P06968; IEUW.
DR MEROPS; A02.0PW; -.
DR InterPro; IPR001995; Asprotease_rtrv.
DR InterPro; IPR001969; Asprotease_site.
DR InterPro; IPR001428; DeoxyUTPase-.
DR InterPro; IPR000467; G_patch.
DR Pfam; PF00077; rvp; 1.
DR Pfam; PF00692; dUTPase; 1.
DR Pfam; PF01585; G_patch; 1.
DR ProDom; PD000946; DeoxyUTPase; 1.
DR SMART; SM00443; G_patch; 1.
DR PROSITE; PS00141; ASP_PROTEASE; 1.
DR PROSITE; PS50175; ASP_PROT_RETROV; 1.
DR PROSITE; PS50174; G_PATCH; 1.
KW Hydrolyase; Aspartyl protease.
FT DOMAIN 275 321 G-PATCH.
FT ACT SITE 193 193 BY SIMILARITY.
SQ SEQUENCE 323 AA; 35126 MW; 5D6CEA38BA32786 CRC64;

Query Match 1.5%; Score 8; DB 1; Length 323;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 161 DLVITPKG 168
    |||||
Db 126 DLVITPKG 133

RESULT 8
CARP_POLTU STANDARD; PRT; 340 AA.
ID CARP_POLTU
AC P15761.
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Polyporopepsin (EC 3.4.23.29) (aspartic proteinase).
OS Polyporus tulipiferæ (Irpex lacteus).
OS Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Polyporaceae; Polyporus.
CX NCBI_TaxID=29885;
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 1-24.
RA Kobayashi H., Sekibata S., Shibuya H., Yoshida S., Kusakabe I.,
RA Murakami K.;
RT "Cloning and sequence analysis of cDNA for Irpex lacteus aspartic
RT proteinase."
RL Agric. Biol. Chem. 53:1927-1933(1989).
CC -1- CATALYTIC ACTIVITY: Milk clotting activity, broad specificity, but
CC fails to cleave I5-Leu-I-Tyr-16 or I6-Tyr-I-Leu-17 of insulin B

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CC chain.
CC -----
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D00589; BAA00467.1; -.
CC PIR; J00057; PEIKL.
CC DR HSSP; P32329; 1YPS.
CC DR MEROPS; A01.019; -.
CC DR InterPro; IPR001461; Aspprotease1.
CC DR InterPro; IPR001969; Aspprotease_site.
CC DR Pfam; PF00026; asp.1.
CC DR PRINTS; PR00792; PEPsin.
CC DR PROSITE; PS00141; ASP_PROTEASE; 2.
CC KM Hydrolyse; Aspartyl protease; Glycoprotein.
CC FT ACT_SITE 32 32
CC FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SQ SEQUENCE 340 AA; 35050 MW; 9BAF837264D42FEF CRC64;

Query Match 1.5%; Score 8; DB 1; Length 340;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 LVDTGSSN 115
Db 30 LVDTGSSN 37

RESULT 9
ID YHDX_ECOLI STANDARD; PRT; 362 AA.
AC PA5767;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical amino-acid ABC transporter_permease protein yhdx.
GN YHDX OR B3269.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blatter F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
CC -1- FUNCTION: PROBABLY PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT
CC SYSTEM YDHMYWZ FOR AN AMINO ACID; PROBABLY RESPONSIBLE FOR THE
CC TRANSLOCATION OF THE SUBSTRATE ACROSS THE MEMBRANE.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (potential).
CC -1- SIMILARITY: BELONGS TO THE BINDING-PROTEIN-DEPENDENT TRANSPORT
CC SYSTEM PERMEASE FAMILY. HISWQ SUBFAMILY. SEEMS TO BE THE ORTHOLOG
CC OF R.LEGMINOSARUM AAPQ.
CC -----
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CC -----
CC DR EMBL; U18997; AAA58073.1; ALT_INIT.
CC DR EMBL; AE000405; AAC76301.1; ALT_INIT.
CC DR Ecogen; EG12835; yhdx.
CC DR InterPro; IPR000515; BPD_transp.
CC DR Pfam; PF00528; BPD_transp.1.
CC DR PROSITE; PS00402; BPD_TRANSP_INN_MEMBER; 1.
CC KM Hypothetical protein; Transport; Amino-acid transport; Transmembrane;
CC Inner membrane; Complete proteome.
CC FT TRANSMEM 21 41 POTENTIAL.
CC FT TRANSMEM 92 112 POTENTIAL.
CC FT TRANSMEM 128 148 POTENTIAL.
CC FT TRANSMEM 180 200 POTENTIAL.
CC FT TRANSMEM 219 239 POTENTIAL.
CC FT TRANSMEM 256 276 POTENTIAL.
CC FT TRANSMEM 333 353 POTENTIAL.
CC SQ SEQUENCE 362 AA; 39749 MW; 946105FBA0761BD6 CRC64;

Query Match 1.5%; Score 8; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LPLLAQWL 17
Db 227 LPLLAQWL 234

RESULT 10
ID ECT1_SCHPO STANDARD; PRT; 365 AA.
AC Q9UT16;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable ethanolamine-phosphate cytidyltransferase (EC 2.7.7.14)
DE (Phosphorylethanolamine transferase) (CTP:phosphoethanolamine
DE cytidyltransferase).
GN SPAC15E1.05C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Baaham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skellon J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Voickert G., Aert R., Robben J., Gymnopreze B.,
RA Weljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritze C., Holzer E., Moesti D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Gillefeu A., Cadieu E., Deyano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong U., Forsburg S.L.,
RA Carrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
```

RT "The genome sequence of Schizosaccharomyces pombe.";
 RL Nature 415:871-880(2002).
 CC -1- CATALYTIC ACTIVITY: CTP + ethanolamine phosphate = diphosphate +
 CC CDP-ethanolamine.
 CC -1- PATHWAY: PHOSPHOLIPID BIOSYNTHESIS; CDP-ETHANOLAMINE SYNTHESIS;
 CC SECOND STEP.
 CC -1- SIMILARITY: BELONGS TO THE CYTIDYLYLTRANSFERASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; AL109770; CAB52424.1; -
 DR InterPro; IPR004821; Cyt tran. rel.
 DR InterPro; IPR004820; Cytidylyltransf.
 DR Pfam; PF01467; Cytidylyltransf; 1.
 DR TIGRPFAMs; TIGR00125; Cyt tran. rel; 2.
 KM Transferase; Nucleotidylyltransferase; Phospholipid biosynthesis.
 FT DOMAIN 1 182 CATALYTIC (POTENTIAL).
 SQ SEQUENCE 365 AA; 41556 MW; ACDB6A974ABB734 CXC64;
 Query Match 1.5%; Score 8; DB 1; Length 365;
 Best Local Similarity 100.0%; Pred. No. 7.9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 304 SGTTLRL 311
 |||||
 Db 191 SGTTLRL 198
 RESULT 11
 LBP_HUMAN STANDARD; PRT; 481 AA.
 ID LBP_HUMAN Q92672; O43438; Q9UD66; Q9H403;
 AC P18428; Q92672; O43438; Q9UD66; Q9H403;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE L15-POLYsaccharide-binding protein precursor (LBP).
 GN LBP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=90385281; PubMed=2402637;
 RA Schumann R.R., Leong S.R., Flagg G.W., Gray P.W., Wright S.D.,
 RA Mathison J.C., Tobias P.S., Ulevitch R.J.;
 RA "Structure and function of lipopolysaccharide binding protein.";
 RL Science 249:1429-1431 (1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=94292492; PubMed=7517398;
 RA Wilde C.G., Seilhamer J.J., McGrogan M., Ashton N., Snable J.L.,
 RA Lane J.C., Leong S.R., Thornton M.B., Miller K.L., Scott R.W.;
 RA "Bactericidal/permeability-increasing protein and lipopolysaccharide
 RT (LPS)-binding protein. LPS binding properties and effects on LPS-
 RT mediated cell activation.";
 RL J. Biol. Chem. 269:17411-17416 (1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Hudacek J.A., Aslanidis C., Schmitz G.;
 RL Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=98110577; PubMed=9441745;
 RA Kirschning C.J., Au-Yang J., Lamping N., Reuter D., Pfeil D.,
 RA Seilhamer J.J., Schumann R.R.;
 RA "Similar organization of the lipopolysaccharide-binding protein (LBP)

RT and phospholipid transfer protein (PLTP) genes suggests a common gene
 RT family of lipid-binding proteins.";
 RL Genomics 46:416-425 (1997).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RT Long Y.Y., Liu J.Q., Xue Y.N., Wang H.X.;
 RT "Cloning and sequencing of human lipopolysaccharide-binding protein
 RT gene.";
 RL Sheng Wu Huaxue Yu Shengwu Wuli Jinzhan 25:469-471 (1998).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Mathews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Graffham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekesch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Leharvalho M.H., Leverisa M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McKay K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prichard S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Rose M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Symmore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:665-871 (2001).
 RN [7]
 RP SEQUENCE OF 1-41 FROM N.A.
 RA Sutton C.L., Smith R.I.F., Centola M.B., Theofan G.;
 RL Submitted (May-1995) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE=98227852; PubMed=9568897;
 RA Beamer L.J., Carroll S.F., Eisenberg D.;
 RA "The BPI/LBP family of proteins: a structural analysis of conserved
 RT regions.";
 RL Protein Sci. 7:906-914 (1998).
 CC -1- FUNCTION: BINDS TO THE LIPID A MOIETY OF BACTERIAL
 CC LIPOLYSACCHARIDES (LPS), A GLYCOLIPID PRESENT IN THE OUTER
 CC MEMBRANE OF ALL GRAM-NEGATIVE BACTERIA. THE LBP/LPS COMPLEX SEEMS
 CC TO INTERACT WITH THE CD14 RECEPTOR.
 CC -1- SIMILARITY: BELONGS TO THE BPI/CETP/LBP/PLTP FAMILY.
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 CC -----
 DR EMBL; M35533; AA59493.1; -
 DR EMBL; X98657; CA67226.1; -
 DR EMBL; X98658; CA67226.1; JOINED.
 DR EMBL; X98659; CA67226.1; JOINED.
 DR EMBL; X98660; CA67226.1; JOINED.
 DR EMBL; X98661; CA67226.1; JOINED.
 DR EMBL; X98662; CA67226.1; JOINED.
 DR EMBL; X98663; CA67226.1; JOINED.

DR EMBL; X98664; CAA67226.1; JOINED.
 DR EMBL; X98665; CAA67226.1; JOINED.
 DR EMBL; X98666; CAA67226.1; JOINED.
 DR EMBL; X98667; CAA67226.1; JOINED.
 DR EMBL; X98668; CAA67226.1; JOINED.
 DR EMBL; AF013500; AAC39547.1; JOINED.
 DR EMBL; AF013501; AAC39547.1; JOINED.
 DR EMBL; AF013502; AAC39547.1; JOINED.
 DR EMBL; AF013503; AAC39547.1; JOINED.
 DR EMBL; AF013504; AAC39547.1; JOINED.
 DR EMBL; AF013505; AAC39547.1; JOINED.
 DR EMBL; AF013506; AAC39547.1; JOINED.
 DR EMBL; AF013507; AAC39547.1; JOINED.
 DR EMBL; AF013508; AAC39547.1; JOINED.
 DR EMBL; AF013509; AAC39547.1; JOINED.
 DR EMBL; AF013510; AAC39547.1; JOINED.
 DR EMBL; AF013511; AAC39547.1; JOINED.
 DR EMBL; AF015067; AAC21962.1; -.
 DR EMBL; AL080249; CAC10462.1; -.
 DR PIR; A35843; A35843.
 DR HSSP; P17213; 1BP1.
 DR Genew; HGNC:5517; LBP.
 DR MIM; 151990; -.
 DR InterPro; IPR001124; LBP_BPI_CETP.
 DR Pfam; PF01273; LBP_BPI_CETP; 1.
 DR SMART; PF02886; LBP_BPI_CETP_C; 1.
 DR SMART; SM00329; BPI; 1.
 DR PROSITE; PS00400; LBP_BPI_CETP; 1.
 KW Lipid transport; Antibiotic; Transmembrane; Glycoprotein; signal.
 FT SIGNAL 1 25
 FT CHAIN 26 481
 FT CARBOHYD 300 300
 FT CARBOHYD 355 355
 FT CARBOHYD 386 386
 FT CARBOHYD 394 394
 FT CONFLICT 6 6
 FT CONFLICT 22 22
 FT CONFLICT 82 82
 FT CONFLICT 128 128
 FT CONFLICT 154 157
 FT CONFLICT 174 174
 FT CONFLICT 257 257
 FT CONFLICT 266 270
 FT CONFLICT 369 369
 FT CONFLICT 436 436
 SQ SEQUENCE 481 AA; 53349 MW; 816E4B9E5E6864D0 CRC64;
 Query Match 1.5%; Score 8; DB 1; Length 481;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGALRAL 8
 DB 1 MGALRAL 8
 ID 60IM_ECOLI STANDARD; PRT; 548 AA.
 AC P25714;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 60 kDa inner-membrane protein.
 GN YIDC OR B3705.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OC NCBI_TaxID=562;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=33315143; PubMed=7686882;
 RA Burland V.D., Plunkett G. II, Daniels D.L., Blattner F.R.;
 RT "DNA sequence and analysis of 136 kilobases of the Escherichia coli
 genome: organizational symmetry around the origin of replication.";
 RL Genomics 16:551-561 (1993).
 RN [2]
 RP SEQUENCE OF 1-2 FROM N.A.
 RX MEDLINE=8606995; PubMed=2415431;
 RA Hansen F.G., Hansen E.B., Aclung T.;
 RT "Physical mapping and nucleotide sequence of the rnpA gene that
 encodes the protein component of ribonuclease P in Escherichia
 coli.";
 RL Gene 38:85-93 (1985).
 RN [3]
 RP TOPOLOGY
 RX MEDLINE=99023968; PubMed=9804807;
 RA Saeel A., Monne M., de Gier J.W., von Heijne G.;
 RT "Membrane topology of the 60-kDa Oxa1p homologue from Escherichia
 coli.";
 RL J. Biol. Chem. 273:30415-30418 (1998).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
 (probable).
 CC -1- SIMILARITY: BELONGS TO THE OXA1 / 60 KDA IMP FAMILY.
 CC -----
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 CC -----
 DR EMBL; L10328; AAA62056.1; -.
 DR EMBL; AE000447; AAC76728.1; -.
 DR EMBL; M11056; -; NOT ANNOTATED_CDS.
 DR EcoGene; EG1197; YidC.
 DR InterPro; IPR001708; 60kDa innermemb.
 DR Pfam; PF02096; 60KD IMP; 1.
 DR PRINTS; PR00701; 60KDINNERMP.
 KW Transmembrane; Inner membrane; Complete proteome.
 FT DOMAIN 1 5
 FT TRANSMEM 6 23
 FT DOMAIN 24 342
 FT TRANSMEM 343 370
 FT TRANSMEM 371 416
 FT TRANSMEM 417 446
 FT TRANSMEM 447 463
 FT TRANSMEM 464 481
 FT TRANSMEM 482 493
 FT TRANSMEM 494 509
 FT TRANSMEM 510 512
 FT TRANSMEM 513 535
 FT DOMAIN 536 548
 SQ SEQUENCE 548 AA; 61526 MW; 95EBC5DAB4F2FCFB CRC64;
 Query Match 1.5%; Score 8; DB 1; Length 548;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 110 DTSSNFA 117
 DB 207 DTSSNFA 214
 ID G1ND_CORGL STANDARD; PRT; 692 AA.
 AC G9X706;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE [Protein-P11] uridylyltransferase (EC 2.7.7.59) (P11 uridylyl-
transferase) (uridylyl removing enzyme) (UTase).
DE GIND OR CGL2059.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Corynebacteriaceae; Corynebacteriaceae;
OC Corynebacterium.
OX NCBI_Taxid=1718;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RX MEDLINE=99243747; PubMed=10227160;
RA Jakoby M.J., Kraemer R., Burkovski A.;
RT "Nitrogen regulation in Corynebacterium glutamicum: isolation of genes
involved and biochemical characterization of corresponding proteins";
RL FEMS Microbiol. Lett. 173:303-310(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RX Nakagawa S.;
RL "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032";
RT Submitted (May-2002) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: MODIFIER, BY URIDYLATION OR DEURIDYLATION THE P11
(GIND) REGULATORY PROTEIN (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: UTP + [protein-P11] = diphosphate + uridylyl-
[protein-P11].
CC -1- SIMILARITY: BELONGS TO THE GIND FAMILY.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ010319; CAB39374.1; -;
DR EMBL; AP005280; BAB99452.1; -;
DR InterPro; IPR002819; HD.
DR InterPro; IPR003607; ME_P1ase_HDC.
DR InterPro; IPR002934; NTF_transf.
DR Pfam; PF01909; NTF_transf_2; 1.
DR Pfam; PF01966; HD; 1.
DR SMART; SM00471; HDC; 1.
DR Transference; Nucleotidyltransferase.
SQ SEQUENCE 692 AA; 75969 MW; A7AC19614C133676 CRC64;
Query Match 1.5%; Score 8; DB 1; Length 692;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 31 LPLRVAAA 38
DB 295 LPLRVAAA 302
RESULT 14
NIDO_HUMAN
ID NIDO_HUMAN STANDARD; PRT; 1247 AA.
AC P14543; Q14942;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Nidogen precursor (Entactin).
GN NID.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90091745; PubMed=2574658;
RA Nagayoshi T., Sanborn D., Hickok N.J., Olsen D.R., Fazio M.J.,

RA Chu M.-L., Knowlton R., Mann K., Deutzmann R., Timpl R., Utto J.;
RT "Human nidogen: complete amino acid sequence and structural domains
deduced from cDNAs, and evidence for polymorphism of the gene.";
RL DNA 8:581-594(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96044428; PubMed=7557988;
RA Zimmermann K., Holschen S., Hafner M., Nisch R.;
RT "Genomic sequences and structural organization of the human nidogen
gene (NID)";
RL Genomics 27:245-250(1995).
RN [3]
RP SEQUENCE OF 667-1247 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=99270475; PubMed=2471408;
RA Olsen D.R., Nagayoshi T., Fazio M., Mattei M.-G., Passage E., Weil D.,
RT Timpl R., Chu M.-L., Utto J.;
RT "Human nidogen: cDNA cloning, cellular expression, and mapping of the
gene to chromosome 1q43.";
RL Am. J. Hum. Genet. 44:876-885(1989).
CC -1- FUNCTION: SULFATED GLYCOPROTEIN WHICH IS WIDELY DISTRIBUTED IN
BASEMENT MEMBRANES AND THAT IS TIGHTLY ASSOCIATED WITH LAMININ.
CC ALSO BINDS TO COLLAGEN IV. IT PROBABLY HAS A ROLE IN CELL-
EXTRACELLULAR MATRIX INTERACTIONS.
CC -1- SUBCELLULAR LOCATION: BASEMENT MEMBRANES.
CC -1- PTM: N- AND O-GLYCOSYLATED.
CC -1- SIMILARITY: CONTAINS 1 THYROGLOBULIN TYPE-I DOMAIN.
CC -1- SIMILARITY: CONTAINS 5 LDL-RECEPTOR YWTD DOMAINS.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M30269; AAA59932.1; -;
DR EMBL; X82245; CAA57709.1; -;
DR EMBL; X84819; CAA57709.1; JOINED.
DR EMBL; X84820; CAA57709.1; JOINED.
DR EMBL; X84821; CAA57709.1; JOINED.
DR EMBL; X84822; CAA57709.1; JOINED.
DR EMBL; X84823; CAA57709.1; JOINED.
DR EMBL; X84824; CAA57709.1; JOINED.
DR EMBL; X84825; CAA57709.1; JOINED.
DR EMBL; X84826; CAA57709.1; JOINED.
DR EMBL; X84827; CAA57709.1; JOINED.
DR EMBL; X84828; CAA57709.1; JOINED.
DR EMBL; X84829; CAA57709.1; JOINED.
DR EMBL; X84830; CAA57709.1; JOINED.
DR EMBL; X84831; CAA57709.1; JOINED.
DR EMBL; X84832; CAA57709.1; JOINED.
DR EMBL; X84833; CAA57709.1; JOINED.
DR EMBL; X84834; CAA57709.1; JOINED.
DR EMBL; X84835; CAA57709.1; JOINED.
DR EMBL; X84836; CAA57709.1; JOINED.
DR EMBL; X84837; CAA57709.1; JOINED.
DR EMBL; M27445; AAA57261.1; -;
DR PIR; A33322; MMHUND.
DR HSSP; P35555; IEMN.
DR Genew; HGNC:7821; NID.
DR MIM; 131390; -;
DR InterPro; IPR000152; Aex_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR000033; Idl_receptor_rep.
DR InterPro; IPR003866; Nidogen_ext.
DR InterPro; IPR000716; Thyroglobulin_1.
DR Pfam; PF00008; EGF; 6.
DR Pfam; PF00058; Idl_recept_b; 3.
DR Pfam; PF00086; thyroglobulin_1; 1.

DR SMART; SM00179; EGF CA; 2.
 DR SMART; SM00001; EGF_Like; 4.
 DR SMART; SM00135; LY; 5.
 DR SMART; SM00539; NIDO; 1.
 DR SMART; SM00211; TY; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 3.
 DR PROSITE; PS00484; THYROGLOBULIN_1; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 5.
 DR PROSITE; PS01187; EGF CA; 2.
 KW Basement membrane; Extracellular matrix; Glycoprotein; Sulfation;
 KW Signal; Calcium-binding; Repeat; EGF-like domain; Cell adhesion.
 FT SIGNAL 1 / 28
 FT CHAIN 29 / 28
 FT DOMAIN 29 669 I (LARGER GLOBULAR DOMAIN).
 FT DOMAIN 670 917 II (CYSTEINE-RICH).
 FT DOMAIN 918 1247 III (SMALLER GLOBULAR DOMAIN).
 FT DOMAIN 386 426 EGF-Like 1.
 FT DOMAIN 668 709 EGF-Like 2.
 FT DOMAIN 710 751 EGF-Like 3.
 FT DOMAIN 758 801 EGF-Like 4.
 FT DOMAIN 802 840 EGF-Like 5.
 FT DOMAIN 872 919 THYROGLOBULIN TYPE 1.
 FT DOMAIN 1030 1073 LDL-RECEPTOR YWTD MOTIF 1.
 FT DOMAIN 1073 1073 LDL-RECEPTOR YWTD MOTIF 2.
 FT DOMAIN 1075 1118 LDL-RECEPTOR YWTD MOTIF 3.
 FT DOMAIN 1124 1163 LDL-RECEPTOR YWTD MOTIF 4.
 FT DOMAIN 1208 1244 EGF-Like 6.
 FT MOD_RES 289 289 SULFATION (POTENTIAL).
 FT MOD_RES 296 296 SULFATION (POTENTIAL).
 FT DISULFID 672 685 BY SIMILARITY.
 FT DISULFID 679 695 BY SIMILARITY.
 FT DISULFID 697 708 BY SIMILARITY.
 FT DISULFID 714 727 BY SIMILARITY.
 FT DISULFID 721 736 BY SIMILARITY.
 FT DISULFID 738 750 BY SIMILARITY.
 FT DISULFID 762 777 BY SIMILARITY.
 FT DISULFID 789 787 BY SIMILARITY.
 FT DISULFID 789 800 BY SIMILARITY.
 FT DISULFID 806 817 BY SIMILARITY.
 FT DISULFID 811 826 BY SIMILARITY.
 FT DISULFID 828 839 BY SIMILARITY.
 FT DISULFID 1212 1223 BY SIMILARITY.
 FT DISULFID 1219 1232 BY SIMILARITY.
 FT DISULFID 1234 1243 BY SIMILARITY.
 FT SITE 702 704 CELL ATTACHMENT SITE.
 FT CARBOHYD 1137 1137 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 33 34 EL -> SS (IN REF. 2).
 FT CONFLICT 37 42 FGPOG -> SAPPR (IN REF. 2).
 FT CONFLICT 1115 1115 H -> T (IN REF. 3).
 SQ SEQUENCE 1247 AA; 136488 MW; 4681583CEC1575B CRC64;

Query Match 1.5%; Score 8; DB 1; Length 1247;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 RALLPL 13
 |||||
 14 RALLPL 21

RESULT 15
 ID DNMI_MOUSE STANDARD; PRT: 1620 AA.
 AC P13854; P97413; Q9QXK6; Q9QSC6;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE DNA (cytosine-5)-methyltransferase 1 (EC 2.1.1.37) (Dnmt1) (DNA methyltransferase MnuI) (DNA MTase MnuI) (MCM1) (Met-1).
 GN DNMT1 OR DNMT OR UTM OR MET1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=89094873; PubMed=3210246;
 RA Bestor T.H., Laudano A., Mattaliano R., Ingram V.;
 RT "Cloning and sequencing of a cDNA encoding DNA methyltransferase of
 RT mouse cells. The carboxyl-terminal domain of the mammalian enzymes is
 RT related to bacterial restriction methyltransferases";
 RL J. Mol. Biol. 203:971-983(1988).
 RN [2]
 RP REVISIONS TO N-TERMINUS.
 RC TISSUE=Embryo;
 RX MEDLINE=97094871; PubMed=8940105;
 RA Yoder J.A., Yen R.-W.C., Vertino P.M., Bestor T.H., Bayliss S.B.;
 RT "New 5' regions of the murine and human genes for DNA (cytosine-5)-
 RT methyltransferase";
 RL J. Biol. Chem. 271:31092-31097(1996).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC STRAIN=C57BL/6; TISSUE=Skeletal muscle;
 RX MEDLINE=20515133; PubMed=11063128;
 RA Aguirre-Arteaga A.M., Grunewald I., Cardoso M.C., Leonhardt H.;
 RT "Expression of an alternative Dnmt1 isoform during muscle
 RT differentiation";
 RL Cell Growth Differ. 11:551-559(2000).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN=C57BL/6;
 RX MEDLINE=20181859; PubMed=10715201;
 RA Margot J.B., Aguirre-Arteaga A.M., Di Giacomo B.V., Pradhan S.,
 RA Roberts R.J., Cardoso M.C., Leonhardt H.;
 RT "Structure and function of the mouse DNA methyltransferase gene: Dnmt1
 RT shows a tripartite structure";
 RL J. Mol. Biol. 297:293-300(2000).
 RN [5]
 RP SEQUENCE OF 1-27 AND 119-1619 FROM N.A. (ISOFORMS 1 AND 2).
 RX MEDLINE=98119799; PubMed=9449671;
 RA Mertineit C., Yoder J.A., Takeito T., Laird D.W., Trasler J.M.,
 RA Bestor T.H.;
 RT "Sex-specific exons control DNA methyltransferase in mammalian germ
 RT cells";
 RL Development 125:889-897(1998).
 RN [6]
 RP SEQUENCE OF 1-144 FROM N.A. (ISOFORMS 1 AND 2), AND SEQUENCE OF 3-6.
 RX STRAIN=129/Sv; and BALB/c; TISSUE=Embryonic stem cells;
 RX MEDLINE=99047652; PubMed=9830015;
 RA Gaudet F., Talbot D., Leonhardt H., Jaenisch R.;
 RT "A short DNA methyltransferase isoform restores methylation in vivo";
 RL J. Biol. Chem. 273:32725-32729(1998).
 RN [7]
 RP SEQUENCE OF 1-119 FROM N.A. (ISOFORM 1).
 RC STRAIN=129/Sv; TISSUE=Embryonic stem cells, and kidney;
 RX MEDLINE=97075093; PubMed=8917520;
 RA Tucker K.L., Talbot D., Lee M.A., Leonhardt H., Jaenisch R.;
 RT "Complementation of methylation deficiency in embryonic stem cells by
 RT a DNA methyltransferase minigene";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:12920-12925(1996).
 RN [8]
 RP SEQUENCE OF 1-272 FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schirni L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Futuro M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carrincci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Guestinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombere P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyshew-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohetsuki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection.",
 RL Nature 409:685-690(2001).
 RP PHOSPHORYLATION OF SER-515, AND MASS SPECTROMETRY.
 RC TISSUE=ERYTHROLEUKEMIA;
 RX MEDLINE=97362284; PubMed=9211941;
 RA Glickman J.F., Pavlovich J.G., Reich N.O.,
 RT "Peptide mapping of the murine DNA methyltransferase reveals a major
 RT phosphorylation site and the start of translation.",
 RL J. Biol. Chem. 272:17851-17857(1997).
 RN [10]
 RP INTERACTION WITH HDAC1.
 RX MEDLINE=20082816; PubMed=10615135;
 RA Fuks F., Burgers W.A., Brehm A., Hughes-Davies L., Kouzarides T.,
 RT "DNA methyltransferase Dnmt1 associates with histone deacetylase
 RT activity.",
 RL Nat. Genet. 24:88-91(2000).
 RN [11]
 RP INTERACTIONS WITH HDAC2 AND DNAP1.
 RX MEDLINE=20347709; PubMed=10888872;
 RA Rountree M.R., Bachman K.E., Baylin S.B.,
 RT "DNMT1 binds HDAC2 and a new co-repressor, DNAP1, to form a complex at
 RT replication foci.",
 RL Nat. Genet. 25:269-277(2000).
 RN [12]
 RP FUNCTION, AND SUBCELLULAR LOCATION.
 RX MEDLINE=21185930; PubMed=11290321.
 RA Howell C.Y., Besor T.H., Ding F., Latham K.E., Mertineit C.,
 RA Treasler J.M., Chaillet J.R.,
 RT "Genomic imprinting disrupted by a maternal effect mutation in the
 RT Dnmt1 gene.",
 RL Cell 104:829-838(2001).
 RN [13]
 RP ALLOSTERIC ACTIVATION.
 RX MEDLINE=21293215; PubMed=11399088;
 RA Facemli M., Hermann A., Pradhan S., Jeltsch A.,
 RT "The activity of the murine DNA methyltransferase Dnmt1 is controlled
 RT by interaction of the catalytic domain with the N-terminal part of
 RT the enzyme leading to an allosteric activation of the enzyme after
 RT binding to methylated DNA.",
 RL J. Mol. Biol. 309:1189-1199(2001).
 CC -1- FUNCTION: Methylates CpG residues. Preferentially methylates
 CC hemimethylated DNA. It is responsible for maintaining methylation
 CC patterns established in development. Isoform 2, in oocytes, may
 CC provide maintenance methyltransferase activity specifically at
 CC imprinted loci during the fourth embryonic S phase. Mediates
 CC transcriptional repression by direct binding to HDAC2.
 CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + DNA = S-adenosyl-L-
 CC homocysteine + DNA containing 5-methylcytosine.
 CC -1- ENZYME REGULATION: Allosterically regulated. The binding of 5-
 CC methylcytosine-containing DNA to the N-terminal parts of Dnmt1
 CC causes an allosteric activation of the catalytic domain by a
 CC direct interaction of its Zn-binding domain with the catalytic
 CC domain.
 CC -1- SUBUNIT: Interacts with HDAC1 and with PCNA. Forms a complex with
 CC DNAP1 and HDAC2, with direct interaction.
 CC -1- SUBCELLULAR LOCATION: Nuclear; it is nucleoplasmic through most of
 CC the cell cycle and associates with replication foci during S-
 CC phase. In germ cells: spermatogonia, preleptotene and leptotene
 CC spermatocytes all express high levels of nuclear protein, while
 CC the protein is not detected in pachytene spermatocytes, despite
 CC the fact they expressed high levels of mRNA. In females, the
 CC protein is not detected in non-growing oocytes, in contrast to the
 CC growing oocytes. During the growing, the protein is no longer
 CC detectable in nuclei but accumulates to very high levels first
 CC throughout the cytoplasm. At the time of ovulation, all the

CC protein is cytoplasmic and is actively associated with the oocyte
 CC cortex. After fecundation, in the preimplantation embryo, the
 CC protein remains cytoplasmic and after implantation, it is
 CC exclusively nuclear in all tissue types. Isoform 2 is sequestered
 CC in the cytoplasm of maturing oocytes and of preimplantation
 CC embryos, except for the 8-cell stage, while isoform 1 is
 CC exclusively nuclear.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1/long form (shown here) and
 CC 2/short form; are produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: Isoform 1 is expressed in embryonic stem cells
 CC and in somatic tissues. Isoform 2 is expressed in oocytes,
 CC preimplantation embryos, testis and in skeletal muscle during
 CC myogenesis.
 CC -1- DEVELOPMENTAL STAGE: In germ cells, it is present at high levels
 CC in spermatogonia and spermatocytes until the pachytene stage,
 CC where it falls to undetectable levels. The transient drop at the
 CC pachytene stage coincides with the disappearance of the 5.2 kb
 CC mRNA and the accumulation of a larger 6.0 kb mRNA. Oocytes
 CC accumulate very large amounts of Dnmt1 protein during the growth
 CC phase.
 CC -1- MISCELLANEOUS: There are three 5' exons, one specific to the
 CC oocyte (1c), one specific to the pachytene spermatocyte and also
 CC found in skeletal muscle (1b) and one found in somatic cells (1a).
 CC Three different mRNAs can be produced which give rise to two
 CC different translation products: isoform 1 (mRNAs-1a) and isoform 2
 CC (mRNAs-1b or -1c).
 CC -1- SIMILARITY: BELONGS TO THE C5-METHYLTRANSFERASE FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 BAH DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 CXXC-TYPE ZINC FINGER.
 CC
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 CC
 CC EMBL: X14805; CAA32910.1; -.
 CC DR EMBL: AF175432; AAF97695.1; -.
 CC DR EMBL: AF162282; AAF19352.1; -.
 CC DR EMBL: AF175431; AAF60965.1; -.
 CC DR EMBL: AF175412; AAF60965.1; JOINED.
 CC DR EMBL: AF175413; AAF60965.1; JOINED.

Query Match 1.5%; Score 8; DB 1; Length 1620;
 Best local similarity 100.0%; Pred. No. 29;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 66 PALASPAG 73
 |||||
 Db 11 PALASPAG 18

Search completed: April 1, 2003, 11:44:55
 Job time : 48 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 1, 2003, 11:40:49 ; Search time 38 Seconds
(without alignments)
2808.748 Million cell updates/sec

Title: US-09-668-314c-2

Perfect score: 518
Sequence: 1 MGALRALPLPLAQMILRA.....RPRDPEVNDSESLVRHRW 518

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_proteint:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriopl:*
- 17: sp_archaeop:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	439	84.7	439	4 Q9H2V8	Q9h2v8 homo sapien
2	378	73.0	396	4 Q9NZL1	Q9nzl1 homo sapien
3	328	63.3	468	4 Q9NZL2	Q9nzl2 homo sapien
4	59	11.4	514	11 Q9JUL8	Q9j1l8 mus musculu
5	38	7.3	255	11 Q9R1P7	Q9r1p7 mus musculu
6	12	2.3	432	4 Q9BYB9	Q9byb9 homo sapien
7	12	2.3	457	4 Q9BYC0	Q9byc0 homo sapien
8	12	2.3	476	4 Q9BYC1	Q9byc1 homo sapien
9	12	2.3	532	4 Q9YLS1	Q9yls1 homo sapien
10	9	1.7	266	11 Q9P0D2	Q9p0d2 homo sapien
11	9	1.7	319	16 Q9CUD5	Q9cud5 mus musculu
12	9	1.7	863	16 Q32940	Q32940 mycobacteri
13	9	1.7	863	16 Q9PCM3	Q9pcw3 xylella fas
14	9	1.7	1121	11 Q9NMK8	Q9nmk8 mus musculu
15	8	1.5	94	2 Q07312	Q07312 rhodobacter
16	8	1.5	96	10 Q9M8Y6	Q9m8y6 arabidopsis

17	1.5	159	16	Q9CP14	Q9cp14 pasteurella
18	1.5	178	10	Q42492	Q42492 canavalia g
19	1.5	202	16	Q9ZM15	Q9zml5 helicobacte
20	1.5	241	16	Q9LOR0	Q9lor0 streptomyce
21	1.5	244	5	Q8M0Y9	Q8m0y9 aphrocallis
22	1.5	250	12	Q72887	Q72887 african cas
23	1.5	254	16	Q983Z3	Q983z3 rhizobium 1
24	1.5	257	12	Q09347	Q09347 cassava gem
25	1.5	257	12	Q09348	Q09348 cassava gem
26	1.5	257	12	Q9WR12	Q9wr12 west africa
27	1.5	257	12	Q09351	Q09351 east africa
28	1.5	257	12	Q8V383	Q8v383 east africa
29	1.5	257	12	Q09350	Q09350 african cas
30	1.5	257	12	Q09349	Q09349 cassava gem
31	1.5	287	10	Q9SH24	Q9sh24 arabidopsis
32	1.5	303	16	Q9RXF5	Q9rxfs deinococcus
33	1.5	318	16	Q92XE4	Q92xe4 rhizobium m
34	1.5	319	16	Q8Z5W7	Q8z5w7 salmoneila
35	1.5	327	3	P78849	P78849 schizosacch
36	1.5	333	16	Q8ZNV8	Q8znv8 salmoneila
37	1.5	341	6	Q46495	Q46495 bos taurus
38	1.5	342	2	Q68868	Q68868 synchococc
39	1.5	352	17	Q9YER7	Q9yer7 aeropyrum p
40	1.5	364	16	Q97LG4	Q97lg4 clostridium
41	1.5	386	10	Q8S1T9	Q8s1t9 oryza sativ
42	1.5	393	16	Q8X5G4	Q8x5g4 escherichia
43	1.5	443	16	Q9RKZ4	Q9rkz4 streptomyce
44	1.5	449	10	Q9S9K4	Q9s9k4 arabidopsis
45	1.5	451	10	Q9JGF1	Q9jgf1 oryza sativ
46	1.5	471	11	Q91XR7	Q91xr7 rattus norv
47	1.5	472	4	Q96PQ4	Q96pq4 homo sapien
48	1.5	472	4	Q8WUX1	Q8wux1 homo sapien
49	1.5	473	5	Q9VEE0	Q9vee0 drosophila
50	1.5	474	5	Q8SQZ9	Q8sqz9 encephalito
51	1.5	476	4	Q9UTU8	Q9utu8 homo sapien
52	1.5	477	4	Q8TCF0	Q8tcfo homo sapien
53	1.5	482	2	Q8RMG9	Q8rmg9 acetobacter
54	1.5	504	4	Q996Z4	Q996z4 homo sapien
55	1.5	504	11	Q9JH29	Q9jhz9 rattus norv
56	1.5	505	11	Q9DGP2	Q9dgp2 mus musculu
57	1.5	505	11	Q9JTL8	Q9jtl8 mus musculu
58	1.5	548	16	Q8ZLN7	Q8zln7 salmoneila
59	1.5	548	16	Q8XB42	Q8xb42 escherichia
60	1.5	548	16	Q8ZKY4	Q8zky4 salmoneila
61	1.5	580	17	Q59381	Q59381 pyrococcus
62	1.5	581	17	Q8U0D8	Q8u0d8 pyrococcus
63	1.5	592	5	Q9VTS5	Q9vts5 drosophila
64	1.5	612	5	Q8T0E6	Q8t0e6 drosophila
65	1.5	637	10	Q82612	Q82612 arabidopsis
66	1.5	671	17	Q8RUA8	Q8r1a8 methanosarc
67	1.5	682	16	Q8XVM2	Q8xvm2 ralsstonia s
68	1.5	904	16	Q9HUM7	Q9hum7 pseudomonas
69	1.5	985	3	Q8X0Z7	Q8x0z7 neurospora
70	1.5	1104	10	Q9FU60	Q9flu60 oryza sativ
71	1.5	1477	3	Q9C250	Q9c250 neurospora
72	1.4	22	4	Q9NNY7	Q9nnv7 homo sapien
73	1.4	32	16	Q98AB6	Q98ab6 rhizobium 1
74	1.4	45	12	Q68620	Q68620 hepatitis c
75	1.4	45	12	Q68613	Q68613 hepatitis c
76	1.4	45	12	Q68614	Q68614 hepatitis c
77	1.4	45	12	Q68617	Q68617 hepatitis c
78	1.4	45	12	Q68618	Q68618 hepatitis c
79	1.4	45	12	Q68619	Q68619 hepatitis c
80	1.4	45	12	Q68625	Q68625 hepatitis c
81	1.4	62	8	Q8WCQ3	Q8wcq3 sphacelaria
82	1.4	62	8	Q8WGQ2	Q8wgq2 sphacelaria
83	1.4	68	5	Q9GTY0	Q9gtv0 tribolium c
84	1.4	76	12	Q68499	Q68499 hepatitis c
85	1.4	76	12	Q68496	Q68496 hepatitis c
86	1.4	76	12	Q68497	Q68497 hepatitis c
87	1.4	76	12	Q68498	Q68498 hepatitis c
88	1.4	77	4	Q8T542	Q8t542 homo sapien
89	1.4	80	12	Q9W8C0	Q9w8c0 hepatitis c

90	7	1.4	80	12	Q9WA47	Q9WA47 hepatitis c	163	7	1.4	114	12	Q9IPK0	Q9IPK0 hepatitis c
91	7	1.4	80	12	Q9WA15	Q9WA15 hepatitis c	164	7	1.4	114	12	Q9IPJ9	Q9IPJ9 hepatitis c
92	7	1.4	80	12	Q9W9M8	Q9W9M8 hepatitis c	165	7	1.4	115	2	P72321	P72321 rhodospirillum rubrum
93	7	1.4	80	12	Q9W9B4	Q9W9B4 hepatitis c	166	7	1.4	119	9	Q9AZT7	Q9AZT7 bacteriophage phi29
94	7	1.4	80	12	Q9W9S3	Q9W9S3 hepatitis c	167	7	1.4	119	11	Q9GX14	Q9GX14 rattus norvegicus
95	7	1.4	80	12	Q9W8S2	Q9W8S2 hepatitis c	168	7	1.4	119	16	Q9CFR1	Q9CFR1 lactococcus lactis
96	7	1.4	80	12	Q9W9M3	Q9W9M3 hepatitis c	169	7	1.4	121	12	O72213	O72213 hepatitis c
97	7	1.4	80	12	Q9W9K3	Q9W9K3 hepatitis c	170	7	1.4	123	15	Q9YV02	Q9YV02 human immunodeficiency virus
98	7	1.4	80	12	Q9W9T7	Q9W9T7 hepatitis c	171	7	1.4	123	15	Q9YU25	Q9YU25 human immunodeficiency virus
99	7	1.4	80	12	Q9W9T6	Q9W9T6 hepatitis c	172	7	1.4	127	11	Q9CPY4	Q9CPY4 mus musculus
100	7	1.4	80	12	Q9W9T5	Q9W9T5 hepatitis c	173	7	1.4	131	16	Q9G0N1	Q9G0N1 mycoplasma mycoides
101	7	1.4	80	12	Q9W9T4	Q9W9T4 hepatitis c	174	7	1.4	132	16	Q9E7H5	Q9E7H5 brucella melitensis
102	7	1.4	80	12	Q9W9T3	Q9W9T3 hepatitis c	175	7	1.4	135	12	Q6B1H8	Q6B1H8 hepatitis c
103	7	1.4	80	12	Q9W9T2	Q9W9T2 hepatitis c	176	7	1.4	137	12	Q911I1	Q911I1 hepatitis c
104	7	1.4	80	12	Q9W9T0	Q9W9T0 hepatitis c	177	7	1.4	137	12	Q911I0	Q911I0 hepatitis c
105	7	1.4	80	12	Q9W9T9	Q9W9T9 hepatitis c	178	7	1.4	137	12	Q911H9	Q911H9 hepatitis c
106	7	1.4	80	12	Q9W9T8	Q9W9T8 hepatitis c	179	7	1.4	137	12	Q911H8	Q911H8 hepatitis c
107	7	1.4	80	12	Q9W9T7	Q9W9T7 hepatitis c	180	7	1.4	137	12	Q911H7	Q911H7 hepatitis c
108	7	1.4	80	12	Q9W9T6	Q9W9T6 hepatitis c	181	7	1.4	137	12	Q911H6	Q911H6 hepatitis c
109	7	1.4	80	12	Q9W9T5	Q9W9T5 hepatitis c	182	7	1.4	137	12	Q911H5	Q911H5 hepatitis c
110	7	1.4	80	12	Q9W9T4	Q9W9T4 hepatitis c	183	7	1.4	137	12	Q911H4	Q911H4 hepatitis c
111	7	1.4	80	12	Q9W9T3	Q9W9T3 hepatitis c	184	7	1.4	137	12	Q911H3	Q911H3 hepatitis c
112	7	1.4	80	12	Q9W9T2	Q9W9T2 hepatitis c	185	7	1.4	137	12	Q911H2	Q911H2 hepatitis c
113	7	1.4	80	12	Q9W9T1	Q9W9T1 hepatitis c	186	7	1.4	137	12	Q911H1	Q911H1 hepatitis c
114	7	1.4	80	12	Q9W9S8	Q9W9S8 hepatitis c	187	7	1.4	137	12	Q911H0	Q911H0 hepatitis c
115	7	1.4	80	12	Q9W9S7	Q9W9S7 hepatitis c	188	7	1.4	137	12	Q911G9	Q911G9 hepatitis c
116	7	1.4	80	12	Q9W9S6	Q9W9S6 hepatitis c	189	7	1.4	137	12	Q911G8	Q911G8 hepatitis c
117	7	1.4	80	12	Q9W9S5	Q9W9S5 hepatitis c	190	7	1.4	137	12	Q911G7	Q911G7 hepatitis c
118	7	1.4	80	12	Q9W9S4	Q9W9S4 hepatitis c	191	7	1.4	137	12	Q911G6	Q911G6 hepatitis c
119	7	1.4	80	12	Q9W9S3	Q9W9S3 hepatitis c	192	7	1.4	137	12	Q911G5	Q911G5 hepatitis c
120	7	1.4	80	12	Q9W9S2	Q9W9S2 hepatitis c	193	7	1.4	137	12	Q911G4	Q911G4 hepatitis c
121	7	1.4	80	12	Q9W9S1	Q9W9S1 hepatitis c	194	7	1.4	137	12	Q911G3	Q911G3 hepatitis c
122	7	1.4	80	12	Q9W9T8	Q9W9T8 hepatitis c	195	7	1.4	137	12	Q911G2	Q911G2 hepatitis c
123	7	1.4	82	17	Q9O3U3	Q9O3U3 hepatitis c	196	7	1.4	137	12	Q911G1	Q911G1 hepatitis c
124	7	1.4	84	17	Q8TWE3	Q8TWE3 methanopyrus kandleri	197	7	1.4	137	12	Q911G0	Q911G0 hepatitis c
125	7	1.4	85	2	Q9APD0	Q9APD0 burkholderia pseudomallei	198	7	1.4	137	12	Q911F9	Q911F9 hepatitis c
126	7	1.4	86	2	Q9W9F8	Q9W9F8 rhodococcus ruber	199	7	1.4	137	12	Q911F8	Q911F8 hepatitis c
127	7	1.4	86	8	Q9S7H6	Q9S7H6 diabolica	200	7	1.4	137	12	Q911F6	Q911F6 hepatitis c
128	7	1.4	86	8	Q9S7H8	Q9S7H8 diabolica	201	7	1.4	137	12	Q911F5	Q911F5 hepatitis c
129	7	1.4	86	8	Q9S7H7	Q9S7H7 diabolica	202	7	1.4	137	12	Q911F4	Q911F4 hepatitis c
130	7	1.4	92	16	Q9BUC3	Q9BUC3 rhizobium lotus	203	7	1.4	137	12	Q911F3	Q911F3 hepatitis c
131	7	1.4	96	16	Q9HYQ7	Q9HYQ7 pseudomonas aeruginosa	204	7	1.4	137	12	Q911F2	Q911F2 hepatitis c
132	7	1.4	97	4	Q16755	Q16755 homo sapien	205	7	1.4	137	12	Q911F1	Q911F1 hepatitis c
133	7	1.4	103	4	Q9ZE77	Q9ZE77 enterococcus faecalis	206	7	1.4	137	12	Q911F0	Q911F0 hepatitis c
134	7	1.4	104	16	Q9ZDE7	Q9ZDE7 listeria monocytogenes	207	7	1.4	137	12	Q911E9	Q911E9 hepatitis c
135	7	1.4	106	17	Q9HNB9	Q9HNB9 halobacterium salinarum	208	7	1.4	137	12	Q911E8	Q911E8 hepatitis c
136	7	1.4	107	3	Q8X1T7	Q8X1T7 pholiotia na	209	7	1.4	137	12	Q911E7	Q911E7 hepatitis c
137	7	1.4	109	12	Q8VAT4	Q8VAT4 white spot syndrome virus	210	7	1.4	137	12	Q911E6	Q911E6 hepatitis c
138	7	1.4	112	5	Q9VLE8	Q9VLE8 drosophila	211	7	1.4	137	12	Q911E5	Q911E5 hepatitis c
139	7	1.4	114	12	Q9IPM8	Q9IPM8 hepatitis c	212	7	1.4	137	12	Q911E4	Q911E4 hepatitis c
140	7	1.4	114	12	Q9IPM7	Q9IPM7 hepatitis c	213	7	1.4	137	12	Q911E3	Q911E3 hepatitis c
141	7	1.4	114	12	Q9IPM6	Q9IPM6 hepatitis c	214	7	1.4	137	12	Q911E2	Q911E2 hepatitis c
142	7	1.4	114	12	Q9IPM5	Q9IPM5 hepatitis c	215	7	1.4	137	12	Q911E1	Q911E1 hepatitis c
143	7	1.4	114	12	Q9IPM4	Q9IPM4 hepatitis c	216	7	1.4	137	12	Q911E0	Q911E0 hepatitis c
144	7	1.4	114	12	Q9IPM3	Q9IPM3 hepatitis c	217	7	1.4	137	12	Q911D9	Q911D9 hepatitis c
145	7	1.4	114	12	Q9IPM2	Q9IPM2 hepatitis c	218	7	1.4	137	12	Q911D8	Q911D8 hepatitis c
146	7	1.4	114	12	Q9IPM1	Q9IPM1 hepatitis c	219	7	1.4	137	12	Q911D7	Q911D7 hepatitis c
147	7	1.4	114	12	Q9IPM0	Q9IPM0 hepatitis c	220	7	1.4	137	12	Q911D6	Q911D6 hepatitis c
148	7	1.4	114	12	Q9IPM7	Q9IPM7 hepatitis c	221	7	1.4	137	12	Q911D5	Q911D5 hepatitis c
149	7	1.4	114	12	Q9IPM6	Q9IPM6 hepatitis c	222	7	1.4	137	12	Q911D4	Q911D4 hepatitis c
150	7	1.4	114	12	Q9IPM5	Q9IPM5 hepatitis c	223	7	1.4	137	12	Q911D3	Q911D3 hepatitis c
151	7	1.4	114	12	Q9IPM4	Q9IPM4 hepatitis c	224	7	1.4	137	12	Q911D2	Q911D2 hepatitis c
152	7	1.4	114	12	Q9IPM3	Q9IPM3 hepatitis c	225	7	1.4	137	12	Q911D1	Q911D1 hepatitis c
153	7	1.4	114	12	Q9IPM2	Q9IPM2 hepatitis c	226	7	1.4	137	12	Q911D0	Q911D0 hepatitis c
154	7	1.4	114	12	Q9IPM1	Q9IPM1 hepatitis c	227	7	1.4	137	12	Q911C9	Q911C9 hepatitis c
155	7	1.4	114	12	Q9IPM0	Q9IPM0 hepatitis c	228	7	1.4	137	12	Q911C8	Q911C8 hepatitis c
156	7	1.4	114	12	Q9IPK8	Q9IPK8 hepatitis c	229	7	1.4	137	12	Q911C7	Q911C7 hepatitis c
157	7	1.4	114	12	Q9IPK7	Q9IPK7 hepatitis c	230	7	1.4	137	12	Q911C6	Q911C6 hepatitis c
158	7	1.4	114	12	Q9IPK6	Q9IPK6 hepatitis c	231	7	1.4	137	12	Q911C5	Q911C5 hepatitis c
159	7	1.4	114	12	Q9IPK5	Q9IPK5 hepatitis c	232	7	1.4	137	12	Q911C4	Q911C4 hepatitis c
160	7	1.4	114	12	Q9IPK4	Q9IPK4 hepatitis c	233	7	1.4	137	12	Q911C3	Q911C3 hepatitis c
161	7	1.4	114	12	Q9IPK3	Q9IPK3 hepatitis c	234	7	1.4	137	12	Q911C2	Q911C2 hepatitis c
162	7	1.4	114	12	Q9IPK2	Q9IPK2 hepatitis c	235	7	1.4	137	12	Q911C1	Q911C1 hepatitis c

236	7	1.4	154	12	Q8Q0E8	Q8qg8 hepatitis c	309	7	1.4	205	8	Q9G8Z9	Q9g8z ochromonas
237	7	1.4	154	12	Q8Q0E7	Q8qge hepatitis c	310	7	1.4	206	10	Q9LSK3	Q9lsk3 arabidopsis
238	7	1.4	160	16	Q98K01	Q98k01 rhizobium l	311	7	1.4	206	10	Q9LSK2	Q9lsk2 arabidopsis
239	7	1.4	161	16	Q9K088	Q9k088 neisseria m	312	7	1.4	206	16	Q8UE19	Q8ue19 agrobacteri
240	7	1.4	161	16	Q9JVB8	Q9jvb8 neisseria m	313	7	1.4	210	2	Q9XCJ9	Q9xcj9 streptococ
241	7	1.4	167	3	Q9C150	Q9c150 candida gla	314	7	1.4	211	2	Q93V18	Q93v18 salmonella
242	7	1.4	168	16	Q2S5I2	Q2s5i2 helicobacte	315	7	1.4	212	16	Q8X580	Q8x580 escherichia
243	7	1.4	168	16	Q9ZJM9	Q9zjm9 helicobacte	316	7	1.4	218	2	Q9XCK5	Q9xc5 streptococ
244	7	1.4	169	12	Q917P8	Q917p8 hepatitis c	317	7	1.4	219	10	Q9S0H9	Q9s0h9 arabidopsis
245	7	1.4	170	16	Q927W0	Q927w0 listeria in	318	7	1.4	219	16	Q981K1	Q981k1 rhizobium l
246	7	1.4	170	16	Q8Y4B8	Q8y4b8 listeria mo	319	7	1.4	222	12	P89443	P89443 herpes simp
247	7	1.4	174	6	Q9SLE0	Q9sle0 canis famli	320	7	1.4	222	12	Q65570	Q65570 bovine herp
248	7	1.4	175	13	Q98T03	Q98t03 brachydanio	321	7	1.4	223	16	Q9L218	Q9l218 streptomyce
249	7	1.4	180	16	P71704	P71704 mycobacteri	322	7	1.4	227	8	Q9XPE9	Q9xpe9 eumeces egr
250	7	1.4	182	16	Q9K2R9	Q9k2r9 streptomyce	323	7	1.4	227	16	Q9R8M2	Q9rm2 deinococcus
251	7	1.4	185	16	Q2S457	Q2s457 helicobacte	324	7	1.4	227	16	Q981Y2	Q981y2 rhizobium l
252	7	1.4	186	12	Q91Y22	Q91y22 hepatitis c	325	7	1.4	230	10	Q8S5J3	Q8s5j3 cryza sativ
253	7	1.4	186	12	Q91Y21	Q91y21 hepatitis c	326	7	1.4	235	2	Q9XCK9	Q9xc9 streptococ
254	7	1.4	186	12	Q91Y20	Q91y20 hepatitis c	327	7	1.4	235	16	Q9URU0	Q9jru0 chlamydia p
255	7	1.4	186	12	Q91Y19	Q91y19 hepatitis c	328	7	1.4	235	16	Q92742	Q92742 chlamydia p
256	7	1.4	186	12	Q91Y18	Q91y18 hepatitis c	329	7	1.4	240	11	Q9D1A3	Q9d1a3 mus musculu
257	7	1.4	186	12	Q91Y17	Q91y17 hepatitis c	330	7	1.4	241	16	Q9PLK3	Q9plk3 chlamydia m
258	7	1.4	186	12	Q91Y16	Q91y16 hepatitis c	331	7	1.4	241	16	Q84728	Q84728 chlamydia t
259	7	1.4	186	12	Q91Y15	Q91y15 hepatitis c	332	7	1.4	244	2	Q93KX0	Q93kx0 yersinia en
260	7	1.4	186	12	Q91Y14	Q91y14 hepatitis c	333	7	1.4	244	16	Q8YX00	Q8yj00 brucella me
261	7	1.4	186	12	Q91Y13	Q91y13 hepatitis c	334	7	1.4	249	2	Q8VMJ4	Q8vmj4 pseudomonas
262	7	1.4	186	12	Q91Y12	Q91y12 hepatitis c	335	7	1.4	249	10	Q9AX28	Q9ax28 cryza sativ
263	7	1.4	186	12	Q91Y11	Q91y11 hepatitis c	336	7	1.4	251	16	Q9KG10	Q9kg10 bacillus ha
264	7	1.4	186	12	Q91Y10	Q91y10 hepatitis c	337	7	1.4	253	2	Q9L4V7	Q9l4v7 streptomyce
265	7	1.4	186	12	Q91Y09	Q91y09 hepatitis c	338	7	1.4	253	2	Q61709	Q61709 caenorhabdi
266	7	1.4	186	12	Q91Y08	Q91y08 hepatitis c	339	7	1.4	254	16	Q9A3X5	Q9a3x5 cauliabacter
267	7	1.4	186	12	Q91Y07	Q91y07 hepatitis c	340	7	1.4	255	10	Q43406	Q43406 brassica ol
268	7	1.4	186	12	Q91Y06	Q91y06 hepatitis c	341	7	1.4	257	2	Q69217	Q69217 azotobacter
269	7	1.4	186	12	Q91Y05	Q91y05 hepatitis c	342	7	1.4	258	2	Q9X414	Q9x414 chlamydophi
270	7	1.4	186	12	Q91Y12	Q91y12 hepatitis c	343	7	1.4	260	10	Q94AV8	Q94av8 arabidopsis
271	7	1.4	186	12	Q91Y11	Q91y11 hepatitis c	344	7	1.4	264	2	Q9UR55	Q9jre5 actinobacil
272	7	1.4	186	12	Q91Y10	Q91y10 hepatitis c	345	7	1.4	266	2	Q9ZFB0	Q9zfb0 rhodobacter
273	7	1.4	186	12	Q91Y09	Q91y09 hepatitis c	346	7	1.4	267	2	Q05382	Q05382 actinobacil
274	7	1.4	186	12	Q91Y08	Q91y08 hepatitis c	347	7	1.4	267	2	Q66261	Q66261 actinobacil
275	7	1.4	186	12	Q91Y06	Q91y06 hepatitis c	348	7	1.4	267	5	Q9VHH4	Q9vh4 dtrosophila
276	7	1.4	186	12	Q91Y05	Q91y05 hepatitis c	349	7	1.4	267	16	Q9HMB2	Q9hmb2 pseudomonas
277	7	1.4	186	12	Q91Y04	Q91y04 hepatitis c	350	7	1.4	267	16	Q9CWM2	Q9cwm2 pasteurella
278	7	1.4	186	12	Q91Y03	Q91y03 hepatitis c	351	7	1.4	268	16	Q8XDY5	Q8xdy5 escherichia
279	7	1.4	186	12	Q91Y02	Q91y02 hepatitis c	352	7	1.4	269	2	Q9RFW5	Q9rfw5 mycoplasma
280	7	1.4	186	12	Q91Y01	Q91y01 hepatitis c	353	7	1.4	269	4	Q9UKP1	Q9ukp1 homo sapien
281	7	1.4	186	12	Q91Y00	Q91y00 hepatitis c	354	7	1.4	270	16	P71638	P71638 mycobacteri
282	7	1.4	186	12	Q91Y09	Q91y09 hepatitis c	355	7	1.4	276	16	Q9ZBN3	Q9zbn3 streptomyce
283	7	1.4	186	12	Q91Y08	Q91y08 hepatitis c	356	7	1.4	277	2	Q9F5Q9	Q9f5q9 vibrio chol
284	7	1.4	186	12	Q91Y07	Q91y07 hepatitis c	357	7	1.4	278	2	Q9RHL8	Q9rhl8 actinobacil
285	7	1.4	186	12	Q91Y06	Q91y06 hepatitis c	358	7	1.4	281	2	Q93Q45	Q93q45 clostridium
286	7	1.4	186	12	Q91Y05	Q91y05 hepatitis c	359	7	1.4	289	11	Q8R296	Q8r296 mus musculu
287	7	1.4	186	12	Q91Y04	Q91y04 hepatitis c	360	7	1.4	289	12	Q9QAI8	Q9gai8 murid herpe
288	7	1.4	186	12	Q91Y03	Q91y03 hepatitis c	361	7	1.4	289	16	Q8ZBW9	Q8zbw9 salmonella
289	7	1.4	186	12	Q91Y02	Q91y02 hepatitis c	362	7	1.4	289	16	Q9XK61	Q9xk61 pseudomonas
290	7	1.4	186	12	Q91Y00	Q91y00 hepatitis c	363	7	1.4	289	17	Q8UZB8	Q8uzb8 pyrococcus
291	7	1.4	186	12	Q91Y19	Q91y19 hepatitis c	364	7	1.4	290	16	Q8YFEB	Q8yfeb brucella me
292	7	1.4	186	12	Q91Y18	Q91y18 hepatitis c	365	7	1.4	291	16	Q9KMY5	Q9kmy5 vibrio chol
293	7	1.4	186	12	Q91Y17	Q91y17 hepatitis c	366	7	1.4	294	5	Q9VB61	Q9vb61 dtrosophila
294	7	1.4	186	12	Q91Y16	Q91y16 hepatitis c	367	7	1.4	295	16	Q9K3X0	Q9k3x0 streptomyce
295	7	1.4	186	12	Q91Y15	Q91y15 hepatitis c	368	7	1.4	298	5	Q9VOA8	Q9vga8 dtrosophila
296	7	1.4	186	16	Q92F66	Q92f66 listeria in	369	7	1.4	299	16	Q8UKB5	Q8ukb5 agrobacteri
297	7	1.4	187	8	Q03012	Q03012 molilugo ver	370	7	1.4	302	16	Q52882	Q52882 rhizobium m
298	7	1.4	189	2	Q9EM69	Q9em69 streptococ	371	7	1.4	305	17	Q8Z299	Q8z299 pyrobaculum
299	7	1.4	192	12	Q81414	Q81414 hepatitis c	372	7	1.4	306	16	Q8ZRU1	Q8zru1 salmonella
300	7	1.4	192	12	Q81432	Q81432 hepatitis c	373	7	1.4	306	16	Q8ZS97	Q8z97 salmonella
301	7	1.4	192	12	Q81435	Q81435 hepatitis c	374	7	1.4	306	16	Q8X9Y6	Q8x9y6 escherichia
302	7	1.4	192	12	Q81397	Q81397 hepatitis c	375	7	1.4	308	2	Q9JPL4	Q9jpl4 neisseria m
303	7	1.4	192	16	Q8ZEG6	Q8zeg6 yersinia pe	376	7	1.4	312	11	Q9D7V4	Q9d7v4 mus musculu
304	7	1.4	195	4	Q96LW6	Q96lw6 homo sapien	377	7	1.4	313	5	Q9VMY0	Q9vm0 dtrosophila
305	7	1.4	197	2	Q9WM61	Q9wm61 streptococ	378	7	1.4	314	2	Q9JPD2	Q9jpd2 rhodocyclu
306	7	1.4	200	16	Q9Z4W8	Q9z4w8 streptomyce	379	7	1.4	315	12	Q98UL4	Q98ul4 hepatitis c
307	7	1.4	203	16	Q8YOD0	Q8yod0 anabaena sp	380	7	1.4	315	12	Q98UL3	Q98ul3 hepatitis c
308	7	1.4	204	17	Q8TUA6	Q8tua6 methanosarc	381	7	1.4	316	16	Q9KMU0	Q9kmu0 vibrio chol

382	7	1.4	319	2	032485	032485 enterobacte	455	7	1.4	381	6	096K11	096K11 camelus dro
383	7	1.4	319	5	09N3J6	09N3J6 caenorhabdi	456	7	1.4	382	8	094RJO	094RJO chimaera mo
384	7	1.4	319	5	08TOB8	08TOB8 drosophila	457	7	1.4	381	13	09PRG9	09PRG9 gallus gall
385	7	1.4	319	16	09CMU4	09CMU4 pasteurella	458	7	1.4	383	5	095S03	095S03 drosophila
386	7	1.4	319	16	08YDM9	08YDM9 bruceella me	459	7	1.4	383	13	09DEC3	09DEC3 xenopus lae
387	7	1.4	320	2	09KHS4	09KHS4 leptospira	460	7	1.4	384	13	091322	091322 rana catesb
388	7	1.4	320	2	09L586	09L586 leptospira	461	7	1.4	385	6	02S080	02S080 sus scrofa
389	7	1.4	320	2	048546	048546 leptospira	462	7	1.4	386	6	09BKP3	09BKP3 caenorhabdi
390	7	1.4	320	16	09JXR6	09JXR6 neisseria m	463	7	1.4	386	6	09GMV7	09GMV7 rhinolphus
391	7	1.4	320	16	09JXR6	09JXR6 neisseria m	464	7	1.4	386	6	09GMV6	09GMV6 canis famli
392	7	1.4	322	5	09N3J7	09N3J7 caenorhabdi	465	7	1.4	386	6	09TTW8	09TTW8 capra hircu
393	7	1.4	322	5	001945	001945 meloidogyne	466	7	1.4	387	6	09GMV9	09GMV9 suncus muri
394	7	1.4	323	16	0989C6	0989C6 rhizobium 1	467	7	1.4	387	6	09GMV8	09GMV8 sorex ungui
395	7	1.4	325	16	092N18	092N18 rhizobium m	468	7	1.4	387	6	046496	046496 bos taurus
396	7	1.4	326	16	054118	054118 streptomyce	469	7	1.4	388	6	046524	046524 felis silve
397	7	1.4	326	16	08YDU4	08YDU4 raietonia s	470	7	1.4	389	3	09Y775	09Y775 candida tro
398	7	1.4	327	16	092WF7	092WF7 rhizobium m	471	7	1.4	389	3	09MYK3	09MYK3 sus scrofa
399	7	1.4	328	16	09KLE3	09KLE3 neisseria m	472	7	1.4	389	6	09MYK2	09MYK2 sus scrofa
400	7	1.4	328	16	09JXS6	09JXS6 neisseria m	473	7	1.4	390	6	09MYK2	09MYK2 sus scrofa
401	7	1.4	330	11	08VCK6	08VCK6 mus musculu	474	7	1.4	390	6	09GK10	09GK10 camelus dro
402	7	1.4	331	16	09PRL2	09PRL2 deinococcus	475	7	1.4	392	17	09U228	09U228 pyrococcus
403	7	1.4	331	16	09T561	09T561 pseudomonas	476	7	1.4	394	16	09PED1	09PED1 xyella fas
404	7	1.4	333	2	09XAT5	09XAT5 thizobium 1	477	7	1.4	394	16	P72780	P72780 synchocyst
405	7	1.4	333	16	08ZEG7	08ZEG7 yersinia pe	478	7	1.4	395	16	005773	005773 mycobacteri
406	7	1.4	335	5	0965L5	0965L5 yersinia pe	479	7	1.4	396	13	093428	093428 chironodrao
407	7	1.4	335	16	09PRG0	09PRG0 campylobact	480	7	1.4	398	16	09RW70	09RW70 deinococcus
408	7	1.4	336	3	074472	074472 echinosacch	481	7	1.4	407	17	09HJF2	09HJF2 thermoplasm
409	7	1.4	336	10	065453	065453 arabidopsis	482	7	1.4	411	2	066380	P71136 chlamydia p
410	7	1.4	337	16	092V77	092V77 rhizobium m	483	7	1.4	411	2	066380	066380 chlamydia p
411	7	1.4	338	12	065547	065547 bovine herp	484	7	1.4	413	3	014413	014413 pichia angu
412	7	1.4	339	16	091IH2	091IH2 pseudomonas	485	7	1.4	413	16	08RG42	08RG42 fusobacteri
413	7	1.4	339	16	08XXA2	08XXA2 raietonia s	486	7	1.4	416	16	0987L1	0987L1 rhizobium 1
414	7	1.4	340	16	098C73	098C73 rhizobium 1	487	7	1.4	416	16	08ZH85	08ZH85 yersinia pe
415	7	1.4	341	2	09XAN4	09XAN4 bacteroides	488	7	1.4	417	8	08WCQ4	08WCQ4 sphacelaria
416	7	1.4	341	2	002728	002728 ovis aries	489	7	1.4	419	10	094HM8	094HM8 oryza sativ
417	7	1.4	341	6	002728	002728 ovis aries	490	7	1.4	423	2	09EZP6	09EZP6 streptococ
418	7	1.4	341	6	019478	019478 mus musculu	491	7	1.4	430	16	08X147	08X147 cistridium
419	7	1.4	345	5	096439	096439 leishmania	492	7	1.4	433	16	09RT22	09RT22 deinococcus
420	7	1.4	345	16	09RRR0	09RRR0 deinococcus	493	7	1.4	433	16	08ZIK4	08ZIK4 yersinia pe
421	7	1.4	345	16	08Z359	08Z359 salmonella	494	7	1.4	436	16	09A1M0	09A1M0 streptococ
422	7	1.4	345	16	08URK3	08URK3 agrobacteri	495	7	1.4	436	16	09JNK7	09JNK7 streptococ
423	7	1.4	346	12	002729	002729 ovis aries	496	7	1.4	436	16	09ZU00	09ZU00 rhizobium m
424	7	1.4	346	12	068543	068543 horseadish	497	7	1.4	437	2	09EZP7	09EZP7 streptococ
425	7	1.4	346	16	09CHK6	09CHK6 bacillus ha	498	7	1.4	438	10	08W347	08W347 oryza sativ
426	7	1.4	347	16	08ZOK4	08ZOK4 lactococcus	499	7	1.4	441	17	08TW66	08TW66 methanopyru
427	7	1.4	350	16	09PRT2	09PRT2 anabaena sp	500	7	1.4	444	5	045891	045891 caenorhabdi
428	7	1.4	353	2	09PRT2	09PRT2 xylella fas	501	7	1.4	446	2	005375	005375 actinobacil
429	7	1.4	353	8	080037	080037 borrelia he	502	7	1.4	448	8	09B8G5	09B8G5 heticodocus
430	7	1.4	354	5	09GYX7	09GYX7 ciconia abd	503	7	1.4	449	17	08TWG3	08TWG3 methanopyru
431	7	1.4	358	2	070899	070899 boophilus m	504	7	1.4	450	5	060989	060989 plasmodium
432	7	1.4	358	10	09PRW5	09PRW5 borrelia he	505	7	1.4	451	16	076965	076965 fusobacteri
433	7	1.4	360	2	070905	070905 nepenthes a	506	7	1.4	451	16	08RHG6	08RHG6 fusobacteri
434	7	1.4	361	16	092S90	092S90 rhizobium m	507	7	1.4	452	10	09L173	09L173 arabidopsis
435	7	1.4	366	2	070900	070900 borrelia he	508	7	1.4	457	8	09SAL3	09SAL3 cladostephu
436	7	1.4	366	2	08SNJ3	08SNJ3 ractus norv	509	7	1.4	457	8	08WGQ0	08WGQ0 sphacelaria
437	7	1.4	367	16	098JF1	098JF1 rhizobium 1	510	7	1.4	457	8	08WGP7	08WGP7 sphacelaria
438	7	1.4	368	16	08UND2	08UND2 agrobacteri	511	7	1.4	460	4	09H8M0	09H8M0 homo sapien
439	7	1.4	371	2	09EZH2	09EZH2 streptococ	512	7	1.4	461	10	09FUL9	09FUL9 zea mays (m
440	7	1.4	371	4	016748	016748 homo sapien	513	7	1.4	465	4	096ND8	096ND8 homo sapien
441	7	1.4	371	4	016746	016746 homo sapien	514	7	1.4	465	5	09VER5	09VER5 drosophila
442	7	1.4	372	16	08U748	08U748 agrobacteri	515	7	1.4	468	17	028528	028528 archaeglob
443	7	1.4	373	10	09SD30	09SD30 arabidopsis	516	7	1.4	470	11	099LK8	099LK8 mus musculu
444	7	1.4	373	10	P93031	P93031 arabidopsis	517	7	1.4	473	4	096A99	096A99 homo sapien
445	7	1.4	374	6	09TWO	09TWO bos taurus	518	7	1.4	474	2	050185	050185 mycobacteri
446	7	1.4	374	16	0927X3	0927X3 listeria in	519	7	1.4	475	10	09SD14	09SD14 arabidopsis
447	7	1.4	375	11	08R5C3	08R5C3 mus musculu	520	7	1.4	477	5	09VJ95	09VJ95 drosophila
448	7	1.4	378	13	09PUR9	09PUR9 pseudopleur	521	7	1.4	482	4	08TBC2	08TBC2 homo sapien
449	7	1.4	379	4	096MC1	096MC1 homo sapien	522	7	1.4	484	2	09Z911	09Z911 magnetoapir
450	7	1.4	379	11	09JUX1	09JUX1 ractus norv	523	7	1.4	484	17	026245	026245 methanobact
451	7	1.4	380	6	046492	046492 bos taurus	524	7	1.4	486	10	09S130	09S130 arabidopsis
452	7	1.4	380	6	09TWS	09TWS capra hircu	525	7	1.4	486	10	038934	038934 arabidopsis
453	7	1.4	380	6	09TVA	09TVA bos taurus	526	7	1.4	486	13	08QX2	08QX2 brachydanio
454	7	1.4	380	6	002723	002723 ovis aries	527	7	1.4	488	2	09ZP57	09ZP57 neisseria m

528	7	1.4	488	16	Q9K165	Q9K165 neisseria m	601	7	1.4	611	8	Q9S1J2	Q9S1J2 phoxinus er
529	7	1.4	490	16	Q9JSR3	Q9JSR3 neisseria m	602	7	1.4	613	13	Q98C87	Q98C87 rhizobium 1
530	7	1.4	491	16	P71586	P71586 mycobacteri	603	7	1.4	615	13	Q42565	Q42565 xenopus lae
531	7	1.4	491	16	Q8U9P9	Q8U9P9 agrobacteri	604	7	1.4	622	5	Q9VZE3	Q9VZE3 drosophila
532	7	1.4	491	17	Q9HN17	Q9HN17 halobacteri	605	7	1.4	625	16	Q9HWN4	Q9HWN4 pseudomonas
533	7	1.4	492	16	Q9CDE6	Q9CDE6 mycobacteri	606	7	1.4	626	16	Q9KQX9	Q9KQX9 vibrio chol
534	7	1.4	493	5	Q16741	Q16741 homo sapien	607	7	1.4	633	16	Q98LR9	Q98LR9 rhizobium 1
535	7	1.4	495	4	Q16742	Q16742 homo sapien	608	7	1.4	638	6	Q62705	Q62705 sus scrofa
536	7	1.4	495	4	Q16749	Q16749 homo sapien	609	7	1.4	638	6	Q62707	Q62707 sus scrofa
537	7	1.4	495	4	Q16874	Q16874 h cytochrom	610	7	1.4	638	15	Q90LX5	Q90LX5 porcine end
538	7	1.4	496	16	Q9HXB9	Q9HXB9 pseudomonas	611	7	1.4	638	15	Q90LX4	Q90LX4 porcine end
539	7	1.4	497	5	Q9GXY2	Q9GXY2 leishmania	612	7	1.4	638	17	Q90LX3	Q90LX3 porcine end
540	7	1.4	501	16	Q8KX19	Q8KX19 ralsctonia s	613	7	1.4	639	17	Q59112	Q59112 pyrococcus
541	7	1.4	501	17	Q8THN4	Q8THN4 methanosarc	614	7	1.4	641	15	Q9K4H5	Q9K4H5 streptomyce
542	7	1.4	504	10	Q9XFX3	Q9XFX3 cynara card	615	7	1.4	641	15	Q8Q6Y9	Q8Q6Y9 porcine end
543	7	1.4	504	16	Q53858	Q53858 mycobacteri	616	7	1.4	644	16	Q69917	Q69917 streptomyce
544	7	1.4	505	10	Q9FRW6	Q9FRW6 nepenthes a	617	7	1.4	646	5	Q21689	Q21689 caenorhabdi
545	7	1.4	506	10	Q39311	Q39311 brassica na	618	7	1.4	649	4	Q9H0T2	Q9H0T2 homo sapien
546	7	1.4	506	10	Q40140	Q40140 lycopersico	619	7	1.4	653	15	Q8Q6Z1	Q8Q6Z1 porcine end
547	7	1.4	506	10	Q65390	Q65390 arabisdopsis	620	7	1.4	653	15	Q8Q6Z0	Q8Q6Z0 porcine end
548	7	1.4	507	10	Q9FRW7	Q9FRW7 nepenthes a	621	7	1.4	659	12	Q66383	Q66383 dengue viru
549	7	1.4	508	10	Q94BP0	Q94BP0 glycine max	622	7	1.4	659	15	Q9Q9X3	Q9Q9X3 porcine end
550	7	1.4	508	10	Q9XEC4	Q9XEC4 arabisdopsis	623	7	1.4	659	15	Q8Q6Y8	Q8Q6Y8 porcine end
551	7	1.4	509	10	Q9S8Z1	Q9S8Z1 helianthus	624	7	1.4	659	15	Q8Q6Y7	Q8Q6Y7 porcine end
552	7	1.4	510	16	Q99WR2	Q99WR2 staphylococ	625	7	1.4	659	15	Q8Q6Y6	Q8Q6Y6 porcine end
553	7	1.4	512	10	Q04593	Q04593 arabisdopsis	626	7	1.4	674	4	Q9H917	Q9H917 homo sapien
554	7	1.4	513	10	Q8VYL3	Q8VYL3 arabisdopsis	627	7	1.4	677	5	Q9V8K7	Q9V8K7 drosophila
555	7	1.4	514	10	Q9FRW9	Q9FRW9 nepenthes a	628	7	1.4	682	16	Q8Z057	Q8Z057 yerstina pe
556	7	1.4	517	11	Q91XS7	Q91XS7 raltus norv	629	7	1.4	689	8	Q37618	Q37618 prototheca
557	7	1.4	519	10	Q9SD16	Q9SD16 arabisdopsis	630	7	1.4	690	16	Q9KLR6	Q9KLR6 agrobacteri
558	7	1.4	525	16	Q99ZD0	Q99ZD0 streptococ	631	7	1.4	690	16	Q8UNO1	Q8UNO1 agrobacteri
559	7	1.4	526	2	Q93N65	Q93N65 coxiella bu	632	7	1.4	699	10	Q9ZU69	Q9ZU69 arabisdopsis
560	7	1.4	526	10	Q82783	Q82783 oryza sativ	633	7	1.4	702	17	Q8ZU82	Q8ZU82 pyrobaculum
561	7	1.4	527	10	Q9SUZ1	Q9SUZ1 arabisdopsis	634	7	1.4	707	16	Q9CD82	Q9CD82 mycobacteri
562	7	1.4	527	16	Q9ZAH8	Q9ZAH8 staphylococ	635	7	1.4	709	5	Q22548	Q22548 caenorhabdi
563	7	1.4	528	16	Q8XRX4	Q8XRX4 ralsctonia s	636	7	1.4	711	5	Q24205	Q24205 drosophila
564	7	1.4	529	10	Q9FC87	Q9FC87 arabisdopsis	637	7	1.4	712	16	Q9ZLS9	Q9ZLS9 rhizobium m
565	7	1.4	529	10	Q94CA1	Q94CA1 arabisdopsis	638	7	1.4	713	1	Q8XZ68	Q8XZ68 pyrococcus
566	7	1.4	529	17	Q8U2T6	Q8U2T6 pyrococcus	639	7	1.4	717	2	Q9X478	Q9X478 enterococcu
567	7	1.4	532	2	P95760	P95760 streptococ	640	7	1.4	721	16	Q9K515	Q9K515 vibrio chol
568	7	1.4	532	5	Q9V8K8	Q9V8K8 drosophila	641	7	1.4	722	3	Q10668	Q10668 echizosach
569	7	1.4	537	6	Q9MZU5	Q9MZU5 sus scrofa	642	7	1.4	725	2	Q68081	Q68081 rhodobacter
570	7	1.4	540	5	Q962U4	Q962U4 plasmodium	643	7	1.4	732	10	Q94HA5	Q94HA5 oryza sativ
571	7	1.4	541	4	Q8TBY2	Q8TBY2 homo sapien	644	7	1.4	741	6	Q9XAU3	Q9XAU3 pseudomonas
572	7	1.4	544	12	Q41936	Q41936 caulobacter	645	7	1.4	748	2	P79370	P79370 oryctolagus
573	7	1.4	547	16	Q9A2T2	Q9A2T2 caulobacter	646	7	1.4	758	11	Q99U52	Q99U52 mus musculu
574	7	1.4	548	10	Q8RU81	Q8RU81 oryza sativ	647	7	1.4	770	4	Q8TER3	Q8TER3 homo sapien
575	7	1.4	551	2	Q68258	Q68258 escherichia	648	7	1.4	779	10	Q8W0Q5	Q8W0Q5 sorghum bic
576	7	1.4	551	5	Q20673	Q20673 caenorhabdi	649	7	1.4	784	16	Q8VAM5	Q8VAM5 listeria mo
577	7	1.4	554	16	Q9PAC4	Q9PAC4 xylella fas	650	7	1.4	788	16	Q9PPA1	Q9PPA1 xylella fas
578	7	1.4	555	5	Q76789	Q76789 caenorhabdi	651	7	1.4	797	4	Q9BYB0	Q9BYB0 homo sapien
579	7	1.4	555	10	Q9C7N0	Q9C7N0 arabisdopsis	652	7	1.4	802	10	Q38802	Q38802 arabisdopsis
580	7	1.4	556	16	Q9KV74	Q9KV74 vibrio chol	653	7	1.4	813	10	Q9LDT8	Q9LDT8 oryza sativ
581	7	1.4	559	10	Q9FKP2	Q9FKP2 arabisdopsis	654	7	1.4	813	12	Q911N8	Q911N8 hepatitis b
582	7	1.4	561	16	Q9CKX7	Q9CKX7 pasteurella	655	7	1.4	830	17	Q27158	Q27158 methanobact
583	7	1.4	562	10	Q81837	Q81837 arabisdopsis	656	7	1.4	832	10	Q9S4T5	Q9S4T5 arabisdopsis
584	7	1.4	565	10	Q8VYV5	Q8VYV5 pseudomonas	657	7	1.4	843	12	Q91524	Q91524 hepatitis b
585	7	1.4	570	16	Q9HWG5	Q9HWG6 pseudomonas	658	7	1.4	854	5	Q9NDZ8	Q9NDZ8 hepatitis b
586	7	1.4	581	16	Q8RI17	Q8RI17 fusobacteri	659	7	1.4	880	16	Q9A1M8	Q9A1M8 streptococ
587	7	1.4	582	11	Q8VHU6	Q8VHU6 raltus norv	660	7	1.4	881	16	Q9A1M7	Q9A1M7 streptococ
588	7	1.4	583	5	Q9BH45	Q9BH45 plasmodium	661	7	1.4	882	11	Q9R0S1	Q9R0S1 mus musculu
589	7	1.4	583	5	Q9BH83	Q9BH83 plasmodium	662	7	1.4	887	5	Q19428	Q19428 caenorhabdi
590	7	1.4	588	16	Q8RCR3	Q8RCR3 thermoaer	663	7	1.4	893	10	Q8S615	Q8S615 oryza sativ
591	7	1.4	589	5	Q8WRY7	Q8WRY7 leishmania	664	7	1.4	902	5	Q9VSA5	Q9VSA5 oryza sativ
592	7	1.4	589	15	Q90LX2	Q90LX2 porcine end	665	7	1.4	907	16	Q9L248	Q9L248 streptomyce
593	7	1.4	600	2	Q9R613	Q9R613 rhodobacter	666	7	1.4	911	16	Q9KNU9	Q9KNU9 streptomyce
594	7	1.4	600	5	Q9U2N6	Q9U2N6 caenorhabdi	667	7	1.4	912	16	Q9K3Y2	Q9K3Y2 streptomyce
595	7	1.4	601	2	Q9R879	Q9R879 rhodobacter	668	7	1.4	931	12	Q9S3T2	Q9S3T2 streptococ
596	7	1.4	601	2	Q53189	Q53189 rhodobacter	669	7	1.4	931	12	Q9QAP6	Q9QAP6 rangiferine
597	7	1.4	601	10	Q80360	Q80360 arabisdopsis	670	7	1.4	933	16	Q8XE39	Q8XE39 escherichia
598	7	1.4	604	6	Q8SPR3	Q8SPR3 sus scrofa	671	7	1.4				
599	7	1.4	609	2	Q05334	Q05334 rhodobacter	672	7	1.4				
600	7	1.4	609	10	Q9AUT9	Q9AUT9 arabisdopsis	673	7	1.4				

674	7	1.4	934	11	Q924X9	Q924x9 mus musculi	747	6	1.2	24	9	Q9T0Q7	Q9T0Q7 bacterioph
675	7	1.4	939	16	Q8YOR3	Q8YOR3 anaena sp	748	6	1.2	25	11	Q9WNG7	Q9WNG7 sigma virus
676	7	1.4	952	16	Q86BM2	Q86bm2 rhizobium l	749	6	1.2	28	12	Q9ZME3	Q9ZME3 rhodopus su
677	7	1.4	964	16	Q8YFR7	Q8yfr7 brucella me	750	6	1.2	30	7	Q31234	Q31234 mus musculi
678	7	1.4	967	2	Q54123	Q54123 staphylococ	751	6	1.2	31	2	Q32325	Q32325 clostridium
679	7	1.4	968	2	Q9F848	Q9F848 streptomyce	752	6	1.2	33	4	Q16148	Q16148 homo sapien
680	7	1.4	970	16	Q92KJ8	Q92KJ8 rhizobium m	753	6	1.2	35	8	Q9S409	Q9S409 synaphobran
681	7	1.4	971	16	Q8UH99	Q8uh99 agrobacteri	754	6	1.2	36	4	Q9UHK5	Q9UHK5 homo sapien
682	7	1.4	991	4	Q15043	Q15043 homo sapien	755	6	1.2	39	5	Q16984	Q16984 acheta dome
683	7	1.4	993	5	Q9VXM6	Q9vxm6 drosophila	756	6	1.2	40	10	Q9SSK6	Q9SSK6 arabidopsis
684	7	1.4	994	11	Q9QVY4	Q9qvy4 mus sp. neu	757	6	1.2	44	16	Q8VJ52	Q8VJ52 mycobacteri
685	7	1.4	1015	2	Q93T50	Q93t50 streptococc	758	6	1.2	45	4	Q13013	Q13013 homo sapien
686	7	1.4	1015	4	Q14572	Q14572 homo sapien	759	6	1.2	44	4	Q12847	Q12847 homo sapien
687	7	1.4	1026	5	Q8SY90	Q8sy90 drosophila	760	6	1.2	45	4	Q8TD77	Q8td77 homo sapien
688	7	1.4	1027	2	Q93T51	Q93t51 streptococc	761	6	1.2	45	6	Q9GK71	Q9GK71 bos taurus
689	7	1.4	1039	16	Q9KEQ8	Q9keq8 bacillus ha	762	6	1.2	46	4	Q96J56	Q96j56 homo sapien
690	7	1.4	1042	4	Q9H4G6	Q9h4g6 homo sapien	763	6	1.2	46	11	Q9R1N8	Q9r1n8 mus musculi
691	7	1.4	1062	4	Q9NSW2	Q9nsw2 homo sapien	764	6	1.2	46	11	Q9WVP4	Q9wvp4 mus spreus
692	7	1.4	1082	11	Q8VJ75	Q8vj75 mus musculi	765	6	1.2	46	11	Q9WTK9	Q9wtk9 mus musculi
693	7	1.4	1130	4	Q9HIV5	Q9hiv5 homo sapien	766	6	1.2	47	12	Q91FM8	Q91fm8 chilo iride
694	7	1.4	1131	16	Q8YTA3	Q8yta3 anaena sp	767	6	1.2	49	2	Q9EVP1	Q9evp1 escherichia
695	7	1.4	1133	17	Q96XX7	Q96xx7 sulfolobus	768	6	1.2	49	13	Q42578	Q42578 xenopus lae
696	7	1.4	1142	16	Q97J24	Q97j24 clostridium	769	6	1.2	52	16	Q9A041	Q9a041 streptococc
697	7	1.4	1153	5	Q9U2G5	Q9u2g5 caenorhabdi	770	6	1.2	54	4	Q13807	Q13807 homo sapien
698	7	1.4	1163	16	Q92P24	Q92p24 rhizobium m	771	6	1.2	56	2	P97248	P97248 escherichia
699	7	1.4	1166	11	Q9OVN4	Q9ovn4 rattus sp.	772	6	1.2	56	5	Q9UAC6	Q9uac6 mesobuthus
700	7	1.4	1172	16	Q9ZBY5	Q9zby5 streptomyce	773	6	1.2	57	9	Q8SDV2	Q8sdv2 bacterioph
701	7	1.4	1177	16	Q8Y054	Q8y054 ralestonia s	774	6	1.2	58	4	Q969L1	Q969l1 homo sapien
702	7	1.4	1194	16	Q53645	Q53645 mycobacteri	775	6	1.2	59	3	Q9UT67	Q9ut67 schizosach
703	7	1.4	1215	11	P97686	P97686 rattus norv	776	6	1.2	59	6	Q28715	Q28715 oryctolagus
704	7	1.4	1235	11	Q9UL54	Q9ul54 homo sapien	777	6	1.2	60	3	Q9L720	Q9l720 caulobacter
705	7	1.4	1235	11	Q9JLS3	Q9jls3 rattus norv	778	6	1.2	60	9	Q12711	Q12711 trichoderma
706	7	1.4	1236	2	Q9JPA4	Q9jpa4 rhodocyclus	779	6	1.2	61	2	Q52860	Q52860 bacterioph
707	7	1.4	1241	16	Q8VXP9	Q8vxp9 mycobacteri	780	6	1.2	61	2	P82170	P82170 locusta mig
708	7	1.4	1253	10	Q9S404	Q9s404 arabidopsis	781	6	1.2	62	5	Q9BEP4	Q9bep4 conus penna
709	7	1.4	1269	5	Q43993	Q43993 dictyosteli	782	6	1.2	63	5	Q94855	Q94855 borrelia bu
710	7	1.4	1324	10	Q94GQ7	Q94gq7 oryza sativ	783	6	1.2	64	2	Q4855	Q4855 thiamophis
711	7	1.4	1330	6	Q97961	Q97961 vulpes vulp	784	6	1.2	64	8	Q36146	Q36146 chlamydia p
712	7	1.4	1379	5	Q9VNG9	Q9vng9 drosophila	785	6	1.2	65	16	Q9K2D5	Q9k2d5 chlamydia
713	7	1.4	1411	2	Q8TY11	Q8ty11 drosophila	786	6	1.2	67	5	Q9VP44	Q9vp44 drosophila
714	7	1.4	1411	2	Q8AUJ93	Q8auj93 actinomyces	787	6	1.2	67	16	Q92EM1	Q92em1 listeria in
715	7	1.4	1429	4	Q9Y5T6	Q9y5t6 homo sapien	788	6	1.2	67	16	Q927S6	Q927s6 listeria in
716	7	1.4	1433	11	Q07563	Q07563 mus musculi	789	6	1.2	67	16	Q8RYV4	Q8ryv4 listeria mo
717	7	1.4	1437	5	Q9GOS1	Q9gq51 dictyosteli	790	6	1.2	68	10	Q8RYJ4	Q8ryj4 oryza sativ
718	7	1.4	1513	16	P96901	P96901 mycobacteri	791	6	1.2	68	16	Q9CGB6	Q9cgb6 lactococcus
719	7	1.4	1628	4	Q9P2P2	Q9p2f2 homo sapien	792	6	1.2	68	16	Q9AUF4	Q9auf4 brassica ca
720	7	1.4	1630	16	Q8RHH7	Q8rhh7 fusobacteri	793	6	1.2	69	12	Q9AUF7	Q9auf7 brassica na
721	7	1.4	1690	2	Q86821	Q86821 streptomyce	794	6	1.2	69	12	Q9WIT0	Q9wit0 canarypox v
722	7	1.4	1740	2	Q9KWX8	Q9kwx8 streptomyce	795	6	1.2	69	16	Q91723	Q91723 pseudomonas
723	7	1.4	1829	5	Q8T2N7	Q8t2n7 dictyosteli	796	6	1.2	70	10	Q9AUF6	Q9auf6 brassica na
724	7	1.4	1886	5	Q9NKU5	Q9nku5 leishmania	797	6	1.2	70	10	Q9AUF5	Q9auf5 brassica ol
725	7	1.4	1937	2	Q8RJY2	Q8rjy2 stigmatalia	798	6	1.2	70	10	Q9AUF4	Q9auf4 brassica ca
726	7	1.4	2014	5	Q22774	Q22774 caenorhabdi	799	6	1.2	71	2	Q9FCW3	Q9fcw3 escherichia
727	7	1.4	2025	10	Q9SHK4	Q9shk4 arabidopsis	800	6	1.2	71	10	P93234	P93234 lycopersico
728	7	1.4	2042	5	Q9W1C5	Q9w1c5 drosophila	801	6	1.2	71	12	Q8QUQ7	Q8quq7 interococcus
729	7	1.4	2479	11	Q63002	Q63002 rattus norv	802	6	1.2	71	17	Q8TZV7	Q8tzv7 pyrococcus
730	7	1.4	2554	5	Q9NKT1	Q9nkt1 leishmania	803	6	1.2	72	10	Q65618	Q65618 arabidopsis
731	7	1.4	2813	4	Q96JPE	Q96jpe homo sapien	804	6	1.2	72	12	Q8VB96	Q8vbp6 white spot
732	7	1.4	2813	4	Q8WKO6	Q8wko6 homo sapien	805	6	1.2	73	8	Q9XOR3	Q9xqr3 pisum sativ
733	7	1.4	2817	4	Q96P79	Q96p79 homo sapien	806	6	1.2	73	8	Q35148	Q35148 merodia ery
734	7	1.4	2862	16	Q8R874	Q8r874 thermoaer	807	6	1.2	73	8	Q9A2N3	Q9a2n3 caulobacter
735	7	1.4	2894	17	Q58791	Q58791 methanococc	808	6	1.2	73	16	Q9A2X8	Q9a2x8 ralestonia s
736	7	1.4	3010	12	Q81760	Q81760 hepatitis c	809	6	1.2	74	16	Q8YXZ8	Q8yxz8 ralestonia s
737	7	1.4	3897	12	Q09461	Q09461 border dise	810	6	1.2	75	2	Q9EYX7	Q9eyx7 photobacter
738	7	1.4	4340	2	Q30764	Q30764 streptomyce	811	6	1.2	75	2	P94755	P94755 erwinia chr
739	7	1.4	4450	5	Q9UBZ8	Q9ubz8 caenorhabdi	812	6	1.2	75	16	Q8XTW9	Q8xtw9 ralestonia s
740	7	1.4	4706	10	Q9FN44	Q9fn44 arabidopsis	813	6	1.2	76	8	Q48083	Q48083 eryx latari
741	7	1.4	5953	16	Q8XS39	Q8xs39 ralestonia s	814	6	1.2	77	8	Q99364	Q99364 elaphe rufo
742	7	1.4	8243	5	Q96554	Q96554 cryptospori	815	6	1.2	77	8	Q9ZXV7	Q9zxv7 elaphe rufo
743	7	1.2				Q9ur72 trichoderma	816	6	1.2	77	10	Q9XJX4	Q9xjx4 oryza sativ
744	7	1.2				Q9pdx2 macaca mulia	817	6	1.2	78	8	Q36087	Q36087 thiamophis
745	7	1.2				Q9s956 zea mays (m	818	6	1.2	78	8	Q36143	Q36143 thiamophis
746	7	1.2				Q9qwb6 mus sp. sgp	819	6	1.2	79	6	Q29452	Q29452 bos taurus

820	6	1.2	79	16	025333	025333 helicobacte	893	6	1.2	94	8	036145	036145 chlamophis
821	6	1.2	80	2	070028	070028 streptomyce	894	6	1.2	94	8	036094	036094 chlamophis
822	6	1.2	80	2	09R6M8	09R6M8 agrobacteri	895	6	1.2	94	16	09CJ90	09CJ90 pasteurella
823	6	1.2	80	8	093165	093165 elaphe bima	896	6	1.2	95	2	049154	049154 methylobact
824	6	1.2	80	10	049028	049028 gracilaria	897	6	1.2	95	8	036000	036000 chlamophis
825	6	1.2	81	8	093352	093352 elaphe taen	898	6	1.2	95	8	035147	035147 merodia ery
826	6	1.2	81	8	093370	093370 dinodon ruf	899	6	1.2	95	10	09FTU0	09FTU0 oryza sativ
827	6	1.2	81	8	099371	099371 dinodon ruf	900	6	1.2	95	15	09JNC6	09JNC6 human immun
828	6	1.2	81	8	099372	099372 zaocys dhun	901	6	1.2	96	8	036001	036001 chlamophis
829	6	1.2	81	8	099373	099373 zaocys dhun	902	6	1.2	96	11	08R401	08R401 ratius norv
830	6	1.2	81	8	099374	099374 zaocys dhun	903	6	1.2	96	12	08OP44	08OP44 dengue viru
831	6	1.2	81	8	099375	099375 pygas korro	904	6	1.2	96	15	038190	038190 human immun
832	6	1.2	81	8	099376	099376 pygas korro	905	6	1.2	97	8	036051	036051 chlamophis
833	6	1.2	81	8	092XW5	092XW5 zaocys dhun	906	6	1.2	97	8	036019	036019 chlamophis
834	6	1.2	81	8	092XW5	092XW5 zaocys dhun	907	6	1.2	97	8	036021	036021 chlamophis
835	6	1.2	81	12	055445	055445 sindbis vir	908	6	1.2	97	8	036029	036029 chlamophis
836	6	1.2	81	12	055447	055447 sindbis vir	909	6	1.2	97	8	035983	035983 chlamophis
837	6	1.2	81	12	055448	055448 sindbis vir	910	6	1.2	97	15	09YF65	09YF65 human immun
838	6	1.2	81	12	055448	055448 sindbis vir	911	6	1.2	98	5	08SYX2	08SYX2 drosophila
839	6	1.2	81	16	09PA00	09PA00 xylella fas	912	6	1.2	98	8	036077	036077 chlamophis
840	6	1.2	81	16	09R1W6	09R1W6 streptomyce	913	6	1.2	98	8	035982	035982 chlamophis
841	6	1.2	82	4	09Y5U9	09Y5U9 homo sapien	914	6	1.2	98	8	021564	021564 sigmodon oc
842	6	1.2	82	5	08T2S0	08T2S0 dictyosteli	915	6	1.2	98	8	036028	036028 thamophis
843	6	1.2	82	11	09CR20	09CR20 mus musculu	916	6	1.2	98	9	080282	080282 xanthomonas
844	6	1.2	82	12	055446	055446 sindbis vir	917	6	1.2	98	8	036124	036124 chlamophis
845	6	1.2	83	4	09H3B2	09H3B2 homo sapien	918	6	1.2	99	8	09G435	09G435 chlamophis
846	6	1.2	84	8	036106	036106 thamophis	919	6	1.2	99	8	036024	036024 chlamophis
847	6	1.2	84	12	08VB94	08VB94 white spot	920	6	1.2	99	12	P88822	P88822 salmitrine
848	6	1.2	84	16	092S15	092S15 thizobium m	921	6	1.2	99	12	073557	073557 laesa virus
849	6	1.2	85	4	08TE25	08TE25 homo sapien	922	6	1.2	99	15	071241	071241 human immun
850	6	1.2	85	5	09W5T0	09W5T0 drosophila	923	6	1.2	99	16	092Y38	092Y38 thizobium m
851	6	1.2	85	8	048086	048086 eryx tatar	924	6	1.2	99	16	08YVNS	08YVNS anaebaena sp
852	6	1.2	85	17	09HJF0	09HJF0 human immun	925	6	1.2	100	8	09TEP8	09TEP8 natix natr
853	6	1.2	85	17	085938	085938 sphingomona	926	6	1.2	100	8	09TEP7	09TEP7 elaphe long
854	6	1.2	88	2	085938	085938 sphingomona	927	6	1.2	100	8	036144	036144 thamophis
855	6	1.2	88	8	036141	036141 thamophis	928	6	1.2	100	8	036025	036025 thamophis
856	6	1.2	88	10	08RWS1	08RWS1 arabidopsis	929	6	1.2	100	8	036027	036027 thamophis
857	6	1.2	88	16	025107	025107 helicobacte	930	6	1.2	100	8	036003	036003 thamophis
858	6	1.2	88	16	092K13	092K13 rhizobium m	931	6	1.2	100	8	035150	035150 merodia fas
859	6	1.2	88	16	09F2U8	09F2U8 streptomyce	932	6	1.2	100	10	023329	023329 arabidopsis
860	6	1.2	89	8	036122	036122 thamophis	933	6	1.2	100	12	091FS4	091FS4 chilo iride
861	6	1.2	89	8	095888	095888 peromyscus	934	6	1.2	100	13	090393	090393 cyprinodon
862	6	1.2	89	10	09AR36	09AR36 oryza sativ	935	6	1.2	101	16	092Y12	092Y12 rhizobium m
863	6	1.2	89	11	09WUG8	09WUG8 mus musculu	936	6	1.2	101	2	046552	046552 bacteroides
864	6	1.2	89	16	09CHR8	09CHR8 lactococcus	937	6	1.2	101	3	096U48	096U48 neurospora
865	6	1.2	89	16	092S83	092S83 rhizobium m	938	6	1.2	101	8	036083	036083 chlamophis
866	6	1.2	90	4	09UQV8	09UQV8 homo sapien	939	6	1.2	101	8	0952Q4	0952Q4 euphorbia p
867	6	1.2	90	8	036745	036745 epiractes s	940	6	1.2	101	10	08S2M7	08S2M7 oryza sativ
868	6	1.2	90	8	08WEO7	08WEO7 sanzania ma	941	6	1.2	101	12	084519	084519 parametium
869	6	1.2	90	8	08WEO6	08WEO6 boa constri	942	6	1.2	101	16	09HVC1	09HVC1 pseudomonas
870	6	1.2	90	8	08WEO5	08WEO5 candoia bib	943	6	1.2	101	16	08YDB6	08YDB6 bruceella me
871	6	1.2	90	8	08WEO4	08WEO4 candoia car	944	6	1.2	101	17	09Y9N7	09Y9N7 aeropyrum p
872	6	1.2	90	8	08WEO3	08WEO3 candoia car	945	6	1.2	102	8	09G121	09G121 chlamophis
873	6	1.2	90	8	08WEO2	08WEO2 candoia car	946	6	1.2	102	8	09G1W2	09G1W2 chlamophis
874	6	1.2	90	8	08WEO1	08WEO1 candoia car	947	6	1.2	102	8	09G1V3	09G1V3 chlamophis
875	6	1.2	90	8	08W7U6	08W7U6 candoia bib	948	6	1.2	102	8	09G1T7	09G1T7 thamophis
876	6	1.2	90	8	08W7N8	08W7N8 candoia asp	949	6	1.2	102	8	036078	036078 thamophis
877	6	1.2	90	8	08W7N7	08W7N7 candoia car	950	6	1.2	102	8	036022	036022 thamophis
878	6	1.2	90	8	08W7N6	08W7N6 candoia asp	951	6	1.2	102	8	036023	036023 thamophis
879	6	1.2	90	12	099CY8	099CY8 bovine herp	952	6	1.2	102	8	09B8P0	09B8P0 philodryas
880	6	1.2	90	13	091063	091063 jordanella	953	6	1.2	102	8	09B8B9	09B8B9 philodryas
881	6	1.2	90	13	090XJ1	090XJ1 acipenser s	954	6	1.2	102	8	09B8N8	09B8N7 philodryas
882	6	1.2	90	13	090XJ5	090XJ5 amia calva	955	6	1.2	102	8	09B8N7	09B8N7 philodryas
883	6	1.2	90	16	P71926	P71926 mycobacteri	956	6	1.2	102	8	09B8N6	09B8N6 philodryas
884	6	1.2	90	16	09K3G8	09K3G8 streptomyce	957	6	1.2	102	8	09B8N3	09B8N3 tropidodrya
885	6	1.2	90	17	09K3G7	09K3G7 pyrococcus	958	6	1.2	102	8	09B8N1	09B8N1 oxyrhopus g
886	6	1.2	91	12	09PYT8	09PYT8 xestica c-ni	959	6	1.2	102	8	09G436	09G436 chlamophis
887	6	1.2	92	2	052631	052631 escherichia	960	6	1.2	102	8	09G434	09G434 chlamophis
888	6	1.2	92	2	052632	052632 escherichia	961	6	1.2	102	8	09G432	09G432 chlamophis
889	6	1.2	92	8	036123	036123 thamophis	962	6	1.2	102	12	P88824	P88824 salmitrine
890	6	1.2	92	16	08YBA0	08YBA0 bruceella me	963	6	1.2	102	16	08X798	08X798 escherichia
891	6	1.2	93	13	091251	091251 profundulus	964	6	1.2	102	16	08YUN7	08YUN7 bruceella me
892	6	1.2	93	17	08TWE6	08TWE6 methanopyru	965	6	1.2	103	8	09TB05	09TB05 azemlops fe

966	6	1.2	103	8	Q9TB04	Q9tb04 agkistrodon
967	6	1.2	103	8	Q9TB03	Q9tb03 agkistrodon
968	6	1.2	103	8	Q9TB02	Q9tb02 glyodius br
969	6	1.2	103	8	Q9TB01	Q9tb01 agkistrodon
970	6	1.2	103	8	Q9TB00	Q9tb00 glyodius st
971	6	1.2	103	8	Q9TA29	Q9ta29 glyodius sa
972	6	1.2	103	8	Q9TA28	Q9ta28 glyodius sh
973	6	1.2	103	8	Q9TA27	Q9ta27 glyodius st
974	6	1.2	103	8	Q9TA26	Q9ta26 agkistrodon
975	6	1.2	103	8	Q9TA25	Q9ta25 ovophis mon
976	6	1.2	103	8	Q9TA24	Q9ta24 trimeresuru
977	6	1.2	103	8	Q9TA23	Q9ta23 trimeresuru
978	6	1.2	103	10	Q8S737	Q8s737 oryza sativ
979	6	1.2	103	11	Q9CUI3	Q9cui3 mus musculu
980	6	1.2	103	13	Q90224	Q90224 aplocheilic
981	6	1.2	103	13	Q90312	Q90312 crenicbthys
982	6	1.2	103	13	Q91931	Q91931 zoogonococcus
983	6	1.2	103	16	Q9RX39	Q9rx39 delnococtus
984	6	1.2	103	16	Q98P21	Q98p21 rhizobium 1
985	6	1.2	103	16	Q84895	Q84895 salmonella
986	6	1.2	104	6	Q29169	Q29169 sus scrofa
987	6	1.2	104	13	Q90242	Q90242 aplocheilic
988	6	1.2	104	13	Q91536	Q91536 xenotoca el
989	6	1.2	104	17	Q9UZM9	Q9uzm9 pyrococcus
990	6	1.2	105	3	Q9P8L3	Q9p8l3 botrytis ci
991	6	1.2	105	4	Q9P1P1	Q9p1p1 homo sapien
992	6	1.2	105	10	Q943N0	Q943n0 oryza sativ
993	6	1.2	105	16	Q9S8L1	Q9s8l1 staphylococ
994	6	1.2	105	16	Q8YH98	Q8yh98 bruceella me
995	6	1.2	106	8	Q9B1R1	Q9b1r1 crotales ho
996	6	1.2	106	8	Q9B426	Q9b426 crotales ho
997	6	1.2	106	8	Q21102	Q21102 homo sapien
998	6	1.2	106	12	Q9YK02	Q9yk02 dengue viru
999	6	1.2	107	2	Q05626	Q05626 streptomyce
1000	6	1.2	107	2	Q9XAT7	Q9xat7 rhodococcus

ALIGNMENTS

RESULT 1

Q9H2V8 PRELIMINARY; PRT; 439 AA.
 AC Q9H2V8;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE CDAL3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PHOCHROMOCYTOMA;
 RI Li Y., Huang Q., Peng, Y., Song H., Yu Y., Xu S., Ren S., Chen Z.,
 Han Z.;
 RA Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF212252; AAG41783.1; -.
 DR HSSP; P00797; 2REN.
 DR InterPro; IPR001461; Aspproteasea1.
 DR InterPro; IPR001969; Aspprotease_site.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPISIN.
 DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
 SQ SEQUENCE 439 AA; 48275 MW; 02EC0E050F11602 CRC64;

Query Match 84.7%; Score 439; DB 4; Length 439;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	1	MDNLOGDSGRGYLLEMLIGTPPOKQIILVDTGSSNFAVAGTPHSHYIDTFDTERSTYR	60
Qy	140	SKGFDVTVKTYQSGWTFGEEDLVITPKGFNTSFLVNIATIFESSENFPLGKWNIGL	199
Db	61	SKGFDVTVKTYQSGWTFGEEDLVITPKGFNTSFLVNIATIFESSENFPLGKWNIGL	120
Qy	200	AYATLAPSSSLSTFPDLSLTQANINPVFSMOMCGAGLPVAGSGTNGSLVLGIEBSLY	259
Db	121	AYATLAPSSSLSTFPDLSLTQANINPVFSMOMCGAGLPVAGSGTNGSLVLGIEBSLY	180
Qy	260	KGDITWYPIKEEWWYQIEILKLEIGGSLNLDREYNADKAIYDSGTTLLRLPOKVEDAV	319
Db	181	KGDITWYPIKEEWWYQIEILKLEIGGSLNLDREYNADKAIYDSGTTLLRLPOKVEDAV	240
Qy	320	VEAVARASLIPESDGFMTSGQLACWTNSETPWSYFPKISIVYLDENSSSFRITLIPOL	379
Db	241	VEAVARASLIPESDGFMTSGQLACWTNSETPWSYFPKISIVYLDENSSSFRITLIPOL	300
Qy	380	YIOPMAGLNYECYRFGISPTNALVIGATWMEGFVITDRQKRVGFAPCAETAGA	439
Db	301	YIOPMAGLNYECYRFGISPTNALVIGATWMEGFVITDRQKRVGFAPCAETAGA	360
Qy	440	AVSEISGPFSTEDVASCVCVPAQSLSEPTLWIVSYALMSVCGATILVILVLLPFCQRR	499
Db	361	AVSEISGPFSTEDVASCVCVPAQSLSEPTLWIVSYALMSVCGATILVILVLLPFCQRR	420
Qy	500	PRDEPVNDESSLVRRHWK	518
Db	421	PRDEPVNDESSLVRRHWK	439

RESULT 2

Q9NZL1 PRELIMINARY; PRT; 396 AA.
 AC Q9NZL1;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Aspartyl protease.
 GN BACE2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20422477; Pubmed=10965118;
 RA Solans A., Bisti Vill X., de la Luna S.;
 RT "A new aspartyl protease on 21q22.3, BACE2, is highly similar to
 Alzheimer's amyloid precursor protein beta-secretase.";
 RL Cytogenet. Cell Genet. 89:177-184 (2000).
 DR EMBL; AF188277; AAF35836.1; -.
 DR HSSP; P00797; 2REN.
 DR MEROPS; A01.041; -.
 DR InterPro; IPR001461; Aspproteasea1.
 DR InterPro; IPR001969; Aspprotease_site.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPISIN.
 DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_2.
 KW Protease.
 SQ SEQUENCE 396 AA; 43013 MW; 5023A7AF391CEAC9 CRC64;

Query Match 73.0%; Score 378; DB 4; Length 396;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGALRALLLPLLAQWLLRAAPELAPAFPLPLRVAATNRVAVTPGPGTPAERHADGL	60
Db	1	MGALRALLLPLLAQWLLRAAPELAPAFPLPLRVAATNRVAVTPGPGTPAERHADGL	60
Qy	61	ALALEPALASPAGANFLAMVDNLOGDSGRGYLLEMLIGTPPOKQIILVDTGSSNFAVAG	120
Db	61	ALALEPALASPAGANFLAMVDNLOGDSGRGYLLEMLIGTPPOKQIILVDTGSSNFAVAG	120


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QY 121 TPHSYIDTYFPTERRSSTYRSKGFVTVKYTGSGMTGFGVGEDLVITIPKGFNTSFLVNIATI 180
Db 121 TPHSYIDTYFPTERRSSTYRSKGFVTVKYTGSGMTGFGVGEDLVITIPKGFNTSFLVNIATI 180
QY 181 PESNFPLPGIKMNGIIGLAAYATLAKPSSSLETFFDSLVTOANI PNVSFMSQMGAGLPLVA 240
Db 181 PESNFPLPGIKMNGIIGLAAYATLAKPSSSLETFFDSLVTOANI PNVSFMSQMGAGLPLVA 240
QY 241 GSGTNGSLVVGIEPSLYKGDWYTPPIKEWYQIETLKIEIGGSLNIDCREYNADKA 300
Db 241 GSGTNGSLVVGIEPSLYKGDWYTPPIKEWYQIETLKIEIGGSLNIDCREYNADKA 300
QY 301 IVDSGTTLLRLPQKVPFVAVEAVARASLIPEFSDGFWTGSOLACMTSETPMSYFPKXISI 360
Db 301 IVDSGTTLLRLPQKVPFVAVEAVARASLIPEFSDGFWTGSOLACMTSETPMSYFPKXISI 360
QY 361 YLRDENSRSRFRITITLPO 378
Db 361 YLRDENSRSRFRITITLPO 378

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RESULT 3

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Q9NZL2 ID Q9NZL2 PRELIMINARY; PRT; 468 AA.
AC Q9NZL2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Aspartyl protease.
GN BACE2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20422477; PubMed=10965118;
RX Solans A., Estivill X., de la Luna S.;
RT "A new aspartyl protease on 21q22.3, BACE2, is highly similar to
RT Alzheimer's amyloid precursor protein beta-secretase.";
RL CytoGene. Cell Genet. 89:177-184 (2000).
DR EMBL; AF188276; AAF35835.1; -.
DR HSSP; P00797; 2REN.
DR MEROPS; A01.041; -.
DR InterPro; IPR001461; AsproteaseA1.
DR InterPro; IPR001969; Asprotease_site.
DR Pfam; PF00026; asp. 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_2.
KM Protease.
SQ SEQUENCE 468 AA; 50324 MW; 717E0920126A0142 CRC64;

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Query Match 63.3%; Score 328; DB 4; Length 468;
Best Local Similarity 100.0%; Pred. No. 6,6e-318;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MGALAPALLLELLAOWMLIRAPPELLAPFTLPLVAAATNVAATPPGPTPAERHAGL 60
Db 1 MGALAPALLLELLAOWMLIRAPPELLAPFTLPLVAAATNVAATPPGPTPAERHAGL 60
QY 61 ALALEPALASPAAGANFLAMVDNIOGDSRGVYLEMLIGTFPQKQILVDTGSSNFAVAG 120
Db 61 ALALEPALASPAAGANFLAMVDNIOGDSRGVYLEMLIGTFPQKQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFPTERRSSTYRSKGFVTVKYTGSGMTGFGVGEDLVITIPKGFNTSFLVNIATI 180
Db 121 TPHSYIDTYFPTERRSSTYRSKGFVTVKYTGSGMTGFGVGEDLVITIPKGFNTSFLVNIATI 180
QY 181 PESNFPLPGIKMNGIIGLAAYATLAKPSSSLETFFDSLVTOANI PNVSFMSQMGAGLPLVA 240
Db 181 PESNFPLPGIKMNGIIGLAAYATLAKPSSSLETFFDSLVTOANI PNVSFMSQMGAGLPLVA 240

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QY 241 GSGTNGSLVVGIEPSLYKGDWYTPPIKEWYQIETLKIEIGGSLNIDCREYNADKA 300
Db 241 GSGTNGSLVVGIEPSLYKGDWYTPPIKEWYQIETLKIEIGGSLNIDCREYNADKA 300
QY 301 IVDSGTTLLRLPQKVPFVAVEAVARASLIPEFSDGFWTGSOLACMTSETPMSYFPKXISI 360
Db 301 IVDSGTTLLRLPQKVPFVAVEAVARASLIPEFSDGFWTGSOLACMTSETPMSYFPKXISI 360

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RESULT 4

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Q9JL18 ID Q9JL18 PRELIMINARY; PRT; 514 AA.
AC Q9JL18;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Aspartyl protease 1.
GN BACE2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Choi D.K., Sugano S., Sakaki Y.;
RT "Molecular characterization of the mouse Aspi gene, a homolog of the
RT human Aspi (Down Syndrome Region aspartyl protease).";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF216310; AAF36599.1; -.
DR HSSP; P32329; 1YPS.
DR MEROPS; A01.041; -.
DR MGD; MGI:1860440; Bace2.
DR InterPro; IPR001461; AsproteaseA1.
DR InterPro; IPR001969; Asprotease_site.
DR Pfam; PF00026; asp. 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_2.
KM Protease.
SQ SEQUENCE 514 AA; 55799 MW; A70725F2CIDF5B47 CRC64;

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Query Match 11.4%; Score 59; DB 11; Length 514;
Best Local Similarity 100.0%; Pred. No. 8,8e-50;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 228 FSWMGAGLPLVAGSGTNGSLVVGIEPSLYKGDWYTPPIKEWYQIETLKIEIGQ 286
Db 224 FSWMGAGLPLVAGSGTNGSLVVGIEPSLYKGDWYTPPIKEWYQIETLKIEIGQ 282

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RESULT 5

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Q9R1P7 ID Q9R1P7 PRELIMINARY; PRT; 255 AA.
AC Q9R1P7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Aspartyl protease (Fragment).
GN BACE2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Accarino M., Fumagalli P., Taramelli R., Ottolenghi S.;
RT "Cloning of a gene from chromosome 21 Down Region encoding a potential
RT transmembrane protease.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF051150; AAD45964.1; -.
DR MEROPS; A01.041; -.
DR MGD; MGI:1860440; Bace2.
DR InterPro; IPR001461; AsproteaseA1.
DR InterPro; IPR001969; Asprotease_site.

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DR PRINTS; PR00792; PEPsin.
 DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
 KM PROTEASE.
 FT NON TER
 SQ SEQUENCE 255 AA; 28685 MW; 53DE317815996D63 CRC64;

Query Match 7.3%; Score 38; DB 11; Length 255;
 Best Local Similarity 100.0%; Pred. No. 4e-29;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 288 LNLDCREYNADKATVDSGTTLRRLRQKVPDAVEAVAR 325
 DB 25 LNLDCREYNADKATVDSGTTLRRLRQKVPDAVEAVAR 62

RESULT 6

Q9BYB9 PRELIMINARY; PRT; 432 AA.

AC Q9BYB9;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Beta-site APP cleaving enzyme I-432.

GN BACE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;

RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=BRIN;
 RX MEDLINE=21408467; PubMed=11516562;

RA Tanahashi H., Tabira T.;
 RT "Three novel alternatively spliced isoforms of the human beta-site APP
 cleaving enzyme (BACE) and their effect on amyloid beta-peptide
 production.";
 RL Neurosci. Lett. 307:9-12(2001).

DR EMBL; AB050438; BAB40933.1; -.
 DR HSSP; P32329; IYPS.

DR InterPro; IPR001461; AspproteaseA1.
 DR InterPro; IPR001969; Aspprotease_site.
 DR Pfam; PF00026; asp. 1.

DR PRINTS; PR00792; PEPsin.
 DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.

SQ SEQUENCE 432 AA; 48212 MW; 96FC81E6F0ED01B CRC64;

Query Match 2.3%; Score 12; DB 4; Length 432;
 Best Local Similarity 100.0%; Pred. No. 0.0054;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 ILVDTGSSNFAV 118
 DB 90 ILVDTGSSNFAV 101

RESULT 7

Q9BYC0 PRELIMINARY; PRT; 457 AA.

AC Q9BYC0;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Beta-site APP cleaving enzyme I-457 (Beta-site APP cleaving enzyme
 type C).

GN BACE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;

RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=BRIN;
 RX MEDLINE=21408467; PubMed=11516562;

RA Tanahashi H., Tabira T.;
 RT "Three novel alternatively spliced isoforms of the human beta-site APP
 cleaving enzyme (BACE) and their effect on amyloid beta-peptide
 production.";
 RL Neurosci. Lett. 307:9-12(2001).

RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=EXOCRINE PANCREAS;
 RA Zaccchetti D., De Pietri Tonelli D., Schnurbus R.;
 RT "New beta-site APP cleaving enzyme isoform (BACE-1c) obtained from
 human pancreas.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB050437; BAB40932.1; -.
 DR EMBL; AF338817; AAK38375.1; -.

DR HSSP; P32329; IYPS.
 DR InterPro; IPR001461; AspproteaseA1.
 DR InterPro; IPR001969; Aspprotease_site.
 DR Pfam; PF00026; asp. 1.

DR PRINTS; PR00792; PEPsin.
 DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.

SQ SEQUENCE 457 AA; 51068 MW; C794C9A5E85FE7A2 CRC64;

Query Match 2.3%; Score 12; DB 4; Length 457;
 Best Local Similarity 100.0%; Pred. No. 0.0056;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 ILVDTGSSNFAV 118
 DB 90 ILVDTGSSNFAV 101

RESULT 8

Q9BYC1 PRELIMINARY; PRT; 476 AA.

AC Q9BYC1;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Beta-site APP cleaving enzyme I-476.

GN BACE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;

RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=BRIN;
 RX MEDLINE=21408467; PubMed=11516562;

RA Tanahashi H., Tabira T.;
 RT "Three novel alternatively spliced isoforms of the human beta-site APP
 cleaving enzyme (BACE) and their effect on amyloid beta-peptide
 production.";
 RL Neurosci. Lett. 307:9-12(2001).

DR EMBL; AB050436; BAB40931.1; -.

DR HSSP; P32329; IYPS.

DR InterPro; IPR001461; AspproteaseA1.
 DR InterPro; IPR001969; Aspprotease_site.
 DR Pfam; PF00026; asp. 1.

DR PRINTS; PR00792; PEPsin.
 DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.

SQ SEQUENCE 476 AA; 52907 MW; 6C8C87F8A953AF66 CRC64;

Query Match 2.3%; Score 12; DB 4; Length 476;
 Best Local Similarity 100.0%; Pred. No. 0.0056;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 ILVDTGSSNFAV 118
 DB 90 ILVDTGSSNFAV 101

RESULT 9

Q9ULS1

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ID 09UTL1 PRELIMINARY; PRT; 532 AA.
AC 09UTL1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE KIAA1149 protein (Fragment).
GN KIAA1149.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RX MEDLINE=20039618; PubMed=10574461;
RA Hitozawa M., Nagase T., Ishikawa K., Kikuno R., Nomura N., Ohara O.;
RT "Characterization of cDNA clones selected by the Genemark analysis
RT from size-fractionated cDNA libraries from human brain.";
RL DNA Res. 6:329-336(1999).
DR EMBL; AB032975; BAA86463.2; -.
DR HSSP; P56272; 1AM5.
DR MEROPS; A01.004; -.
DR InterPro; IPR001461; Asparticaseal.
DR InterPro; IPR001669; Asparticaseal.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
FT NON TER 1
SQ SEQUENCE 532 AA; 58720 MW; 98B135D0D5FBD2E8 CRC64;

Query Match 2.3%; Score 12; DB 4; Length 532;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 ILVDTGSSNFAV 118
Db 121 ILVDTGSSNFAV 132

RESULT 10
09P0D2 PRELIMINARY; PRT; 213 AA.
AC 09P0D2;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE HSPC104 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CORD BLOOD;
RA Zhang Q.H., Ye M., Zhou J., Shen Y., Wu X.Y., Guan Z.Q., Wang L.,
RA Fan H.Y., Mao Y.F., Dai M., Huang Q.H., Chen S.J., Chen Z.;
RT "Human partial CDS cloned from cd34+ stem cells.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161367; AAF28927.1; -.
DR InterPro; IPR001461; Asparticaseal.
DR Pfam; PF00026; asp; 1.
FT NON TER 1
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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 370 SFRITLIPQ 378
Db 119 SFRITLIPQ 127

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RESULT 11
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AC 09CUD5;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Beta-site App cleaving enzyme (Fragment).
GN BACE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=BRIN;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA Kuent P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirini L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK014390; BAB29317.1; -.
DR MEROPS; A01.004; -.
DR MGD; MGI:1346542; Bace.
DR InterPro; IPR001461; Asparticaseal.
DR Pfam; PF00026; asp; 1.
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Db 121 SFRITLIPQ 129

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DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Possible sugar transport protein (Probable ABC-transport protein,
DE inner membrane component).
GN M1426 OR M1CB2052.28.
GN Mycobacterium leprae.
OS Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_Taxid=1769;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TN;
RX MEDLINE=2118732; PubMed=11234002;
RA Cole S.T., Sigmeier K., Parkhill J., James K.D., Thomson N.R.,

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RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
RA Holroyd S., Hornsby T., Jagsels K., Lacroix C., Maclean J., Moule S.,
RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrett B.G.;
RT "Massive gene decay in the leprosy bacillus.";
RL Nature 409:1007-1011 (2001)
CC -1- FUNCTION: PROBABLY PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT
CC SYSTEM. PROBABLY RESPONSIBLE FOR THE TRANSLLOCATION OF THE
CC SUBSTRATE ACROSS THE MEMBRANE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
CC PROTEIN-DEPENDENT TRANSPORT SYSTEMS.
DR EMBL; Z98604; CAB11326.1; -;
DR EMBL; AL583922; CAC30377.1; -;
DR Lepronia; ML1426; -;
DR InterPro; IPR000515; BPD transp.
DR Pfam; PF00528; BPD transp. 1.
DR PROSITE; PS00402; BPD_TRANS_PNN_MEMBR; 1.
KW Sugar transport; Transmembrane; Transport; Complete proteome.
SQ SEQUENCE 319 AA; 34868 MW; D1FD52DBE850DFC7 CRC64;
Query Match 1.7%; Score 9; DB 16; Length 319;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 294 AILVLIVL 302
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AC Q9PCW3;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical protein Xf1641.
GN Xf1641.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xylella.
CX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9A5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Brites M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carter H.,
RA Coutinho N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Facinani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frome M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hohnsels J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lamais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Neto L.E.S.,
RA Nhani A.Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A.Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E.Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A.Jr.,

RA da Silva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159 (2000).
DR EMBL; AE003991; AAF84450.1; -;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 863 AA; 95838 MW; 4FC65FC0A020876C CRC64;
Query Match 1.7%; Score 9; DB 16; Length 863;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 59 GLALALEPA 67
Db 153 GLALALEPA 161
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ID Q99MX8 PRELIMINARY; PRT; 1121 AA.
AC Q99MX8;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Macrophage hemoglobin scavenger receptor CD163 precursor.
GN CD163.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21243729; PubMed=11345593;
RA Schaefer D.J., Boretto F.S., Hongegger A., Roehler D., Linscheld P.,
RA Steage H., Muller C., Schoedon G., Schaffner A.;
RT "Molecular cloning and characterization of the mouse CD163 homologue,
RT a highly glucocorticoid-inducible member of the scavenger receptor
RT cysteine-rich family.";
RL Immunogenetics 53:170-177 (2001).
DR EMBL; AF274883; AAK16065.1; -;
DR MGD; MGI:2135946; Cd163.
DR InterPro; IPR001190; Srcr_receptor.
DR Pfam; PF00530; SRCR; 9.
DR PRINTS; PR00258; SPERACTRCPTR.
DR SMART; SM00202; SRCR_1; UNKNOWN_3.
DR PROSITE; PS00420; SRCR_1; UNKNOWN_3.
DR PROSITE; PS50287; SRCR_2; 9.
KW Receptor; Signal.
FT SIGNAL 1
FT SIGNAL 38
SQ SEQUENCE 1121 AA; 120889 MW; 04428DF18AD26187 CRC64;
Query Match 1.7%; Score 9; DB 11; Length 1121;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1051 VCGALLVL 1059
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AC 007312;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE Hypothetical 9.6 kDa protein.
GN URK6 OR URK3.
OS Rhodospirillum rubrum (Rhodospirillum rubrum).
OC Bacteria; Proteobacteria; alpha subdivision; Rhodospirillum group;

OC Rhodobacter.
 OX NCBI_TaxID=1061;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97363217; PubMed=9219542;
 RA Herter S.M., Schiltz E., Drews G.;
 RT "Protein and gene structure of the NADH-binding fragment of
 Rhodobacter capsulatus NADH:ubiquinone oxidoreductase.";
 RL Eur. J. Biochem. 246:800-808(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B10;
 RA Dupuis A., Issartel J.P.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; Y09884; CAA71015.1; -;
 DR EMBL; AF029365; AAC24993.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 94 AA; 9613 MW; 0BAF868376A8F04 CRC64;

Query Match 1.5%; Score 8; DB 2; Length 94;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 2 RALLPL 9

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GenCore version 5.1.4 p5_4578
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OM protein - protein search, using sw model

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Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

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SUMMARIES

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2	406	100.0	413	22	AAE02610
3	406	100.0	413	22	ABE78619
4	406	100.0	475	22	AAE10657
5	406	100.0	475	22	AAE02609
6	406	100.0	475	22	ABE78618
7	406	100.0	481	22	AAE75592
8	406	100.0	518	19	AAE61362
9	406	100.0	518	20	AAE41714
10	406	100.0	518	20	AAE22239

41	406	100.0	518	20	AAE13799	Human aspartyl pro
12	406	100.0	518	21	AAE44270	Human PRO852 (UNQ4
13	406	100.0	518	21	AAE88424	Human aspartyl pro
14	406	100.0	518	22	AAE10628	Human aspartyl pro
15	406	100.0	518	22	AAE10656	Human ASP 1 protei
16	406	100.0	518	22	AAE29059	Human PRO polypept
17	406	100.0	518	22	AAE06858	Human aspartyl pro
18	406	100.0	518	22	AAE06602	Human aspartyl pro
19	406	100.0	518	22	AAU07201	Human aspartyl pro
20	406	100.0	518	22	AAE02580	Human aspartyl pro
21	406	100.0	518	22	AAE02568	Human aspartyl pro
22	406	100.0	518	22	ABE78589	Human Asp-1 protei
23	406	100.0	518	23	ABE78617	Human Asp-1 protei
24	406	100.0	518	23	ABE06531	Human aspartyl pro
25	406	100.0	518	23	ABE07453	Human BACE2 amino
26	389	95.8	439	23	ABE90365	Human polypeptide
27	373	91.9	423	22	AAE04796	Human aspartyl pro
28	294	72.4	355	22	AAE93925	Human protein sequ
29	235	57.9	423	22	AAE88479	Human membrane or
30	59	14.5	514	22	AAE84204	Amino acid sequenc
31	59	14.5	50	22	AAE18665	Peptide #5099 enco
32	31	12.3	89	22	AAE25497	Human protein sequ
33	15	3.7	62	22	AAE23623	Novel human enzyme
34	12	3.0	387	22	AAE23068	Novel human enzyme
35	12	3.0	390	22	AAE23069	Novel human enzyme
36	12	3.0	415	21	AAE07899	Amino acid sequenc
37	12	3.0	425	21	AAE88437	Human Asp2 amino a
38	12	3.0	425	22	AAE10641	T7-Caspase-Caspase
39	12	3.0	425	22	AAE06871	T7-Caspase-Caspase
40	12	3.0	425	22	AAE06615	T7-Caspase-Caspase
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42	12	3.0	425	22	AAE02593	T7-Caspase-Caspase
43	12	3.0	425	23	ABE78602	T7-Caspase-Caspase
44	12	3.0	427	23	AAE93866	Human polypeptide,
45	12	3.0	428	22	AAE10646	Human-Asp 2 (b) pro
46	12	3.0	428	22	AAE06891	Human-Asp2 (b) del
47	12	3.0	428	22	AAU06620	Human-pro-Asp 2 (b)
48	12	3.0	428	22	AAU07219	Human aspartyl pro
49	12	3.0	428	22	AAE02598	Human aspartyl pro
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51	12	3.0	433	21	AAE88433	Human-pro-Asp-2 (a)
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53	12	3.0	433	22	AAE06870	Human-pro-Asp2 (a)
54	12	3.0	433	22	AAU06614	Human-pro-Asp 2 (a)
55	12	3.0	433	22	AAU07213	T7-Human aspartyl
56	12	3.0	433	22	AAE02592	Human-pro-Asp-2 (a)
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58	12	3.0	434	22	AAE10647	Human-Asp 2 (b) pro
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60	12	3.0	434	22	AAU06621	Human-pro-Asp 2 (b)
61	12	3.0	434	22	AAU07220	Human aspartyl pro
62	12	3.0	434	22	AAE02599	Human aspartyl pro
63	12	3.0	434	23	ABE78608	Human Asp-2 (b) del
64	12	3.0	446	21	AAE88431	T7-Caspase-human-p
65	12	3.0	446	22	AAE10638	T7-Human-pro-Asp 2
66	12	3.0	446	22	AAE06868	T7-Human-pro-Asp2 (
67	12	3.0	446	22	AAU06612	Human T7-Human-pro
68	12	3.0	446	22	AAU07211	T7-human aspartyl
69	12	3.0	446	22	AAE02590	T7-Human-pro-Asp-2
70	12	3.0	446	23	ABE78599	T7-human-pro-Asp-2
71	12	3.0	453	21	AAE88438	Modified human asp
72	12	3.0	453	22	AAE10642	Human-Asp 2 (a) pro
73	12	3.0	453	22	AAE06872	Human-Asp2 (a) del
74	12	3.0	453	22	AAU06616	Human-pro-Asp 2 (a)
75	12	3.0	453	22	AAU07215	Human aspartyl pro
76	12	3.0	453	22	AAE02594	Human-Asp-2 (a) del
77	12	3.0	453	23	ABE78603	Human Asp-2 (a) del
78	12	3.0	456	21	AAE07897	Active enzyme port
79	12	3.0	459	21	AAE88432	T7-caspase-human-p
80	12	3.0	459	21	AAE88439	Modified human asp
81	12	3.0	459	22	AAE10639	T7-caspase-human-p
82	12	3.0	459	22	AAE10643	Human-Asp 2 (a) pro
83	12	3.0	459	22	AAE06869	T7-Caspase-Human-p

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85	12	3.0	459	22	AAU06613	Human T7-Caspase-H	158	8	2.0	592	22	ABB67339	Drosophila melanog
86	12	3.0	459	22	AAU06617	Human-pro-Asp 2(a)	159	7	1.7	25	22	ABB44227	Protophila #9783 enco
87	12	3.0	459	22	AAU07212	T7-caspase-human a	160	7	1.7	25	22	AAU63163	Human brain expres
88	12	3.0	459	22	AAU07216	Human aspartyl pro	161	7	1.7	25	22	AAU75977	Human bone marrow
89	12	3.0	459	22	AAE02591	T7-Caspase-human-p	162	7	1.7	25	22	AAU36085	Peptide #10122 enc
90	12	3.0	459	22	AAE02595	Human-Asp-2(a) del	163	7	1.7	34	21	AAU12350	Fragment of human
91	12	3.0	459	22	ABB78600	T7-caspase-human-p	164	7	1.7	34	21	AAU65900	Arabidopsis thalia
92	12	3.0	459	22	ABB78604	Human Asp-2(a) delc	165	7	1.7	41	22	AAU51187	Human secreted pro
93	12	3.0	460	21	AAU07898	Amino acid sequenc	166	7	1.7	47	22	AAU31051	Novel human secret
94	12	3.0	460	21	AAU88426	Human aspartyl pro	167	7	1.7	61	22	AAU42241	Propionibacterium
95	12	3.0	476	22	AAE10630	Human aspartyl pro	168	7	1.7	68	22	AAU20237	Human novel endocr
96	12	3.0	476	22	AAE06860	Human aspartyl pro	169	7	1.7	79	21	AAU56899	Arabidopsis thalia
97	12	3.0	476	22	AAE06909	Human aspartyl pr	170	7	1.7	86	22	AAU51186	Human secreted pro
98	12	3.0	476	22	AAE06604	Human aspartyl pro	171	7	1.7	88	22	AAU03578	Human polypeptide
99	12	3.0	476	22	AAU07203	Human aspartyl pro	172	7	1.7	90	22	AAU47158	Propionibacterium
100	12	3.0	476	22	AAE02582	Human aspartyl pro	173	7	1.7	95	22	AAU00007	Platidic trioseph
101	12	3.0	476	22	AAE02619	Murine aspartyl pr	174	7	1.7	105	23	AAU02662	Human ORFX protein
102	12	3.0	476	22	ABB78591	Human Asp-2(b) pro	175	7	1.7	109	22	ABG11071	Novel human diagno
103	12	3.0	476	23	ABB06410	Human aspartyl pro	176	7	1.7	109	22	ABG23787	Novel human diagno
104	12	3.0	476	23	ABB06120	Human NS protein s	177	7	1.7	112	22	ABU67791	Drosophila melanog
105	12	3.0	488	22	AAE65572	Human memapsin 2.	178	7	1.7	115	22	AAU88647	Human immune/haema
106	12	3.0	488	22	AAE61334	Memapsin 2 protei	179	7	1.7	117	23	ABP33337	Human ORF2310 prot
107	12	3.0	488	22	AAU99488	Amino acid sequenc	180	7	1.7	120	21	AAU03247	Human secreted pro
108	12	3.0	501	19	AAU59807	Human beta-secret	181	7	1.7	121	20	AAU12208	Human 5' EST secre
109	12	3.0	501	21	AAU94767	Murine beta-secret	182	7	1.7	126	22	AAU39144	Human polypeptide
110	12	3.0	501	21	AAU94768	Rat beta-secretase	183	7	1.7	130	22	AAU01648	Human polypeptide
111	12	3.0	501	21	AAU94769	Human aspartyl pr	184	7	1.7	139	22	AAU99857	Human kidney relat
112	12	3.0	501	21	AAU07896	Amino acid sequenc	185	7	1.7	139	22	AAU42672	Human xcretory re
113	12	3.0	501	21	AAU88425	Human aspartyl pro	186	7	1.7	140	20	AAU06823	P. methanolic pro
114	12	3.0	501	21	AAU88427	Human aspartyl pr	187	7	1.7	140	20	AAU38359	P. methanolic pro
115	12	3.0	501	22	AAE10629	Human aspartyl pro	188	7	1.7	140	21	AAU39840	S. cerevisiae prot
116	12	3.0	501	22	AAE10631	Human aspartyl pr	189	7	1.7	140	21	AAU19018	Amino acid sequenc
117	12	3.0	501	22	AAE06859	Human aspartyl pr	190	7	1.7	140	21	AAU51057	P. methanolic pro
118	12	3.0	501	22	AAE06861	Murine aspartyl pr	191	7	1.7	140	22	AAE05416	Pichia methanolic
119	12	3.0	501	22	AAU06603	Human Aspartyl pr	192	7	1.7	140	22	AAE07567	Amino acid sequenc
120	12	3.0	501	22	AAU06605	Mouse Aspartyl pro	193	7	1.7	140	22	AAU61193	P. methanolic pro
121	12	3.0	501	22	AAU07202	Human aspartyl pro	194	7	1.7	140	22	AAU72372	P. methanolic pro
122	12	3.0	501	22	AAU07204	Mouse aspartyl pro	195	7	1.7	140	22	AAU49227	Protein derived fr
123	12	3.0	501	22	AAU84948	Mouse aspartic sec	196	7	1.7	140	23	AAU019974	Human secreted pro
124	12	3.0	501	22	AAE02581	Human aspartyl pro	197	7	1.7	145	22	ABU50641	Human ORF3631 prot
125	12	3.0	501	22	AAE02583	Murine aspartyl pr	198	7	1.7	145	22	ABP34658	Novel human enzyme
126	12	3.0	501	23	ABB78590	Human Asp-2(a) pro	199	7	1.7	156	22	AAU23445	Novel human diagno
127	12	3.0	501	23	ABB78592	Mouse Asp-2(a) pro	200	7	1.7	157	22	ABG22859	Human ORFX protein
128	12	3.0	501	23	ABB06409	Human aspartyl pro	201	7	1.7	166	23	ABP01194	Peptide #3609 enco
129	12	3.0	503	22	AAE66573	Human pro-memapsin	202	7	1.7	175	22	AAU17175	Peptide #3705 enco
130	12	3.0	503	22	AAE61335	T7 promoter and ve	203	7	1.7	175	22	AAU29668	Human polypeptide
131	12	3.0	503	23	AAU99489	Pro-memapsin 2 enc	204	7	1.7	175	22	AAU40930	Peptide #3552 enco
132	12	3.0	509	23	AAU52697	Partial amino acid	205	7	1.7	175	22	AAU04870	Arabidopsis thalia
133	12	3.0	790	19	AAU59808	Novel human diagno	206	7	1.7	209	21	AAU04117	Arabidopsis thalia
134	12	3.0	969	22	AAU09611	N terminus of 15KD	207	7	1.7	209	21	AAU1858	Arabidopsis thalia
135	9	2.2	45	23	AAU78524	Novel human diagno	208	7	1.7	209	21	AAU54004	Human colon cancer
136	9	2.2	269	22	ABG18048	Novel human diagno	209	7	1.7	231	22	AAU75438	Human protein HP03
137	9	2.2	322	22	AAE04797	Human aspartyl pro	210	7	1.7	233	22	AAU61608	Human triacylglyce
138	9	2.2	351	20	AAU35918	Extended human sec	211	7	1.7	235	20	AAU35512	Human triacylglyce
139	8	2.0	67	23	ABP11020	Human ORFX protein	212	7	1.7	241	20	AAU37435	Arabidopsis thalia
140	8	2.0	105	21	AAU45058	Arabidopsis thalia	213	7	1.7	253	22	AAE10135	Human secreted pro
141	8	2.0	131	22	AAU23632	Novel human enzyme	214	7	1.7	261	22	AAU40710	Novel human diagno
142	8	2.0	239	22	ABG09608	Novel human diagno	215	7	1.7	262	21	AAU58184	Propionibacterium
143	8	2.0	262	22	AAU41741	Human polypeptide	216	7	1.7	265	23	ABU72331	Rat protein isolat
144	8	2.0	285	21	AAU12862	Arabidopsis thalia	217	7	1.7	267	22	ABU64636	Drosophila melanog
145	8	2.0	287	21	ABU12861	Herbicidally activ	218	7	1.7	268	22	AAU69751	Escherichia coli e
146	8	2.0	307	21	ABU12861	Arabidopsis thalia	219	7	1.7	269	22	AAU67213	Novel human diagno
147	8	2.0	313	22	ABG09606	Novel human diagno	220	7	1.7	272	22	AAU49513	Propionibacterium
148	8	2.0	335	22	ABG18051	Novel human diagno	221	7	1.7	276	23	AAU14745	Human triacylglyce
149	8	2.0	341	20	AAU32039	Bovine pregnancy a	222	7	1.7	280	23	AAU14743	Human triacylglyce
150	8	2.0	358	20	AAU41391	Bovine pregnancy a	223	7	1.7	289	21	AAU04116	Arabidopsis thalia
151	8	2.0	380	20	AAU32041	Bovine pregnancy a	224	7	1.7	289	21	AAU1857	Arabidopsis thalia
152	8	2.0	472	22	AAU39955	Human polypeptide	225	7	1.7	289	21	AAU54003	Arabidopsis thalia
153	8	2.0	473	22	ABU71149	Drosophila melanog	226	7	1.7	289	23	AAU77494	Human lipid metabo
154	8	2.0	475	22	ABU91454	Herbicidally activ	227	7	1.7	290	22	AAU63105	Propionibacterium
155	8	2.0	504	23	AAU84277	Human endometrial	228	7	1.7	306	22	AAU68408	Escherichia coli p
156	8	2.0	548	22	AAU98365	Escherichia coli p	229	7	1.7	320	15	AAU62044	Leptospira OmpL.

230	7	1.7	320	18	AAW14278	Leptospira alstoni
231	7	1.7	323	21	AAB12341	Fragment of human
232	7	1.7	326	22	AAB66589	Human pepsin. Hom
233	7	1.7	326	22	AAB61351	Pepsin protein. H
234	7	1.7	327	22	AAM00099	Plasidic trioseph
235	7	1.7	339	22	ABG15392	Novel human diagno
236	7	1.7	346	22	ABB54038	Lactococcus lactis
237	7	1.7	354	17	AAW14463	Yeast glycoprotein
238	7	1.7	359	23	ABB90878	Herbically activ
239	7	1.7	363	18	AAW24256	Ammonifex histidin
240	7	1.7	369	22	ABG04177	Novel human diagno
241	7	1.7	373	21	AAG04115	Arabidopsis thalia
242	7	1.7	373	21	AAG11856	Arabidopsis thalia
243	7	1.7	373	21	AAAG5402	Arabidopsis thalia
244	7	1.7	379	23	AAU72876	Human aspartyl pro
245	7	1.7	380	20	AAV32036	Bovine pregnancy a
246	7	1.7	380	20	AAV32048	Bovine pregnancy a
247	7	1.7	387	20	AAV32052	Bovine pregnancy a
248	7	1.7	388	22	AAV32058	Cat pregnancy asso
249	7	1.7	388	22	AAU27708	Human full-length
250	7	1.7	392	20	AAV32057	Bovine pregnancy a
251	7	1.7	395	23	AAE14744	Human triacylglyce
252	7	1.7	397	18	AAW31628	Aspergillus oryzae
253	7	1.7	397	23	AAE17308	Human lysosomal ac
254	7	1.7	399	22	AAE67513	Amino acid sequenc
255	7	1.7	399	22	AAU77496	Human lipid metabo
256	7	1.7	409	15	AAW48060	Sequence of protea
257	7	1.7	410	13	AAW28030	Pichia pastoris pr
258	7	1.7	420	21	ABW80665	Candida boitdini p
259	7	1.7	428	20	AAV09000	E. coli suza prote
260	7	1.7	433	21	AAW30824	Arabidopsis thalia
261	7	1.7	433	21	AAW31636	Arabidopsis thalia
262	7	1.7	450	22	AAV57041	Plasmodium vivax P
263	7	1.7	451	22	AAW66063	Murine protein: SE
264	7	1.7	456	21	AAV71062	Human membrane tra
265	7	1.7	456	22	AAW78336	Human protein sequ
266	7	1.7	460	22	AAW94655	Human protein sequ
267	7	1.7	465	22	ABW66239	Drosophila melanog
268	7	1.7	470	22	AAW66083	Murine TMGO 202.
269	7	1.7	489	22	ABW11767	Human membrane tra
270	7	1.7	489	22	AAW79320	Human protein sequ
271	7	1.7	506	21	AAW17818	Arabidopsis thalia
272	7	1.7	508	21	AAW31635	Arabidopsis thalia
273	7	1.7	513	21	AAW45529	Arabidopsis thalia
274	7	1.7	522	21	AAW17817	Arabidopsis thalia
275	7	1.7	525	23	ABP28514	Streptococcus poly
276	7	1.7	656	22	ABG26839	Novel human diagno
277	7	1.7	674	22	AAW94461	Human protein sequ
278	7	1.7	674	22	AAW95164	Human protein sequ
279	7	1.7	674	22	ABG66691	Human novel polype
280	7	1.7	692	22	ABG22381	Novel human diagno
281	7	1.7	702	23	ABP28373	Streptococcus poly
282	7	1.7	702	23	AAW47575	Drosophila cell cy
283	7	1.7	726	22	AAW66716	Human transcriptio
284	7	1.7	731	23	AAE14746	Human triacylglyce
285	7	1.7	733	23	ABW57374	Mouse ischaemic co
286	7	1.7	775	21	AAV67250	Mouse protein tyro
287	7	1.7	775	21	AAV67251	Mutant mouse PRP-P
288	7	1.7	784	23	ABW47322	Listeria monocytoc
289	7	1.7	802	17	AAW90848	Gibberellin (Gal),
290	7	1.7	802	23	ABW92819	Herbically activ
291	7	1.7	863	22	ABW63583	Drosophila melanog
292	7	1.7	868	22	ABG24427	Novel human diagno
293	7	1.7	880	23	ABP27173	Streptococcus poly
294	7	1.7	896	22	ABG28532	Novel human diagno
295	7	1.7	925	22	ABG15391	Novel human diagno
296	7	1.7	933	23	ABP28348	Streptococcus poly
297	7	1.7	1133	23	ABG28516	Novel human diagno
298	7	1.7	1191	22	AAW80219	Human protein sequ
299	7	1.7	1193	22	ABW18089	Novel human diagno
300	7	1.7	1379	22	ABW57823	Drosophila melanog
301	7	1.7	1429	20	AAW93941	Human btx protein.
302	7	1.7	1429	22	ABG05537	Novel human diagno
303	7	1.7	2042	22	ABW59689	Drosophila melanog
304	6	1.5	8	23	ABW06440	Beta-secretase rel
305	6	1.5	8	23	ABW07485	Theobroma cacao as
306	6	1.5	12	21	AAW09319	Hepatitis GB virus
307	6	1.5	12	22	AAW50475	Bacterial A1a pep
308	6	1.5	14	22	ABW55906	Vascular dementia-
309	6	1.5	14	22	AAW72296	ADAMTS-R1 immunog
310	6	1.5	15	22	AAW78131	Human actin 49 pep
311	6	1.5	15	23	ABW81892	Transcriptional el
312	6	1.5	16	22	AAW93379	Vaccine related MH
313	6	1.5	18	23	AAW78513	Human and mouse BA
314	6	1.5	19	18	AAW22374	S. pneumoniae HSP7
315	6	1.5	19	18	AAW72292	ADAMTS-7 immunogen
316	6	1.5	20	9	AAW82056	Pep-13 comprising
317	6	1.5	21	18	AAW10215	Endoglycoseramidas
318	6	1.5	24	15	AAW47014	Cathepsin B positi
319	6	1.5	24	15	AAW9380	Vaccine related MH
320	6	1.5	26	22	AAW76928	Human colon cancer
321	6	1.5	27	23	AAW49941	Human D40 associat
322	6	1.5	27	23	AAW49962	Human D40 associat
323	6	1.5	30	23	AAW49997	Human D40 associat
324	6	1.5	31	21	AAW15670	Alpha V beta 3 rec
325	6	1.5	31	21	AAW49997	Human 5' EST relat
326	6	1.5	31	22	AAW77180	Human colon cancer
327	6	1.5	32	22	ABW42768	Peptide #10274 enc
328	6	1.5	32	22	ABW26061	Protein #8060 enco
329	6	1.5	32	22	AAW63659	Human brain.expres
330	6	1.5	32	22	AAW64973	Human bone marrow
331	6	1.5	32	22	AAW20905	Peptide #7339 enco
332	6	1.5	32	22	AAW6581	Peptide #10618 enc
333	6	1.5	32	23	ABW45734	Human peptide enco
334	6	1.5	34	20	AAW92216	Analogue of parath
335	6	1.5	34	20	AAU06673	Human novel foetal
336	6	1.5	35	22	ABW30124	Peptide #2775 enco
337	6	1.5	35	22	ABW35296	Peptide #2802 enco
338	6	1.5	35	22	ABW35296	Peptide #7067 enco
339	6	1.5	35	22	ABW39561	Protein #2737 enco
340	6	1.5	35	22	ABW20738	Protein #6281 enco
341	6	1.5	35	22	ABW24282	Human brain expres
342	6	1.5	35	22	AAW65125	Human brain expres
343	6	1.5	35	22	AAW60260	Human bone marrow
344	6	1.5	35	22	AAW68497	Human bone marrow
345	6	1.5	35	22	AAW72887	Human bone marrow
346	6	1.5	35	22	AAW16303	Peptide #2737 enco
347	6	1.5	35	22	AAW19767	Peptide #6201 enco
348	6	1.5	35	22	AAW28796	Peptide #2833 enco
349	6	1.5	35	22	AAW33118	Peptide #7155 enco
350	6	1.5	35	22	AAW04039	Peptide #2721 enco
351	6	1.5	35	23	ABW38078	Human peptide enco
352	6	1.5	35	23	ABW42721	Human peptide enco
353	6	1.5	36	22	ABW03311	Human musculoskele
354	6	1.5	40	10	AAW90808	N-terminal sequenc
355	6	1.5	43	19	AAW74950	Human secreted pro
356	6	1.5	44	23	AAW78527	N terminus of 11kD
357	6	1.5	45	19	AAW79315	Staphylococcus aur
358	6	1.5	45	22	AAW87000	Human immune/haema
359	6	1.5	45	22	AAW79300	Human immune/haema
360	6	1.5	46	21	AAW68490	Human polypeptide
361	6	1.5	46	22	AAW66213	Arabidopsis thalia
362	6	1.5	47	22	ABW11222	Human immune/haema
363	6	1.5	47	22	ABW36429	Peptide #3873 enco
364	6	1.5	47	22	AAW57187	Peptide #3935 enco
365	6	1.5	47	22	AAW69592	Human brain expres
366	6	1.5	47	22	AAW69592	Human bone marrow
367	6	1.5	47	22	AAW29928	Peptide #3965 enco
368	6	1.5	47	22	AAW05051	Peptide #3773 enco
369	6	1.5	47	23	ABW39213	Human peptide enco
370	6	1.5	48	23	ABW29630	Human peptide enco
371	6	1.5	49	22	ABW44808	Peptide #2281 enco
372	6	1.5	49	22	ABW50577	Human secreted pro
373	6	1.5	49	22	ABW20224	Protein #2223 enco
374	6	1.5	49	22	AAW55610	Human brain expres
375	6	1.5	49	22	AAW67995	Human bone marrow

376	6	1.5	49	22	AA15811	Peptide #2245 enco	449	6	1.5	67	22	AA16795	Peptide #3229 enco
377	6	1.5	49	22	AA28321	Peptide #2358 enco	450	6	1.5	67	22	AA29277	Peptide #3314 enco
378	6	1.5	49	22	AA03549	Peptide #2231 enco	451	6	1.5	67	22	AA04513	Peptide #3195 enco
379	6	1.5	49	22	ABG37527	Human peptide enco	452	6	1.5	67	23	ABG38553	Human peptide enco
380	6	1.5	50	22	AAU40556	Protonibacterium	453	6	1.5	68	21	AA845596	Fragment of human
381	6	1.5	51	19	AAW71570	Hepatocyte nuclear	454	6	1.5	68	22	ABR31892	Peptide #4543 enco
382	6	1.5	51	22	AAU41435	Protonibacterium	455	6	1.5	68	22	ABR37130	Peptide #4636 enco
383	6	1.5	52	22	AAU61713	Human immune/haema	456	6	1.5	68	22	ABR22441	Protein #4440 enco
384	6	1.5	52	22	AA034336	Human polypeptide	457	6	1.5	68	22	AA57849	Human brain expres
385	6	1.5	52	23	AA03436	Streptococcus poly	458	6	1.5	68	22	AAW70267	Human bone marrow
386	6	1.5	52	23	ABP26180	Streptococcus poly	459	6	1.5	68	22	AA118095	Peptide #4529 enco
387	6	1.5	53	23	AAU41231	Protonibacterium	460	6	1.5	68	22	AA30604	Peptide #4412 enco
388	6	1.5	55	16	AAW80193	Internal portion o	461	6	1.5	68	22	AAW05730	Peptide #4412 enco
389	6	1.5	55	19	AAW79444	Staphylococcus aur	462	6	1.5	68	23	ABG39911	Human peptide enco
390	6	1.5	55	21	AAW79444	Human secreted pro	463	6	1.5	68	23	ABP07588	Human ORFX protein
391	6	1.5	55	22	ABG60250	Human ovarian anti	464	6	1.5	69	21	AAU7411	Arabidopsis thalia
392	6	1.5	55	22	AAU64206	Protonibacterium	465	6	1.5	70	22	ABG18828	Novel human diagno
393	6	1.5	55	22	ABR39033	Peptide #6539 enco	466	6	1.5	71	19	AAW60973	Streptococcus pneu
394	6	1.5	55	22	ABR40396	Peptide #7902 enco	467	6	1.5	71	21	AAU5743	Arabidopsis thalia
395	6	1.5	55	22	ABR23977	Protein #5976 enco	468	6	1.5	71	22	AAU45743	Protonibacterium
396	6	1.5	55	22	ABR24768	Protein #6767 enco	469	6	1.5	72	22	AAU62168	Protonibacterium
397	6	1.5	55	22	AAW94384	Human reproductiv	470	6	1.5	72	23	ABP05481	Human ORFX protein
398	6	1.5	55	22	AAW59687	Human brain expres	471	6	1.5	73	17	AAW04202	Peptide encoded by
399	6	1.5	55	22	AAW61204	Human brain expres	472	6	1.5	73	17	AAW04190	Peptide encoded by
400	6	1.5	55	22	AAW72263	Human bone marrow	473	6	1.5	73	17	AAW04199	Peptide encoded by
401	6	1.5	55	22	AAW73923	Human bone marrow	474	6	1.5	73	21	AAU43580	Arabidopsis thalia
402	6	1.5	55	22	AAW19522	Peptide #5956 enco	475	6	1.5	73	22	ABG03752	Novel human diagno
403	6	1.5	55	22	AAW20159	Peptide #6593 enco	476	6	1.5	73	23	ABP05087	Human ORFX protein
404	6	1.5	55	22	AAW32522	Peptide #6559 enco	477	6	1.5	73	23	ABP10798	Human ORFX protein
405	6	1.5	55	22	AAW34102	Peptide #8139 enco	478	6	1.5	74	22	AAU53361	Protonibacterium
406	6	1.5	55	23	ABG61721	Novel ovarian rela	479	6	1.5	74	22	AAW07082	Human polypeptide
407	6	1.5	55	23	ABG42078	Human peptide enco	480	6	1.5	75	22	AAW99788	Human excytory re
408	6	1.5	55	23	ABG43811	Human peptide enco	481	6	1.5	75	22	AAU42603	Human kidney relat
409	6	1.5	56	23	AAU47306	Protonibacterium	482	6	1.5	76	22	AAU67129	Protonibacterium
410	6	1.5	56	23	ABP34242	Human ORP3215 proc	483	6	1.5	77	22	AAW90374	Human immune/haema
411	6	1.5	57	22	ABR44299	Peptide #9805 enco	484	6	1.5	77	22	AAO10251	Human polypeptide
412	6	1.5	57	22	ABR25802	Protein #7801 enco	485	6	1.5	77	23	ABP02872	Human ORFX protein
413	6	1.5	57	22	AAW63185	Human brain expres	486	6	1.5	78	19	AAW98260	H. pylori GHP 144
414	6	1.5	57	22	AAW75999	Human bone marrow	487	6	1.5	78	21	AAAB3208	Pinus radiata tran
415	6	1.5	57	22	AAW6107	Peptide #10144 enc	488	6	1.5	79	23	ABP00842	Human ORFX protein
416	6	1.5	57	20	ABG45406	Human peptide enco	489	6	1.5	80	22	ABG00065	Novel human diagno
417	6	1.5	58	20	AAV59754	Human normal ovari	490	6	1.5	80	22	ABG11887	Novel human diagno
418	6	1.5	58	22	AAU18640	Human lung antigen	491	6	1.5	80	22	AAW85493	Human immune/haema
419	6	1.5	59	13	AAW27732	Salp20.SR. Vaccin	492	6	1.5	80	23	ABP43203	Human ovarian anti
420	6	1.5	59	14	AAW43264	Human novel foetal	493	6	1.5	81	22	AAO6868	Human polypeptide
421	6	1.5	59	22	AAW20680	Human reproductiv	494	6	1.5	82	19	AAV21011	Human glial fibril
422	6	1.5	59	22	AAW94522	Human ORFX protein	495	6	1.5	82	21	AAW82196	Human artemin neur
423	6	1.5	59	23	ABP02996	Human ORFX protein	496	6	1.5	82	22	ABR31944	Peptide #4595 enco
424	6	1.5	59	23	AAU80947	Caulobacter cresce	497	6	1.5	82	22	ABR37183	Peptide #4689 enco
425	6	1.5	60	22	AAU54616	Protonibacterium	498	6	1.5	82	22	ABR22487	Protein #4486 enco
426	6	1.5	60	22	AAU62553	Protonibacterium	499	6	1.5	82	22	AAW57895	Human brain expres
427	6	1.5	60	22	AAW87965	Human immune/haema	500	6	1.5	82	22	AAW70313	Human bone marrow
428	6	1.5	61	22	AAW69147	M. catarrhalis str	501	6	1.5	82	22	AAW18151	Peptide #4585 enco
429	6	1.5	61	21	AAW03465	Human secreted pro	502	6	1.5	82	22	AAW25544	Human protein sequ
430	6	1.5	62	21	AAO10476	Human polypeptide	503	6	1.5	82	22	AAW30654	Peptide #4691 enco
431	6	1.5	62	21	AAW37069	Arabidopsis thalia	504	6	1.5	82	22	AAW05777	Peptide #4459 enco
432	6	1.5	62	21	AAW86274	Human secreted pro	505	6	1.5	82	23	ABG39957	Human peptide enco
433	6	1.5	62	22	AAW63837	Human ORFX protein	506	6	1.5	83	22	AAU44883	Protonibacterium
434	6	1.5	62	22	ABP09488	Human ORFX protein	507	6	1.5	83	22	ABG28088	Novel human diagno
435	6	1.5	63	22	AAU50416	Protonibacterium	508	6	1.5	83	23	ABP01679	Human ORFX protein
436	6	1.5	63	22	AAU57838	Protonibacterium	509	6	1.5	83	23	AAU21240	Human parathyroid
437	6	1.5	63	22	AAU59994	Protonibacterium	510	6	1.5	84	13	AAW21179	Human parathyroid
438	6	1.5	64	21	AAW38199	Human secreted pro	511	6	1.5	84	13	AAW23516	Bovine parathyroid
439	6	1.5	65	21	AAW45293	Human secreted pro	512	6	1.5	84	13	AAW23323	Bovine parathyroid
440	6	1.5	65	21	AAW45294	Sequence #7 homolo	513	6	1.5	84	13	AAW23455	Porcine parathyroi
441	6	1.5	65	21	AAW45294	Protein fragment #	514	6	1.5	84	22	AAU52779	Protonibacterium
442	6	1.5	65	23	ABP04162	Human secreted pro	515	6	1.5	84	22	AAU20156	Human novel endocr
443	6	1.5	67	22	ABG27225	Novel human diagno	516	6	1.5	85	21	AAU21627	Zea mays protein f
444	6	1.5	67	22	ABR30615	Peptide #3266 enco	517	6	1.5	85	21	AAV44773	Protein-1 compoisi
445	6	1.5	67	22	ABR35779	Peptide #3285 enco	518	6	1.5	85	22	ABR6337	Drosophila melanog
446	6	1.5	67	22	ABR21202	Protein #3201 enco	519	6	1.5	85	22	AAU55013	Protonibacterium
447	6	1.5	67	22	AAW56587	Human brain expres	520	6	1.5	85	22	ABG15570	Novel human diagno
448	6	1.5	67	22	AAW68968	Human bone marrow	521	6	1.5	85	22	AAW84225	Human immune/haema

522	6	1.5	86	21	AAAG26123	Zea mays protein f	595	6	1.5	119	22	AA007689	Human polypeptide
523	6	1.5	86	22	AAU47872	Propionibacterium	596	6	1.5	120	20	AAW97368	Murine growth horm
524	6	1.5	86	22	AAU90093	Human immune/haema	597	6	1.5	121	23	ABP42309	Human ovarian anti
525	6	1.5	86	23	ABP06241	Human ORFX protein	598	6	1.5	121	23	ABP29062	Streptococcus poly
526	6	1.5	86	23	AAU49087	Human p34cdc2-rela	599	6	1.5	122	21	AAAG51931	Arabidopsis thalia
527	6	1.5	89	23	ABBS3965	Lactococcus lactis	600	6	1.5	122	22	AAU23079	Novel human enzyme
528	6	1.5	90	21	AAU91528	Human secreted pro	601	6	1.5	122	22	AAU32987	Novel human secret
529	6	1.5	90	22	ABG09609	Novel human diagno	602	6	1.5	123	20	AAU3491	S. aureus IgG-bind
530	6	1.5	90	22	AAU29662	Novel human secret	603	6	1.5	123	21	AAU44772	Wheat serine O-ace
531	6	1.5	91	16	AAU69587	Non-specific lipid	604	6	1.5	124	20	AAU35862	Chlamydia pneumoni
532	6	1.5	92	20	AAU90173	Human heart muscle	605	6	1.5	124	20	AAU97371	Murine/porcine chi
533	6	1.5	92	21	AAU38067	Arabidopsis thalia	606	6	1.5	124	22	ABG16821	Novel human diagno
534	6	1.5	92	23	ABP31398	Human transport pr	607	6	1.5	125	22	AAU91635	C glutathicum prote
535	6	1.5	93	23	AAU87348	Novel central nerv	608	6	1.5	126	20	AAU35836	Chlamydia pneumoni
536	6	1.5	94	8	AAU70567	Product of ORF 9 f	609	6	1.5	126	21	AAU38066	Arabidopsis thalia
537	6	1.5	94	23	AAU75733	M. Sactiva cyclin b	610	6	1.5	126	21	AAU56294	Arabidopsis thalia
538	6	1.5	95	20	AAU68822	Human tumour antig	611	6	1.5	126	21	AAU74772	Neisseria gonorrhoe
539	6	1.5	95	22	AAU46604	Propionibacterium	612	6	1.5	126	21	AAU74774	Neisseria meningit
540	6	1.5	95	22	AAU67642	Propionibacterium	613	6	1.5	126	22	AAU23696	Novel human enzyme
541	6	1.5	96	22	AAU45975	Propionibacterium	614	6	1.5	126	22	AAU17488	Novel signal trans
542	6	1.5	96	23	ABP00399	Human ORFX protein	615	6	1.5	126	22	AAU21848	Novel human neopla
543	6	1.5	97	21	AAU53531	Human colon cancer	616	6	1.5	128	22	AAU44649	Propionibacterium
544	6	1.5	98	22	ABG13902	Novel human diagno	617	6	1.5	130	20	AAU11561	Human 5' ESR secre
545	6	1.5	99	22	ABG20720	Novel human diagno	618	6	1.5	130	21	ABBS177	Eucalyptus grandis
546	6	1.5	100	22	AAU29661	Novel human secret	619	6	1.5	130	21	AAU60242	Human secreted pro
547	6	1.5	101	21	AAU43039	Human ORFX ORF2803	620	6	1.5	130	21	AAU60573	Human secreted pro
548	6	1.5	101	22	ABG25580	Novel human diagno	621	6	1.5	130	22	AAU681535	S. epidermidis ope
549	6	1.5	102	21	AAU33715	Zea mays protein f	622	6	1.5	131	22	AAU60855	Sunflower blight A
550	6	1.5	103	21	AAU01742	Human secreted pro	623	6	1.5	131	22	AAU01967	Human polypeptide
551	6	1.5	103	23	ABG60203	Human DITHP polype	624	6	1.5	131	23	ABBS3213	Human ORF119 prote
552	6	1.5	103	23	ABP32558	Human glycoprotein	625	6	1.5	132	22	AAU003503	Human polypeptide
553	6	1.5	104	21	AAU01771	Simian immunodefic	626	6	1.5	132	23	ABBS47865	Listeria monocytog
554	6	1.5	104	21	AAU14790	Human Zeis67, a no	627	6	1.5	133	21	AAU41267	Human ORFX ORF1031
555	6	1.5	105	21	AAU33677	Arabidopsis thalia	628	6	1.5	133	21	AAU607905	Arabidopsis thalia
556	6	1.5	105	22	ABG02738	Novel human diagno	629	6	1.5	133	22	ABBS12302	Human secreted pro
557	6	1.5	105	22	ABG15142	Novel human diagno	630	6	1.5	133	22	AAU05039	Human polypeptide
558	6	1.5	105	22	AAU68385	Human immune/haema	631	6	1.5	134	22	ABBS11292	Human HSP-124 pro
559	6	1.5	105	23	ABP34337	Human kinase-like	632	6	1.5	134	22	AAU06644	Human polypeptide
560	6	1.5	107	21	AAU40186	Arabidopsis thalia	633	6	1.5	134	22	AAU681720	S. epidermidis ope
561	6	1.5	107	21	AAU84598	Fragment of human	634	6	1.5	135	22	AAU30249	Novel human secret
562	6	1.5	107	22	ABG12998	Novel human diagno	635	6	1.5	136	20	AAU13003	Human secreted pro
563	6	1.5	108	19	AAU74953	Human secreted pro	636	6	1.5	136	22	ABG19495	Novel human diagno
564	6	1.5	108	21	AAU60968	Arabidopsis thalia	637	6	1.5	137	21	AAU40578	Human ORFX ORF342
565	6	1.5	108	21	AAU40185	Arabidopsis thalia	638	6	1.5	137	22	AAU67542	Propionibacterium
566	6	1.5	108	22	AAU48674	Propionibacterium	639	6	1.5	137	23	ABP07284	Human ORFX protein
567	6	1.5	108	23	ABP34346	Human transport pr	640	6	1.5	138	21	AAU15943	E. coli proliferat
568	6	1.5	109	22	AAU76057	Human colon cancer	641	6	1.5	138	22	AAU48920	Propionibacterium
569	6	1.5	110	22	AAU71946	Human bone marrow	642	6	1.5	139	22	AAU682949	S. epidermidis ope
570	6	1.5	111	12	AAU12604	SIB 134 intestinal	643	6	1.5	140	13	AAU25864	HCV polypeptide 11
571	6	1.5	111	19	AAU85920	S. pneumoniae deri	644	6	1.5	140	14	AAU41742	Hepatitis C virus
572	6	1.5	111	22	AAU29683	Novel human secret	645	6	1.5	141	21	AAU608706	Arabidopsis thalia
573	6	1.5	111	22	AAU02691	Human polypeptide	646	6	1.5	141	21	AAU642719	Arabidopsis thalia
574	6	1.5	112	19	AAU79423	Staphylococcus aur	647	6	1.5	142	21	AAU37788	Arabidopsis thalia
575	6	1.5	112	21	AAU05248	Arabidopsis thalia	648	6	1.5	142	23	ABP42390	Human ovarian anti
576	6	1.5	112	21	AAU60967	Arabidopsis thalia	649	6	1.5	143	21	AAU32914	Pinus radiata tran
577	6	1.5	112	22	AAU60191	Propionibacterium	650	6	1.5	143	22	ABG29743	Novel human diagno
578	6	1.5	113	22	AAU86909	Novel human connec	651	6	1.5	144	21	AAU30702	Arabidopsis thalia
579	6	1.5	113	22	ABG02741	Novel human diagno	652	6	1.5	145	21	AAU44766	Corn serine O-acet
580	6	1.5	113	23	ABG65559	Human breast speci	653	6	1.5	145	22	AAU56954	Propionibacterium
581	6	1.5	114	22	AAU90032	C glutathicum prote	654	6	1.5	145	22	AAU85561	Human secreted pro
582	6	1.5	115	22	AAU61434	Propionibacterium	655	6	1.5	145	23	ABG64721	Human albumin fusi
583	6	1.5	115	22	AAU65123	Propionibacterium	656	6	1.5	146	23	ABBS9479	Human polypeptide
584	6	1.5	115	22	AAU33001	Novel human secret	657	6	1.5	147	21	AAU64111	Human polypeptide
585	6	1.5	116	21	AAU27159	Zea mays protein f	658	6	1.5	148	22	AAU30940	Novel human secret
586	6	1.5	116	22	ABG21772	Novel human diagno	659	6	1.5	148	22	AAU05046	Human polypeptide
587	6	1.5	116	22	AAU96587	Human reproductive	660	6	1.5	149	22	ABG03013	Novel human diagno
588	6	1.5	116	22	AAU04858	Human polypeptide	661	6	1.5	150	22	ABG17930	Novel human diagno
589	6	1.5	117	18	AAU03684	Group B Streptococ	662	6	1.5	151	22	AAU02623	Human polypeptide
590	6	1.5	117	22	AAU17913	Peptide CS4 from d	663	6	1.5	151	22	AAU03607	Human polypeptide
591	6	1.5	117	22	AAU89871	Human immune/haema	664	6	1.5	151	22	AAU41423	Human polypeptide
592	6	1.5	118	22	AAU75718	Human colon cancer	665	6	1.5	151	23	ABBS3951	Lactococcus lactis
593	6	1.5	119	22	ABG16822	Novel human diagno	666	6	1.5	152	21	AAU24037	Arabidopsis thalia
594	6	1.5	119	22	AAU00450	Human polypeptide	667	6	1.5	153	22	AAU67120	Cat mammary tumour

668	6	1.5	153	22	AAB67121	Cat mammary tumour	741	6	1.5	174	22	AAB99092	Sheep GnRH recepto
669	6	1.5	153	23	ABP51252	Human MDDT SEQ ID	742	6	1.5	175	23	AAE14463	PRRSV-VR2332 membr
670	6	1.5	155	22	AAU49062	Propionibacterium	743	6	1.5	175	20	AAW97686	Staphylococcus aur
671	6	1.5	156	20	AAW88760	Polypeptide fragme	744	6	1.5	177	22	ABG28840	Novel human diagno
672	6	1.5	156	20	AAW88743	Secreted protein e	745	6	1.5	177	22	AAE04126	Human gene 2 encod
673	6	1.5	156	21	AAW89396	Human secreted pro	746	6	1.5	177	23	ABG64339	Human albumin fusi
674	6	1.5	156	21	AAW89396	Zea mays protein f	747	6	1.5	178	23	ABG62070	Novel human diagno
675	6	1.5	156	22	AAU45177	Propionibacterium	748	6	1.5	180	22	ABG05504	Novel human diagno
676	6	1.5	156	22	ABG24722	Novel human diagno	749	6	1.5	181	21	AAU00966	Murine Fibroblast
677	6	1.5	156	22	ABG50510	Human secreted pro	750	6	1.5	183	21	AAW52084	Human secreted pro
678	6	1.5	156	22	ABG50575	Human secreted pro	751	6	1.5	184	17	AAW14452	Carb gene product.
679	6	1.5	156	22	ABG89112	Human polypeptide	752	6	1.5	184	19	AAW42098	Human Rab protein
680	6	1.5	157	19	AAW74761	Human secreted pro	753	6	1.5	184	21	AAW54285	Human pancreatic c
681	6	1.5	157	21	AAW16609	Arabidopsis thalia	754	6	1.5	184	22	AAU19393	Human g protein-co
682	6	1.5	157	21	AAW16609	Zea mays protein f	755	6	1.5	185	20	AAW40951	Ara h 3 allergen f
683	6	1.5	157	21	AAW50326	Arabidopsis thalia	756	6	1.5	185	21	AAW07861	Arabidopsis thalia
684	6	1.5	157	22	ABG18088	Novel human diagno	757	6	1.5	185	21	AAW48908	Arabidopsis thalia
685	6	1.5	158	22	ABW70690	Drosophila melano	758	6	1.5	185	21	AAW48925	Arabidopsis thalia
686	6	1.5	158	22	AAU58116	Propionibacterium	759	6	1.5	185	21	AAW51559	Human KGD1 protein
687	6	1.5	158	23	ABP03837	Human ORFX protein	760	6	1.5	186	19	AAW74804	Human secreted pro
688	6	1.5	159	21	AAW20633	Arabidopsis thalia	761	6	1.5	186	22	AAU20264	Human novel endocr
689	6	1.5	159	21	AAW30701	Arabidopsis thalia	762	6	1.5	186	22	AAW39637	Human polypeptide
690	6	1.5	161	21	AAW07904	Arabidopsis thalia	763	6	1.5	187	22	ABW29828	Peptide #2849 enco
691	6	1.5	161	22	ABW76812	Cucumber green mot	764	6	1.5	187	22	ABW30193	Peptide #2844 enco
692	6	1.5	161	22	ABW76813	Cucumber green mot	765	6	1.5	187	22	ABW35356	Peptide #2862 enco
693	6	1.5	162	23	ABP34372	Human DNA/RNA bind	766	6	1.5	187	22	ABW20418	Protein #2417 enco
694	6	1.5	162	23	ABP05171	Human ORFX protein	767	6	1.5	187	22	ABW20798	Human #2797 enco
695	6	1.5	163	21	AAW40873	Human ORFX ORF637	768	6	1.5	187	22	AAW55817	Human brain expres
696	6	1.5	164	19	AAW38705	S. pneumoniae phos	769	6	1.5	187	22	AAW56187	Human bone marrow
697	6	1.5	164	22	ABW16143	Novel human diagno	770	6	1.5	187	22	AAW68191	Human bone marrow
698	6	1.5	165	21	AAW18779	Zea mays protein f	771	6	1.5	187	22	AAW68860	Human bone marrow
699	6	1.5	165	21	ABP01262	Human ORFX protein	772	6	1.5	187	22	AAW16368	Peptide #2802 enco
700	6	1.5	166	13	AAW25886	HK11. Hepatitis C	773	6	1.5	187	22	AAW28865	Peptide #2902 enco
701	6	1.5	167	21	AAW25013	Arabidopsis thalia	774	6	1.5	187	22	AAW04106	Peptide #2788 enco
702	6	1.5	167	22	ABW59605	Drosophila melano	775	6	1.5	187	23	ABW37719	Human peptide enco
703	6	1.5	167	22	AAU17388	Novel signal trans	776	6	1.5	187	23	ABW38138	Human peptide enco
704	6	1.5	167	23	AAW50340	ETEC CS4 pilus Csa	777	6	1.5	188	20	AAW127843	Human secreted pro
705	6	1.5	170	21	AAW09107	Arabidopsis thalia	778	6	1.5	188	23	ABW28307	Human secreted pro
706	6	1.5	170	21	AAW09127	Arabidopsis thalia	779	6	1.5	190	15	AAW60615	Human PDGF-B 109 s
707	6	1.5	171	21	AAW10157	Arabidopsis thalia	780	6	1.5	190	22	ABW21570	Novel human diagno
708	6	1.5	171	21	AAW51725	Human nervous syst	781	6	1.5	190	22	AAW60052	Human protein SEQ
709	6	1.5	171	22	ABW16034	Arabidopsis thalia	782	6	1.5	191	22	ABW69131	Drosophila melano
710	6	1.5	171	22	AAW01948	Staphylococcus epi	783	6	1.5	191	22	AAW64518	Human immune/hema
711	6	1.5	171	23	ABW40360	PRRSV-Ter Huurne m	784	6	1.5	192	16	AAW69646	Hepatitis C virus
712	6	1.5	172	23	AAW14468	PRRSV-Ter Huurne m	785	6	1.5	192	17	AAW89517	Hepatitis C virus
713	6	1.5	172	23	AAW14466	PRRSV-Ter Huurne m	786	6	1.5	192	18	AAW20512	H. pylori cell env
714	6	1.5	172	23	AAW14467	PRRSV-Ter Huurne m	787	6	1.5	193	21	AAW38007	Human secreted pro
715	6	1.5	172	23	AAW14469	PRRSV-Ter Huurne m	788	6	1.5	193	22	AAW16973	Human novel secret
716	6	1.5	172	23	AAW14470	PRRSV-Ter Huurne m	789	6	1.5	193	23	ABW02895	Human ORFX protein
717	6	1.5	173	13	AAW29945	Deduced from Leils	790	6	1.5	194	20	AAW37221	Amino acid sequenc
718	6	1.5	173	16	AAW74642	PRRS virus (Spanis	791	6	1.5	196	18	AAW10505	Alphalapha2 regio
719	6	1.5	173	17	AAW94705	PRRSV Leiyetad ORF	792	6	1.5	196	18	AAW10508	Alphalapha2 regio
720	6	1.5	173	17	AAW88706	Porcine reproducti	793	6	1.5	196	21	AAW23032	Human putative mit
721	6	1.5	173	21	AAW43980	Human cancer assoc	794	6	1.5	196	23	ABW33192	Human ovarian anti
722	6	1.5	173	22	AAW07138	Porcine reproducti	795	6	1.5	197	22	AAW78892	Human protein SEQ
723	6	1.5	173	22	AAW92280	C glutamicum prote	796	6	1.5	197	22	AAW73495	Human transferase
724	6	1.5	173	22	AAW73955	Human colon cancer	797	6	1.5	197	22	AAW33600	Human protein sequ
725	6	1.5	173	23	ABW89598	Human polypeptide	798	6	1.5	198	22	AAW79876	Human protein SEQ
726	6	1.5	173	23	AAW76139	Porcine reproducti	799	6	1.5	199	22	AAW83443	Human polypeptide
727	6	1.5	173	23	AAW76141	Porcine reproducti	800	6	1.5	199	23	ABW83443	Ribosomal protein
728	6	1.5	173	23	AAW14462	PRRSV-Ter Huurne m	801	6	1.5	199	23	ABW85008	Lactococcus lactis
729	6	1.5	173	23	AAW14465	PRRSV-Ter Huurne m	802	6	1.5	200	21	AAW68705	Amino acid sequenc
730	6	1.5	173	23	AAW14471	PRRSV-Ter Huurne m	803	6	1.5	200	22	AAW90998	C glutamicum prote
731	6	1.5	174	17	AAW94711	PRRSV ISU-3927 mem	804	6	1.5	201	22	AAU30978	Novel human diagno
732	6	1.5	174	17	AAW94702	PRRSV VR 2385 vira	805	6	1.5	202	22	ABW25180	Novel human diagno
733	6	1.5	174	17	AAW94709	PRRSV ISU-79 membr	806	6	1.5	203	23	ABW60116	Human DITP polype
734	6	1.5	174	17	AAW94707	PRRSV ISU-1894 mem	807	6	1.5	204	21	AAW22061	Arabidopsis thalia
735	6	1.5	174	17	AAW94708	PRRSV ISU-22 membr	808	6	1.5	204	22	AAW44559	Propionibacterium
736	6	1.5	174	17	AAW94710	PRRSV ISU-55 membr	809	6	1.5	204	22	AAW81799	S. epidermidis ope
737	6	1.5	174	17	AAW92514	VR-2332 ORF 6 prod	810	6	1.5	205	23	ABW55248	Lactococcus lactis
738	6	1.5	174	21	AAW58674	Porcine reproducti	811	6	1.5	206	21	AAW36630	Arabidopsis thalia
739	6	1.5	174	22	AAU15951	Human novel secret	812	6	1.5	206	22	AAU47730	Propionibacterium
740	6	1.5	174	22	AAW90622	C glutamicum prote	813	6	1.5	206	23	ABW92911	Herbically activ

814	6	1.5	207	22	AAE03655	Human extracellular	887	6	1.5	235	20	AAV05674	Maize diphenyl oxi
815	6	1.5	207	23	AAU83629	Human PRO protein,	888	6	1.5	236	22	AAW94238	Human reproductive
816	6	1.5	208	21	AAU08705	Arabidopsis thalia	889	6	1.5	237	20	AAV02654	Human secreted pro
817	6	1.5	208	21	AAU42718	Arabidopsis thalia	890	6	1.5	237	21	AAU94585	Alternatively spli
818	6	1.5	208	23	AAU79290	Rat FGF-related pr	891	6	1.5	237	21	AAU92037	Human artemin (GDN
819	6	1.5	209	23	ABR93083	Herbicidally activ	892	6	1.5	237	21	AAU87321	Human signal pepti
820	6	1.5	209	18	AAU11177	S. pneumoniae N-(5	893	6	1.5	237	21	AAU68706	A human neublastin
821	6	1.5	209	22	ABG17441	Novel human diagno	894	6	1.5	237	21	AAU66721	Membrane-bound pro
822	6	1.5	210	21	AAU18636	Amino acid sequenc	895	6	1.5	237	22	ABG05288	Novel human diagno
823	6	1.5	210	22	AAU68416	Amino acid sequenc	896	6	1.5	237	22	AAU29134	Human PRO polypept
824	6	1.5	210	22	AAU00958	Murine Fibroblast	897	6	1.5	237	22	AAU65244	Human PRO51 (UNOS
825	6	1.5	210	21	AAE24375	Human FGF-21 prote	898	6	1.5	237	23	ABG30699	Human artemin poly
826	6	1.5	211	21	AAU36629	Arabidopsis thalia	899	6	1.5	239	21	AAU05704	Arabidopsis thalia
827	6	1.5	211	23	AAU76144	Ralstonia solanace	900	6	1.5	239	21	AAU29617	Arabidopsis thalia
828	6	1.5	212	21	AAU26292	Arabidopsis thalia	901	6	1.5	239	21	AAU45610	Arabidopsis thalia
829	6	1.5	212	22	ABG29278	Novel human diagno	902	6	1.5	239	22	ABU64172	Drosophila melanog
830	6	1.5	212	22	AAU99966	Hordeum vulgare AG	903	6	1.5	239	22	AAU58883	Propionibacterium
831	6	1.5	213	21	AAU09106	Arabidopsis thalia	904	6	1.5	239	22	AAU87500	Human DNA polymera
832	6	1.5	213	21	AAU25232	Arabidopsis thalia	905	6	1.5	240	22	AAU94913	Human protein sequ
833	6	1.5	213	21	AAU26291	C. pneumoniae prot	906	6	1.5	240	23	AAU74427	Mouse protein sequ
834	6	1.5	214	21	AAU34657	Human colon cancer	907	6	1.5	241	9	AAU80597	Cv-sis gene encode
835	6	1.5	215	21	AAU53324	Actinobacillus ple	908	6	1.5	241	14	AAU40967	Recombinant platel
836	6	1.5	215	21	AAU96096	Actinobacillus ple	909	6	1.5	241	15	AAU34772	Human pancreatic c
837	6	1.5	215	22	AAU23663	Human EST encoded	910	6	1.5	241	21	AAU54090	Drosophila melanog
838	6	1.5	215	22	AAU23663	Human EST encoded	911	6	1.5	241	22	AAU70112	Putative P. abyssi
839	6	1.5	217	22	AAU34785	Novel human diagno	912	6	1.5	241	22	AAU99134	Human polypeptide,
840	6	1.5	217	22	ABG22862	C glutamicum prote	913	6	1.5	241	22	AAU93374	S. epidermidis ope
841	6	1.5	218	23	AAU90916	Aeropyrum pernix e	914	6	1.5	241	22	AAU83027	Propionibacterium
842	6	1.5	218	23	AAU18235	Amino acid sequenc	915	6	1.5	243	22	AAU41710	Novel human secret
843	6	1.5	220	21	AAU84583	Short splice varia	916	6	1.5	243	22	AAU31720	Mouse neurogenic d
844	6	1.5	220	21	AAU44776	A human pre-pro-ne	917	6	1.5	244	18	AAU22443	Amino acid sequenc
845	6	1.5	220	21	AAU68710	Human PRO3562 prot	918	6	1.5	244	19	AAU80804	Murine neuroD3 p
846	6	1.5	220	22	AAU50978	Human PRO3562 poly	919	6	1.5	244	19	AAU57103	Rat neurogenin 1 p
847	6	1.5	220	23	ABG30698	Human artemin poly	920	6	1.5	244	19	AAU54944	Mouse neurogenin 1
848	6	1.5	220	23	ABR95581	Human angiogenesis	921	6	1.5	244	19	AAU54944	Myrothectum verruc
849	6	1.5	220	23	AAU86158	Human PRO3562 poly	922	6	1.5	244	20	AAU50503	Rat neurogenin-1 (
850	6	1.5	220	23	ABR84975	Human PRO3562 prot	923	6	1.5	244	21	AAU70565	Murine neurogenin-
851	6	1.5	221	22	AAU63772	Human prostate can	924	6	1.5	244	21	AAU70566	Novel human diagno
852	6	1.5	222	20	AAU37759	Amino acid sequenc	925	6	1.5	244	21	ABG00011	Human polypeptide,
853	6	1.5	222	22	AAU35175	Enterococcus faeca	926	6	1.5	244	22	AAU93260	Human polypeptide,
854	6	1.5	223	20	AAU97845	Human truncated bo	927	6	1.5	245	18	AAU25783	Anti-T3 antibody d
855	6	1.5	223	21	AAU36473	Human LMP-1 amino	928	6	1.5	247	21	AAU43617	Arabidopsis thalia
856	6	1.5	224	20	AAU06931	C. albicans antige	929	6	1.5	247	22	AAU05363	Mouse high affinit
857	6	1.5	224	20	AAU61638	Novel human diagno	930	6	1.5	247	23	AAU872363	Murine protein iso
858	6	1.5	225	13	AAU29646	AAEPV Spheroidin a	931	6	1.5	248	19	AAU72906	Mycobacterium tube
859	6	1.5	225	15	AAU55573	AAEPV spheroidin G	932	6	1.5	248	20	AAU21923	Amino acid sequenc
860	6	1.5	225	19	AAU41298	AAEPV entomopoxir	933	6	1.5	248	22	ABG18105	Novel human diagno
861	6	1.5	225	20	AAU30166	Protein encoded by	934	6	1.5	248	23	AAU78814	Bacillus sp. Autot
862	6	1.5	225	21	AAU42241	Human ORFX ORF2005	935	6	1.5	249	22	AAU86195	Putative P. abyssi
863	6	1.5	225	21	AAU22119	Maize glutathione-	936	6	1.5	250	21	AAU84383	Human ORFX ORF147
864	6	1.5	226	13	AAU22673	v-sis protein P28s	937	6	1.5	250	21	AAU60893	Arabidopsis thalia
865	6	1.5	227	23	AAU09105	Herbicidally activ	938	6	1.5	250	21	AAU44830	Zea mays protein f
866	6	1.5	227	23	ABR91925	Arabidopsis thalia	939	6	1.5	250	22	AAU64830	Autoinducer inacti
867	6	1.5	227	23	ABR48599	Listeria monocytog	940	6	1.5	250	22	ABR60669	Drosophila melanog
868	6	1.5	228	21	AAU93559	A human GDNF-relat	941	6	1.5	250	23	AAU50476	Listeria sp. strai
869	6	1.5	228	21	AAU44775	Long splice varian	942	6	1.5	250	23	AAU78804	Autoinducer inacti
870	6	1.5	228	22	ABR63150	Drosophila melanog	943	6	1.5	250	23	AAU78805	Autoinducer inacti
871	6	1.5	230	22	ABR60542	Drosophila melanog	944	6	1.5	250	23	AAU78807	Autoinducer inacti
872	6	1.5	230	22	ABG23889	Novel human diagno	945	6	1.5	250	23	AAU78808	Autoinducer inacti
873	6	1.5	230	22	AAU40569	Human polypeptide	946	6	1.5	250	23	AAU78809	Autoinducer inacti
874	6	1.5	230	23	ABP28496	Streptococcus poly	947	6	1.5	250	23	AAU78810	Autoinducer inacti
875	6	1.5	231	21	AAU97009	S. cerevisiae esse	948	6	1.5	250	23	AAU78811	Autoinducer inacti
876	6	1.5	231	22	ABG07188	Novel human diagno	949	6	1.5	250	23	AAU78812	Autoinducer inacti
877	6	1.5	231	22	ABG29059	Novel human diagno	950	6	1.5	251	18	AAU20277	H. pylori surface
878	6	1.5	231	22	AAU25880	Human protein sequ	951	6	1.5	251	22	AAU55293	Human protein sequ
879	6	1.5	232	22	ABR67478	Drosophila melanog	952	6	1.5	252	18	AAU28247	Amino acid sequenc
880	6	1.5	233	22	ABR68857	Drosophila melanog	953	6	1.5	252	21	AAU28247	Arabidopsis thalia
881	6	1.5	234	18	AAU10509	Soluble fused MHC	954	6	1.5	252	22	AAU39891	Propionibacterium
882	6	1.5	234	21	AAU08704	Arabidopsis thalia	955	6	1.5	252	22	AAU59819	Propionibacterium
883	6	1.5	234	21	AAU42717	Arabidopsis thalia	956	6	1.5	253	22	ABG16451	Novel human diagno
884	6	1.5	234	22	AAU60290	Propionibacterium	957	6	1.5	253	23	ABP41998	Human ovarian anti
885	6	1.5	234	23	ABP28911	Streptococcus poly	958	6	1.5	254	21	AAU22059	Arabidopsis thalia
886	6	1.5	235	20	AAU35400	Amino acid sequenc	959	6	1.5	254	21	AAU32612	Arabidopsis thalia

960	6	1.5	254	22	ABB64503	Drosophila melanog
961	6	1.5	256	22	AAC92545	C glutamicum prote
962	6	1.5	257	22	AAB96285	Putative p. abyssi
963	6	1.5	258	22	ABR65793	Drosophila melanog
964	6	1.5	258	22	ABP38691	Staphylococcus epi
965	6	1.5	259	22	AUJ36010	Helicobacter pylori
966	6	1.5	259	22	AAB46975	H. pylori Murb pro
967	6	1.5	260	22	AUJ17427	Novel signal trans
968	6	1.5	260	22	AAB79890	Corynebacterium gl
969	6	1.5	260	22	AUJ1802	Novel human neopla
970	6	1.5	261	22	AA41917	Human polypeptide
971	6	1.5	262	21	AAB42498	Human ORFX ORF262
972	6	1.5	262	21	AAB85539	Human secreted pro
973	6	1.5	262	22	AA673661	Human colon cancer
974	6	1.5	262	22	ABG64720	Human albumin fusi
975	6	1.5	263	21	AA617344	Arabidopsis thalia
976	6	1.5	264	16	AA681425	Hepatitis GB virus
977	6	1.5	264	21	AAB09032	Hepatitis GB virus
978	6	1.5	264	21	AAV44702	Wheat dwarf virus
979	6	1.5	264	21	AAV44703	Wheat dwarf virus
980	6	1.5	266	21	AA606098	Arabidopsis thalia
981	6	1.5	266	21	AA649376	Arabidopsis thalia
982	6	1.5	266	22	AUJ38887	C. pneumoniae CT13
983	6	1.5	266	22	AAG89903	C. glutamicum prote
984	6	1.5	266	23	ABR49459	Listeria monocytog
985	6	1.5	267	18	AAW1027	H. pylori putative
986	6	1.5	268	20	AAW88210	Pseudomonas aerugi
987	6	1.5	269	21	AA649398	Arabidopsis thalia
988	6	1.5	270	22	AAW39394	Human polypeptide
989	6	1.5	270	22	ABR28795	Human hydrolyase-11
990	6	1.5	271	9	AA680595	Recombinant placel
991	6	1.5	271	14	AA640963	PDGF Bv-sis. Simi
992	6	1.5	271	15	AA634468	Recombinant placel
993	6	1.5	271	22	ABR58271	Drosophila melanog
994	6	1.5	271	23	ABR47658	Listeria monocytog
995	6	1.5	272	13	AA625590	RING10 proteasome
996	6	1.5	272	17	AAW06437	Human proteasome s
997	6	1.5	272	22	ABR59895	Drosophila melanog
998	6	1.5	273	22	AAU40181	Propionibacterium
999	6	1.5	273	22	AA630638	C glutamicum prote
1000	6	1.5	274	21	ABR43146	Human ORFX ORF2910

ALIGNMENTS

RESULT 1
AAE10658
ID AAE10658 standard; Protein: 413 AA.
XX
AC AAE10658;
XX
DT 10-DEC-2001 (first entry)
XX
DE Acid-Processed hu-Asp 1 lacking TM domain and containing (His)6 tag.
XX
KM Human; aspartyl protease 1; Aspl1; amyloid precursor protein; APP;
KM Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
KM Amyloid plaque; neuronal loss; proteolytic; neurotrophic; neuroprotective.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN GB2357767-A.
PD
XX 04-JUL-2001.
PF 22-SEP-2000; 2000GB-0023315.
XX
PR 23-SEP-1999; 99US-0155493.
PR 23-SEP-1999; 99US-0404133.
PR 23-SEP-1999; 99US-0520881.
PR 13-OCT-1999; 99US-0416901.

PR 06-DEC-1999; 99US-0169232.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Bienkowiecki MJ, Gurney M;
XX
DR WPI; 2001-444208/48.
XX
XX
PT Polypeptide comprising fragments of human aspartyl protease with
PT Amyloid precursor protein processing activity and alpha-secretase
PT activity, for identifying modulators useful in treating Alzheimer's
PT disease -
PS
XX
XX
XX Example 14; Page 158; 187pp; English.
CC The patent discloses human aspartyl protease 1 (hu-Asp1) or modified
CC Asp1 proteins which lack transmembrane domain or amino terminal
CC domain or cytoplasmic domain and retains alpha-secretase activity
CC and amyloid protein precursor (APP) processing activity. The proteins
CC of the invention are useful for assaying hu-Asp1 alpha-secretase
CC activity, which in turn is useful for identifying modulators of
CC hu-Asp1 alpha-secretase activity, where modulators that increase
CC hu-Asp1 alpha-secretase activity are useful for treating Alzheimer's
CC disease (AD) which causes progressive dementia with consequent
CC formation of amyloid plaques, neurofibrillary tangles, gliosis and
CC neuronal loss. Hu-Asp1 protease substrate is useful for assaying
CC hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein with
CC the substrate under acidic conditions and determining the level
CC of hu-Asp1 proteolytic activity. The present sequence is the acid-
CC processed form of human Asp 1 protein lacking a transmembrane (TM)
CC domain and containing (His)6 tag.
XX
SQ Sequence 413 AA;
Query Match 100.0%; Score 406; DB 22; Length 413;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ALEPALASPAGANFLAMVDNLQDSDGRGYLEMLIGTPPOKLOILDVDTSSNFAVAGTP 60
DB 1 ALERPLASPAANFLAMVDNLQDSDGRGYLEMLIGTPPOKLOILDVDTSSNFAVAGTP 60
OY 61 HSYIDTYFDTERSSSTYRSKGFDTVKYTGSGWTFPGEDLVITPKGNTSLVNIATTFE 120
DB 61 HSYIDTYFDTERSSSTYRSKGFDTVKYTGSGWTFPGEDLVITPKGNTSLVNIATTFE 120
OY 121 SENPFLPGIKNGNGLGLAYATLAKPSSLETFPPSLVTQANIPVFSQMCGAGLPVAGS 180
DB 121 SENPFLPGIKNGNGLGLAYATLAKPSSLETFPPSLVTQANIPVFSQMCGAGLPVAGS 180
OY 181 GTNGSLVLGGIEPSLVKGDIMYTPPIKEWYVQTEILKLEIGQSINLDCREYNADKAIV 240
DB 181 GTNGSLVLGGIEPSLVKGDIMYTPPIKEWYVQTEILKLEIGQSINLDCREYNADKAIV 240
OY 241 DSGTTLRLPKVTDVAEVAARASLIPEFSDGFWTSQALACWTNSETPMSPFKISITYL 300
DB 241 DSGTTLRLPKVTDVAEVAARASLIPEFSDGFWTSQALACWTNSETPMSPFKISITYL 300
OY 301 RDNSSRSRFRITLIPOLYIQPMGAGLNEYCRFGISSTNALVIGATVMGFGVITPDRA 360
DB 301 RDNSSRSRFRITLIPOLYIQPMGAGLNEYCRFGISSTNALVIGATVMGFGVITPDRA 360
OY 361 QKRVGFASPCAEIAGAAVSEISGPFSTEDVANSVCVPAQSISEPIL 406
DB 361 QKRVGFASPCAEIAGAAVSEISGPFSTEDVANSVCVPAQSISEPIL 406
RESULT 2
AAE02610
ID AAE02610 standard; Protein: 413 AA.
XX
XX AAE02610;
AC

DT 10-AUG-2001 (first entry)
 XX Human acid-processed form of aspartyl protease-1 deltatm (His)6 protein.
 DE Human acid-processed form of aspartyl protease-1 deltatm (His)6 protein.
 XX Human acid-processed form of aspartyl protease-1 deltatm (His)6 protein.
 KW Human; alpha-secretase; amyloid precursor protein; APP; therapy;
 KW Alzheimer's disease; antialzheimer's; aspartyl protease 1; Aspl;
 KW beta-secretase; acid-processed Asp-1 deltatm (His)6 protein.
 XX Homo sapiens.
 OS Synthetic.
 PN W0200123533-A2.
 XX 05-APR-2001.
 PD 22-SEP-2000; 2000WO-US26080.
 PF 23-SEP-1999; 99US-0155493.
 PR 23-SEP-1999; 99WO-US20881.
 PR 13-OCT-1999; 99US-0416901.
 PR 06-DEC-1999; 99US-0169232.
 XX (PHAA) PHARMACIA & UPJOHN CO.
 PA Gurney M, Bienkowski MJ;
 PI WPI; 2001-290516/30.
 DR Enzymes that cleave the alpha-secretase site of the amyloid precursor
 XX protein, useful for the treatment of Alzheimer's disease -
 PT Example 14; Page 186-187; 189pp; English.
 PS The present invention relates to enzymes for cleaving the alpha-
 XX secretase site of the amyloid precursor protein (APP) and methods of
 CC identifying those enzymes. The methods may be used to identify enzymes
 CC that may be used to cleave the alpha-secretase cleavage site of the APP
 CC protein. The enzymes may be used to treat or modulate the progress of
 CC Alzheimer's disease. The present sequence is human acid-processed form of
 CC Aspartyl protease-1 (Asp-1) deltatm (His)6 protein which is used for the
 CC expression of pre-pro-human-Aspartyl protease 1 (Aspl). The protein is
 CC obtained by replacing C-terminal transmembrane and cytoplasmic domains
 CC with a hexahistidine purification tag in the human Aspartyl protease 1.
 XX
 SQ Sequence 413 AA;
 Query Match 100.0%; Score 406; DB 22; Length 413;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 361 QKRVGFAPSPCAEIAAGAVSEISGPFSTEDVANSNCVPAQSISEIL 406
 DB 361 QKRVGFAPSPCAEIAAGAVSEISGPFSTEDVANSNCVPAQSISEIL 406
 RESULT 3
 ID ABB78619 standard; Protein; 413 AA.
 XX ABB78619;
 AC ABB78619;
 XX 16-JUL-2002 (first entry)
 DT Asp-1delatm(his)6 acid-processed form SEQ ID NO:68.
 DE Asp-1delatm(his)6 acid-processed form SEQ ID NO:68.
 XX Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease;
 KW proteolytic; chromosome 21.
 XX Homo sapiens.
 XX GB2367060-A.
 PN 27-MAR-2002.
 PD 29-OCT-2001; 2001GB-0025934.
 PF 23-SEP-1999; 99US-155493P.
 PR 23-SEP-1999; 99US-0404133.
 PR 23-SEP-1999; 99WO-US20881.
 PR 13-OCT-1999; 99US-0416901.
 PR 06-DEC-1999; 99US-169232P.
 PR 22-SEP-2000; 2000GB-0023315.
 XX (PHAA) PHARMACIA & UPJOHN CO.
 PA Bienkowski MJ, Gurney M;
 XX WPI; 2002-396337/43.
 DR Human aspartyl protease 1 substrates useful in assays to detect
 XX aspartyl protease activity, e.g. for the diagnosis of Alzheimer's
 PT disease -
 PT Example 14; Page 158-159; 182pp; English.
 PS The present invention describes a human aspartyl protease 1 (hu-Aspl)
 XX substrate (I) which comprises a peptide of no more than 50 amino acids,
 CC and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-
 CC Glu-Pro. Also described are: (1) a method (II) for assaying hu-Aspl
 CC proteolytic activity, comprising: (a) contacting a hu-Aspl protein with
 CC (1) under acidic conditions; and (b) determining the level of hu-Aspl
 CC nucleolytic activity; (2) a purified polynucleotide (III) comprising a
 CC nucleotide sequence that hybridises under stringent conditions to the
 CC non-coding strand complementary to a defined 1804 nucleotide sequence
 CC (see AB152456) where the nucleotide sequence encodes a polypeptide having
 CC Aspl proteolytic activity and lacks nucleotides encoding a transmembrane
 CC domain; (3) a purified polynucleotide (III') comprising a sequence that
 CC hybridises under stringent conditions to (III) (the nucleotide sequence
 CC encodes a polypeptide further lacking a pro-peptide domain corresponding
 CC to amino acids 23-62 of hu-Aspl (see ABB78589)); (4) a vector (IV)
 CC comprising (III) or (III'); and (5) a host cell (V) transformed or
 CC transfected with (III), (III') and/or (IV). The hu-Aspl protease
 CC substrate (I) may be used as an enzyme substrate in assays to detect
 CC aspartyl protease activity, (II) and therefore diagnose diseases
 CC associated with aberrant hu-Aspl expression and activity such as
 CC Alzheimer's disease. Hu-Aspl has been localised to chromosome 21, while
 CC hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
 CC sequence represents the Asp-1delatm(his)6 acid-processed form amino acid
 XX sequence, which is used in an example from the present invention.
 SQ Sequence 413 AA;

Query Match 100.0%; Score 406; DB 23; Length 413;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALEPALSPAGANFLAVNDNLQDSDGRGYLEMLIGTPPOKQLVDTGSSNFAVAGTP 60
 DB 1 ALEPALSPAGANFLAVNDNLQDSDGRGYLEMLIGTPPOKQLVDTGSSNFAVAGTP 60
 QY HSYIDTYDTERSSSTYRSKGFDTVKYTOGSGWTFVGEDLVITIPKGFNTSLVNIATIFE 120
 DB 61 HSYIDTYDTERSSSTYRSKGFDTVKYTOGSGWTFVGEDLVITIPKGFNTSLVNIATIFE 120
 QY 121 SENFPLPGIKWNGILGLAVATLAKPSSSLETFPDSLVTOANIPIVFSQMGAGLPVAGS 180
 DB 121 SENFPLPGIKWNGILGLAVATLAKPSSSLETFPDSLVTOANIPIVFSQMGAGLPVAGS 180
 QY 181 GTNGSLVLGGIEPSLYKGDITWYTPIKEWYQIEILKLEIGGOSLNDCREYNADKAI 240
 DB 181 GTNGSLVLGGIEPSLYKGDITWYTPIKEWYQIEILKLEIGGOSLNDCREYNADKAI 240
 QY 241 DSGTTLRLPKVDFDAVEAVARASLIPEFSDGFWTGSQLAQWNTSETPMSYFPKISITL 300
 DB 241 DSGTTLRLPKVDFDAVEAVARASLIPEFSDGFWTGSQLAQWNTSETPMSYFPKISITL 300
 QY 301 RDENSSRSFRITITLPOLYIQPMGAGLNYECYRFGISPTNALVIGATVMGCFYVIPRA 360
 DB 301 RDENSSRSFRITITLPOLYIQPMGAGLNYECYRFGISPTNALVIGATVMGCFYVIPRA 360
 QY 361 QKRVGFAPCAEITAGAAVSEISGPFSTEDVANSNCVPAQSLSEPTL 406
 DB 361 QKRVGFAPCAEITAGAAVSEISGPFSTEDVANSNCVPAQSLSEPTL 406

RESULT 4
 ID AAE10657 standard; Protein: 475 AA.
 AC AAE10657;
 DT 10-DEC-2001 (first entry)
 DE Secreted recombinant hu-Asp 1 with (His)6 tag and lacking TM domain.
 KW Human; aspartyl protease 1; Aspl1; amyloid precursor protein; APP; Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
 KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective.
 OS Homo sapiens.
 OS Synthetic.
 PN GB2357767-A.
 PD 04-JUL-2001.
 PF 22-SEP-2000; 2000GB-0023315.
 PR 23-SEP-1999; 99US-0155493.
 PR 23-SEP-1999; 99US-0404133.
 PR 23-SEP-1999; 99MO-US20881.
 PR 13-OCT-1999; 99US-0416901.
 PR 06-DEC-1999; 99US-0169232.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 PI Bienkowski MJ, Gurney M;
 WP1; 2001-444208/48.
 PT Polypeptide comprising fragments of human aspartyl protease with
 PT amyloid precursor protein processing activity and alpha-secretase
 PT activity, for identifying modulators useful in treating Alzheimer's
 PT disease -
 XX

PS Example 14; Page 156-158; 187pp; English.
 XX The patent discloses human aspartyl protease 1 (hu-Aspl) or modified
 CC Aspl proteins which lack transmembrane domain or amino terminal
 CC domain or cytoplasmic domain and retains alpha-secretase activity
 CC and amyloid protein precursor (APP) processing activity. The proteins
 CC of the invention are useful for assaying hu-Aspl alpha-secretase
 CC activity, which in turn is useful for identifying modulators of
 CC hu-Aspl alpha-secretase activity, where modulators that increase
 CC hu-Aspl alpha-secretase activity are useful for treating Alzheimer's
 CC disease (AD) which causes progressive dementia with consequent
 CC formation of amyloid plaques, neurofibrillary tangles, gliosis and
 CC neuronal loss. Hu-Aspl protease substrate is useful for assaying
 CC hu-Aspl proteolytic activity, by contacting hu-Aspl protein with
 CC the substrate under acidic conditions and determining the level
 CC of hu-Aspl proteolytic activity. The present sequence is secreted
 CC recombinant human Asp 1 protein lacking a transmembrane (TM) domain
 CC and containing a (His)6 tag. This sequence is generated from human
 CC Asp 1 protein by the deletion of its C-terminal TM domain and addition
 CC of hexa-histidine tag at its C-terminus.
 SO Sequence 475 AA;

Query Match 100.0%; Score 406; DB 22; Length 475;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALEPALSPAGANFLAVNDNLQDSDGRGYLEMLIGTPPOKQLVDTGSSNFAVAGTP 60
 DB 63 ALEPALSPAGANFLAVNDNLQDSDGRGYLEMLIGTPPOKQLVDTGSSNFAVAGTP 122
 QY 61 HSYIDTYDTERSSSTYRSKGFDTVKYTOGSGWTFVGEDLVITIPKGFNTSLVNIATIFE 120
 DB 123 HSYIDTYDTERSSSTYRSKGFDTVKYTOGSGWTFVGEDLVITIPKGFNTSLVNIATIFE 182
 QY 121 SENFPLPGIKWNGILGLAVATLAKPSSSLETFPDSLVTOANIPIVFSQMGAGLPVAGS 180
 DB 183 SENFPLPGIKWNGILGLAVATLAKPSSSLETFPDSLVTOANIPIVFSQMGAGLPVAGS 242
 QY 181 GTNGSLVLGGIEPSLYKGDITWYTPIKEWYQIEILKLEIGGOSLNDCREYNADKAI 240
 DB 243 GTNGSLVLGGIEPSLYKGDITWYTPIKEWYQIEILKLEIGGOSLNDCREYNADKAI 302
 QY 241 DSGTTLRLPKVDFDAVEAVARASLIPEFSDGFWTGSQLAQWNTSETPMSYFPKISITL 300
 DB 303 DSGTTLRLPKVDFDAVEAVARASLIPEFSDGFWTGSQLAQWNTSETPMSYFPKISITL 362
 QY 301 RDENSSRSFRITITLPOLYIQPMGAGLNYECYRFGISPTNALVIGATVMGCFYVIPRA 360
 DB 363 RDENSSRSFRITITLPOLYIQPMGAGLNYECYRFGISPTNALVIGATVMGCFYVIPRA 422
 QY 361 QKRVGFAPCAEITAGAAVSEISGPFSTEDVANSNCVPAQSLSEPTL 406
 DB 423 QKRVGFAPCAEITAGAAVSEISGPFSTEDVANSNCVPAQSLSEPTL 468

RESULT 5
 ID AAE02609 standard; Protein: 475 AA.
 AC AAE02609;
 DT 10-AUG-2001 (first entry)
 DE Human secreted aspartyl protease-1 (Asp-1) deltatm (His)6 protein.
 KW Human; alpha-secretase; amyloid precursor protein; APP; therapy;
 KW Alzheimer's disease; antialzheimer's; aspartyl protease 1; Aspl1;
 KW beta-secretase; secreted Asp-1 deltatm (His)6 protein.
 OS Homo sapiens.
 OS Synthetic.
 XX

PN W0200123533-A2.
 XX
 PD 05-APR-2001.
 XX
 PF 22-SEP-2000; 2000WO-US26080.
 XX
 PR 23-SEP-1999; 99US-0155493.
 PR 23-SEP-1999; 99WO-US20881.
 PR 13-OCT-1999; 99US-0416901.
 PR 06-DEC-1999; 99US-0169232.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Gurney M, Bienkowski MJ;
 XX
 DR WPI; 2001-290516/30.
 XX
 PT Enzymes that cleave the alpha-secretase site of the amyloid precursor
 PT protein, useful for the treatment of Alzheimer's disease -
 XX
 PS Example 14; Page 184-186; 189pp; English.
 XX
 CC The present invention relates to enzymes for cleaving the alpha-
 CC secretase site of the amyloid precursor protein (APP) and methods of
 CC identifying those enzymes. The methods may be used to identify enzymes
 CC that may be used to cleave the alpha-secretase cleavage site of the APP
 CC protein. The enzymes may be used to treat or modulate the progress of
 CC Alzheimer's disease. The present sequence is human secreted recombinant
 CC Aspartyl protease-1 (Asp-1) deltatm (His)6 protein which is used for the
 CC expression of pre-pro-human-aspartyl protease 1 (Asp1). The protein is
 CC obtained by replacing C-terminal transmembrane and cytoplasmic domains
 CC with a hexahistidine purification tag in the human Aspartyl protease 1.
 XX
 SQ Sequence 475 AA;
 Query Match 100.0%; Score 406; DB 22; Length 475;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALPALASPAGANFLAVNDLQGDGSGRGYLEMLIGTPPOKQILVDTGSSNFAVAGTP 60
 DB 63 ALPALASPAGANFLAVNDLQGDGSGRGYLEMLIGTPPOKQILVDTGSSNFAVAGTP 122
 QY 61 HSYIDYFDTERSSSTYRSKGFDTVTKYTGSGWTFVGEDLVITPKGFNTSFLVNIATIFE 120
 DB 123 HSYIDYFDTERSSSTYRSKGFDTVTKYTGSGWTFVGEDLVITPKGFNTSFLVNIATIFE 182
 QY 121 SENFPLPGIKWNGILGLAVATLAKPSSSLETFPDSLVTOANIPNVFSWQMGAGLIPVAGS 180
 DB 183 SENFPLPGIKWNGILGLAVATLAKPSSSLETFPDSLVTOANIPNVFSWQMGAGLIPVAGS 242
 QY 181 GTNGSGLVGGIEPSLYGDIWYPIKEWYQIETILETGGGSLNDCERYNDAKIV 240
 DB 243 GTNGSGLVGGIEPSLYGDIWYPIKEWYQIETILETGGGSLNDCERYNDAKIV 302
 QY 241 DSGTTLRLPKQVDAVEAVARASLIEPFDGFWTGSQACMTSETPMWFFPKISITL 300
 DB 303 DSGTTLRLPKQVDAVEAVARASLIEPFDGFWTGSQACMTSETPMWFFPKISITL 362
 QY 301 RDESSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFDRA 360
 DB 363 RDESSRSFRITILPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFDRA 422
 QY 361 QKRGVFAASPCAETAGAVSEISGPFSTEDVANSNCVPAQSISEPTL 406
 DB 423 QKRGVFAASPCAETAGAVSEISGPFSTEDVANSNCVPAQSISEPTL 468

XX 16-JUL-2002 (first entry)
 DT
 XX
 DE Secreted recombinant Asp-1deltatm(his)6 amino acid SEQ ID NO:67.
 XX
 KM Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease;
 KM proteolytic; chromosome 21.
 XX
 OS Homo sapiens.
 XX
 PN GB2367060-A.
 XX
 PD 27-MAR-2002.
 XX
 PF 29-OCT-2001; 2001GB-0025934.
 XX
 PR 23-SEP-1999; 99US-155493P.
 PR 23-SEP-1999; 99US-0404133.
 PR 23-SEP-1999; 99WO-US20881.
 PR 13-OCT-1999; 99US-0416901.
 PR 06-DEC-1999; 99US-169232P.
 PR 22-SEP-2000; 2000GB-0023315.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Bienkowski MJ, Gurney M;
 XX
 DR WPI; 2002-396337/43.
 XX
 PT Human aspartyl protease 1 substrates useful in assays to detect
 PT aspartyl protease activity, e.g. for the diagnosis of Alzheimer's
 PT disease -
 XX
 PS Example 14; Page 156-158; 182pp; English.
 XX
 CC The present invention describes a human aspartyl protease 1 (hu-Asp1)
 CC substrate (I) which comprises a peptide of no more than 50 amino acids,
 CC and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-
 CC Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1
 CC proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with
 CC (1) under acidic conditions; and (b) determining the level of hu-Asp1
 CC proteolytic activity; (2) a purified polynucleotide (III) comprising a
 CC nucleotide sequence that hybridises under stringent conditions to the
 CC non-coding strand complementary to a defined 1804 nucleotide sequence
 CC (see AB152456) where the nucleotide sequence encodes a polypeptide having
 CC Asp1 proteolytic activity and lacks nucleotides encoding a transmembrane
 CC domain; (3) a purified polynucleotide (III') comprising a sequence that
 CC hybridises under stringent conditions to (III) (the nucleotide sequence
 CC encodes a polypeptide further lacking a pro-peptide domain corresponding
 CC to amino acids 23-62 of hu-Asp1 (see AB875891); (4) a vector (IV)
 CC comprising (III) or (III'); and (5) a host cell (V) transformed or
 CC transfected with (III), (III') and/or (IV). The hu-Asp1 protease
 CC substrate (I) may be used as an enzyme substrate in assays to detect
 CC aspartyl protease activity, (II) and therefore diagnose diseases
 CC associated with aberrant hu-Asp1 expression and activity such as
 CC Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while
 CC hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
 CC sequence represents a secreted recombinant Asp-1deltatm(his)6 amino acid
 CC sequence, which is used in an example from the present invention.
 XX
 SQ Sequence 475 AA;
 Query Match 100.0%; Score 406; DB 23; Length 475;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALPALASPAGANFLAVNDLQGDGSGRGYLEMLIGTPPOKQILVDTGSSNFAVAGTP 60
 DB 63 ALPALASPAGANFLAVNDLQGDGSGRGYLEMLIGTPPOKQILVDTGSSNFAVAGTP 122
 QY 61 HSYIDYFDTERSSSTYRSKGFDTVTKYTGSGWTFVGEDLVITPKGFNTSFLVNIATIFE 120
 DB 123 HSYIDYFDTERSSSTYRSKGFDTVTKYTGSGWTFVGEDLVITPKGFNTSFLVNIATIFE 182

QY 121 SENFPLPGIKKNGILGLAVATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVAGS 180
 DB 183 SENFPLPGIKKNGILGLAVATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVAGS 242
 QY 181 GTNGSLVGLGIEPSLYKGDWYTPRIKEWYQIEILKLEIGGSLNDCREYNADKAIV 240
 DB 243 GTNGSLVGLGIEPSLYKGDWYTPRIKEWYQIEILKLEIGGSLNDCREYNADKAIV 302
 QY 241 DSGTTLRLPQKVPDAVVEAVARASLIPEFSDGFWTGSOLACWNTSETPMSYFPKISITL 300
 DB 303 DSGTTLRLPQKVPDAVVEAVARASLIPEFSDGFWTGSOLACWNTSETPMSYFPKISITL 362
 QY 301 RDENSSRSFRITILPOLYIQPMGAGLNECYRFGISPTNALVIGATWEGFYIIPDRA 360
 DB 363 RDENSSRSFRITILPOLYIQPMGAGLNECYRFGISPTNALVIGATWEGFYIIPDRA 422
 QY 361 QKRVGFAPSPCAEITAGAAVSEISGPFSTEDVANSNCVPAQSLSEPTL 406
 DB 423 QKRVGFAPSPCAEITAGAAVSEISGPFSTEDVANSNCVPAQSLSEPTL 468

RESULT 7
 AAG75592
 ID AAG75592 standard; Protein; 481 AA.
 AC AAG75592;
 DT 03-SEP-2001 (first entry)
 DE Human colon cancer antigen protein SEQ ID NO:6356.
 KW Human: colon cancer; colon cancer antigen; diagnosis; detection;
 KM Colorectal carcinoma; chromosome 21.
 OS Homo sapiens.
 XX MO200122920-A2.
 PN 05-APR-2001.
 PD 28-SEP-2000; 2000WO-US26524.
 PF 29-SEP-1999; 99US-0157137.
 PR 03-NOV-1999; 99US-0163280.
 XX (HUMA-) HUMAN GENOME SCT INC.
 PI Ruben SM, Barash SC, Birse CE, Rosen CA;
 XX WPI; 2001-235357/24.
 DR N-PSDB; AAH34997.
 PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
 useful for preventing, diagnosing and/or treating colorectal cancers -
 PS Claim 11; Page 7815-7817; 9803pp; English.

AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
 cancer-associated nucleic acid molecules (N) and proteins (P), where
 the proteins are collectively known as colon cancer antigens. The colon
 cancer antigens have cytosolic activity and can be used in gene
 therapy and vaccine production. N and P may be used in the prevention,
 diagnosis and treatment of diseases associated with inappropriate P
 expression. For example, N and P may be used to treat disorders
 associated with decreased expression by rectifying mutations or deletions
 in a patient's genome that affect the activity of P by expressing
 inactive proteins or to supplement the patients own production of P.
 Additionally, N may be used to produce the colon cancer-associated Ps
 by inserting the nucleic acids into a host cell and culturing the cell
 to express the proteins. N and P can be used in the prevention, diagnosis
 and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
 and AAB77789 represent sequences used in the exemplification of the

CC present invention.
 CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
 CC missing at time of publication, meaning no sequences are present for
 CC SEQ ID NO:1027 to 1052, 7921 and 7922.
 XX Sequence 481 AA;
 SQ Query Match 100.0%; Score 406; DB 22; Length 481;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALEPALSPAGAAFLAMVDNLQDSGRGYLLEMLIGTPPKQILVDTGSSNFAVAGTP 60
 DB 26 ALEPALSPAGAAFLAMVDNLQDSGRGYLLEMLIGTPPKQILVDTGSSNFAVAGTP 85
 QY 61 HSYIDYEDTSSSTYRSKGFVTVKTYQSGWTFVGEDVLTIPKFNTPFLVNIATITFE 120
 DB 86 HSYIDYEDTSSSTYRSKGFVTVKTYQSGWTFVGEDVLTIPKFNTPFLVNIATITFE 145
 QY 121 SENFPLPGIKKNGILGLAVATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVAGS 180
 DB 146 SENFPLPGIKKNGILGLAVATLAKPSSSLETFPDSLVTQANIPNVFSMOMCGAGLPVAGS 205
 QY 181 GTNGSLVGLGIEPSLYKGDWYTPRIKEWYQIEILKLEIGGSLNDCREYNADKAIV 240
 DB 206 GTNGSLVGLGIEPSLYKGDWYTPRIKEWYQIEILKLEIGGSLNDCREYNADKAIV 265
 QY 241 DSGTTLRLPQKVPDAVVEAVARASLIPEFSDGFWTGSOLACWNTSETPMSYFPKISITL 300
 DB 266 DSGTTLRLPQKVPDAVVEAVARASLIPEFSDGFWTGSOLACWNTSETPMSYFPKISITL 325
 QY 301 RDENSSRSFRITILPOLYIQPMGAGLNECYRFGISPTNALVIGATWEGFYIIPDRA 360
 DB 326 RDENSSRSFRITILPOLYIQPMGAGLNECYRFGISPTNALVIGATWEGFYIIPDRA 385
 QY 361 QKRVGFAPSPCAEITAGAAVSEISGPFSTEDVANSNCVPAQSLSEPTL 406
 DB 386 QKRVGFAPSPCAEITAGAAVSEISGPFSTEDVANSNCVPAQSLSEPTL 431

RESULT 8
 AAW61362
 ID AAW61362 standard; Protein; 518 AA.
 AC AAW61362;
 DT 25-SEP-1998 (first entry)
 DE Aspartic proteinase Aspl.
 KW Aspl; Aspartic proteinase; Alzheimer's disease; cancer; melanoma.
 XX Homo sapiens.
 OS Homo sapiens.
 XX EP848062-A2.
 PN 17-JUN-1998.
 PD 01-DEC-1997; 97EP-0309648.
 PF 14-DEC-1996; 96GB-0026022.
 PR (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PI Chapman CG, Evans JR, Powell DJ, Southan C;
 XX WPI; 1998-314477/28.
 DR N-PSDB; AAV27962.
 PT New isolated polynucleotide encodes Aspartic protease polypeptide -
 used to diagnosis, treat and vaccinate against Alzheimer's disease,
 cancer and melanoma

XX Claim 11, Page 7, 19pp; English.
 XX The human ASP1 protein is structurally related to other proteins of the
 CC Aspartic proteinase family. ASP 1 polypeptides and polynucleotides can
 CC be used to diagnosis, treat and vaccinate against Alzheimer's disease,
 CC cancer and melanoma.
 XX
 SQ Sequence 518 AA;

Query Match 100.0%; Score 406; DB 19; Length 518;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALEPPLASPAAGANFLAVNDLQSGSGRYLEMLIGTTPQKQLIVDTGSSNFAVAGTP 60
 Db 63 ALEPPLASPAAGANFLAVNDLQSGSGRYLEMLIGTTPQKQLIVDTGSSNFAVAGTP 122
 QY 61 HSYIDTYDTERSSSTYRSKGFDTVTKYTGSGWTGFGEDLVTPKGFNTSFLVNIAITFE 120
 Db 123 HSYIDTYDTERSSSTYRSKGFDTVTKYTGSGWTGFGEDLVTPKGFNTSFLVNIAITFE 182
 QY 121 SENFPLPGIKKNGILGLAVATLAKSSLETFEDSLVQANIPNVFSQMCGAGLPVAGS 180
 Db 183 SENFPLPGIKKNGILGLAVATLAKSSLETFEDSLVQANIPNVFSQMCGAGLPVAGS 242
 QY 181 GTNGSLVGLGIEPSLYKGDIMWYPIKEWYQIILKLEIGGSLINDCREYNADKAIY 240
 Db 243 GTNGSLVGLGIEPSLYKGDIMWYPIKEWYQIILKLEIGGSLINDCREYNADKAIY 302
 QY 241 DSGTTLRLPKQKVDPAVEAVARASLIPEFSDGFMTGSQLACWNTSETPMSYFPKISITL 300
 Db 303 DSGTTLRLPKQKVDPAVEAVARASLIPEFSDGFMTGSQLACWNTSETPMSYFPKISITL 362
 QY 301 RDEMSRSFRITLIPOLYIOPMGMGLNVECYRFGISPTALVIGATVMGFIYTFDRA 360
 Db 363 RDEMSRSFRITLIPOLYIOPMGMGLNVECYRFGISPTALVIGATVMGFIYTFDRA 422
 QY 361 QKRVGFAPCAEITAGAVSEISGFSTEDVANSVCVPAQSISEPTIL 406
 Db 423 QKRVGFAPCAEITAGAVSEISGFSTEDVANSVCVPAQSISEPTIL 468

RESULT 9
 ID AAY41714 standard; Protein; 518 AA.
 XX AAY41714;

DT 07-DEC-1999 (first entry)
 XX
 DE Human PRO852 protein sequence.

KM Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
 KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
 XX secreted protein; transmembrane protein.

OS Homo sapiens.
 XX
 XX W09946281-A2.

PD 16-SEP-1999.

PF 08-MAR-1999; 99WO-US05028.

PR 10-MAR-1998; 98US-0077450.

PR 11-MAR-1998; 98US-0077632.

PR 11-MAR-1998; 98US-0077641.

PR 12-MAR-1998; 98US-0077649.

PR 13-MAR-1998; 98US-0077791.

PR 17-MAR-1998; 98US-0078004.

PR 20-MAR-1998; 98US-0040220.

PR 20-MAR-1998; 98US-0078910.
 PR 20-MAR-1998; 98US-0078936.
 PR 25-MAR-1998; 98US-0078939.
 PR 26-MAR-1998; 98US-0079294.
 PR 27-MAR-1998; 98US-0079656.
 PR 27-MAR-1998; 98US-0079663.
 PR 27-MAR-1998; 98US-0079664.
 PR 27-MAR-1998; 98US-0079689.
 PR 27-MAR-1998; 98US-0079728.
 PR 30-MAR-1998; 98US-0079786.
 PR 30-MAR-1998; 98US-0079920.
 PR 30-MAR-1998; 98US-0079923.
 PR 31-MAR-1998; 98US-0080105.
 PR 31-MAR-1998; 98US-0080107.
 PR 31-MAR-1998; 98US-0080165.
 PR 01-APR-1998; 98US-0080194.
 PR 01-APR-1998; 98US-0080237.
 PR 01-APR-1998; 98US-0080328.
 PR 01-APR-1998; 98US-0080333.
 PR 01-APR-1998; 98US-0080334.
 PR 08-APR-1998; 98US-0081049.
 PR 08-APR-1998; 98US-0081070.
 PR 08-APR-1998; 98US-0081071.
 PR 09-APR-1998; 98US-0081195.
 PR 09-APR-1998; 98US-0081203.
 PR 09-APR-1998; 98US-0081229.
 PR 15-APR-1998; 98US-0081817.
 PR 15-APR-1998; 98US-0081838.
 PR 15-APR-1998; 98US-0081952.
 PR 15-APR-1998; 98US-0081955.
 PR 21-APR-1998; 98US-0082568.
 PR 21-APR-1998; 98US-0082569.
 PR 22-APR-1998; 98US-0082700.
 PR 22-APR-1998; 98US-0082704.
 PR 22-APR-1998; 98US-0082804.
 PR 23-APR-1998; 98US-0082767.
 PR 23-APR-1998; 98US-0082796.
 PR 27-APR-1998; 98US-0083336.
 PR 28-APR-1998; 98US-0083332.
 PR 29-APR-1998; 98US-0083382.
 PR 29-APR-1998; 98US-0083495.
 PR 29-APR-1998; 98US-0083496.
 PR 29-APR-1998; 98US-0083499.
 PR 29-APR-1998; 98US-0083500.
 PR 29-APR-1998; 98US-0083545.
 PR 29-APR-1998; 98US-0083554.
 PR 29-APR-1998; 98US-0083558.
 PR 29-APR-1998; 98US-0083559.
 PR 30-APR-1998; 98US-0083742.
 PR 05-MAY-1998; 98US-0084366.
 PR 05-MAY-1998; 98US-0084414.
 PR 06-MAY-1998; 98US-0084441.
 PR 07-MAY-1998; 98US-0084598.
 PR 07-MAY-1998; 98US-0084600.
 PR 07-MAY-1998; 98US-0084627.
 PR 07-MAY-1998; 98US-0084637.
 PR 07-MAY-1998; 98US-0084639.
 PR 07-MAY-1998; 98US-0084640.
 PR 07-MAY-1998; 98US-0084643.
 PR 13-MAY-1998; 98US-0085313.
 PR 13-MAY-1998; 98US-0085318.
 PR 13-MAY-1998; 98US-0085339.
 PR 15-MAY-1998; 98US-0085573.
 PR 15-MAY-1998; 98US-0085579.
 PR 15-MAY-1998; 98US-0085580.
 PR 15-MAY-1998; 98US-0085582.
 PR 15-MAY-1998; 98US-0085689.
 PR 15-MAY-1998; 98US-0085697.
 PR 15-MAY-1998; 98US-0085700.
 PR 15-MAY-1998; 98US-0085704.
 PR 18-MAY-1998; 98US-0086023.
 PR 22-MAY-1998; 98US-0086392.
 PR 22-MAY-1998; 98US-0086414.

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PR 22-MAY-1998; 98US-0086430.
PR 22-MAY-1998; 98US-0086486.
PR 28-MAY-1998; 98US-0087098.
PR 28-MAY-1998; 98US-0087106.
PR 28-MAY-1998; 98US-0087208.
PR 30-JUL-1998; 98US-0094651.
PR 11-SEP-1998; 98US-0100038.
XX
PA (GETH) GENENTECH INC.
XX
PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX WPI; 1999-551358/46.
DR N-PSDB; AA234056.
XX
XX New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders -
XX
XX Claim 12; Fig 73; 530pp; English.
XX
XX The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as
CC sources of probes, primers, for chromosome mapping, and for generation
CC of antisense sequences. They can also be used to create transgenic
CC animals. The proteins can be used to treat a variety of diseases and
CC disorders, depending on their function. Diseases that may be treated
CC include blood coagulation disorders, cancers and cellular adhesion
CC disorders. They may also be used to raise antibodies. AA33891 to
CC AA34338, and AA41685 to AA41774 represent polynucleotide and
CC polypeptide sequence given in the exemplification of the present
CC invention.
XX
SQ Sequence 518 AA;
Query Match 100.0%; Score 406; DB 20; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALEPLASPAAGANFLAVNDLQDSDGSGRYLEMLIGTPPOKQILVDTGSSNFAVAGTP 60
DB 63 ALEPLASPAAGANFLAVNDLQDSDGSGRYLEMLIGTPPOKQILVDTGSSNFAVAGTP 122
QY 61 HSYIDTYEDTERSSSTYRSKGFVDVTKYTOGSMTFVGEEDLVITIPKGFNTSFLVNIATIFE 120
DB 123 HSYIDTYEDTERSSSTYRSKGFVDVTKYTOGSMTFVGEEDLVITIPKGFNTSFLVNIATIFE 182
QY 121 SENFPLPGIKWNGILGLAVATLAKPSSSLETFPDSLVTOANI PNVFSSMOMCGAGLPVAGS 180
DB 183 SENFPLPGIKWNGILGLAVATLAKPSSSLETFPDSLVTOANI PNVFSSMOMCGAGLPVAGS 242
QY 181 GNGGSLVVGGEISLKYGDWYTPPIKEWYQOIEILKLEIGGOSLNDCEYNAADKAIY 240
DB 243 GNGGSLVVGGEISLKYGDWYTPPIKEWYQOIEILKLEIGGOSLNDCEYNAADKAIY 302
QY 241 DSGTTLRLPQKVPDAVVEAVARASLIPFSDGFWTGSOLACWNSSETPMWSYFPKISITL 300
DB 303 DSGTTLRLPQKVPDAVVEAVARASLIPFSDGFWTGSOLACWNSSETPMWSYFPKISITL 362
QY 301 RDENSSRSFRITILPOLYIQPMGAGLNEYCYRFGISPTNALVI GATVMEGFYIIFDRA 360
DB 363 RDENSSRSFRITILPOLYIQPMGAGLNEYCYRFGISPTNALVI GATVMEGFYIIFDRA 422
QY 361 OKRVGFASPCAETAGAVSEISGPFSTEDVANSNCVPAQSISEPTL 406
DB 423 OKRVGFASPCAETAGAVSEISGPFSTEDVANSNCVPAQSISEPTL 468

XX
DT 20-SEP-1999 (first entry)
XX
XX Human CSP56, aspartyl-type protease, protein sequence.
DE
XX Metastatic marker protein; human, cancer metastasis; breast cancer;
KW colon cancer; diagnosis; therapy; tumour; metastatic potential;
KW CSP56; aspartyl-type protease.
XX
OS Homo sapiens.
XX
XX MO9934004-A2
XX
PD 08-JUL-1999.
XX
XX 24-DEC-1998; 98WO-US27608.
XX
XX 31-DEC-1997; 97US-0070112.
XX
XX (CHIR) CHIRON CORP.
XX
XX Gliese K, Xin H;
XX
XX WPI; 1999-430248/36.
DR N-PSDB; AAX84708.
XX
XX New polynucleotides associated with cancer metastasis
PS
XX Claim 4; Page 78-80; 80pp; English.
XX
XX This sequence represents a polypeptide of the invention, and is
CC an aspartyl-type protease, designated CSP56. The polynucleotides (PNs) of
CC the invention encode metastatic marker protein variants. The PNs and
CC polypeptides can be used as markers for cancer metastasis. The products
CC can be used for identifying metastatic tissue or metastatic potential of
CC a tissue, e.g. breast or colon tissue. They can also be used for
CC screening test compounds for the ability to suppress the metastatic
CC potential of a tumour. The products can be used for developing products
CC for the therapy of cancers, particularly breast or colon cancer.
XX
SQ Sequence 518 AA;
Query Match 100.0%; Score 406; DB 20; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALEPLASPAAGANFLAVNDLQDSDGSGRYLEMLIGTPPOKQILVDTGSSNFAVAGTP 60
DB 63 ALEPLASPAAGANFLAVNDLQDSDGSGRYLEMLIGTPPOKQILVDTGSSNFAVAGTP 122
QY 61 HSYIDTYEDTERSSSTYRSKGFVDVTKYTOGSMTFVGEEDLVITIPKGFNTSFLVNIATIFE 120
DB 123 HSYIDTYEDTERSSSTYRSKGFVDVTKYTOGSMTFVGEEDLVITIPKGFNTSFLVNIATIFE 182
QY 121 SENFPLPGIKWNGILGLAVATLAKPSSSLETFPDSLVTOANI PNVFSSMOMCGAGLPVAGS 180
DB 183 SENFPLPGIKWNGILGLAVATLAKPSSSLETFPDSLVTOANI PNVFSSMOMCGAGLPVAGS 242
QY 181 GNGGSLVVGGEISLKYGDWYTPPIKEWYQOIEILKLEIGGOSLNDCEYNAADKAIY 240
DB 243 GNGGSLVVGGEISLKYGDWYTPPIKEWYQOIEILKLEIGGOSLNDCEYNAADKAIY 302
QY 241 DSGTTLRLPQKVPDAVVEAVARASLIPFSDGFWTGSOLACWNSSETPMWSYFPKISITL 300
DB 303 DSGTTLRLPQKVPDAVVEAVARASLIPFSDGFWTGSOLACWNSSETPMWSYFPKISITL 362
QY 301 RDENSSRSFRITILPOLYIQPMGAGLNEYCYRFGISPTNALVI GATVMEGFYIIFDRA 360
DB 363 RDENSSRSFRITILPOLYIQPMGAGLNEYCYRFGISPTNALVI GATVMEGFYIIFDRA 422
QY 361 OKRVGFASPCAETAGAVSEISGPFSTEDVANSNCVPAQSISEPTL 406
DB 423 OKRVGFASPCAETAGAVSEISGPFSTEDVANSNCVPAQSISEPTL 468

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Team Leader Sampler Name: _____ Team: # _____

Remark: _____

RESULT 11
 ID AAY13799 standard; Protein; 518 AA.
 XX AAY13799;
 AC AAY13799;
 XX 21-SEP-1999 (first entry)
 DT 21-SEP-1999 (first entry)
 XX Human aspartyl protease, CSP56.
 DE Human aspartyl protease, CSP56.
 XX
 KM CSP56; human; aspartyl protease; diagnosis; neoplasia; tumour;
 KW breast tumour; colon tumour.
 XX Homo sapiens.
 OS Homo sapiens.
 XX
 PN WO9933963-A1.
 XX
 PD 08-JUL-1999.
 XX
 PF 14-DEC-1998; 98WO-US26547.
 XX
 PR 31-DEC-1997; 97US-0070112.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PI Glese KW, Xin H;
 XX
 PT WPI; 1999-430240/36.
 DR N-PSDB; AAX89297.
 XX
 PT Human CSP56 protein for diagnosis of neoplasia
 PS
 PS Claim 2; Fig 2A; 51pp; English.
 CC This represents a human CSP56 protein, a novel aspartyl protease. The
 CC CSP56 protein can be used in methods for diagnosing neoplasia, for
 CC determining the metastatic potential of a tumour, and for screening test
 CC compounds for the ability to suppress the metastatic potential of a
 CC tumour. The tumours are preferably from breast or colon.
 CC
 XX
 SQ Sequence 518 AA;
 Query Match 100.0%; Score 406; DB 20; Length 518;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALEPALSPAGANFLAVNDVLDGDSGRGYIEMLTGTPPKQLVDTGSSNFAVAGTP 60
 DB 63 ALEPALSPAGANFLAVNDVLDGDSGRGYIEMLTGTPPKQLVDTGSSNFAVAGTP 122
 QY 61 HSYIDTYDTERSSYTRKSGDVYTKYQGSWTFVGEDLVTPKGFMTSLVNIATIFE 120
 DB 123 HSYIDTYDTERSSYTRKSGDVYTKYQGSWTFVGEDLVTPKGFMTSLVNIATIFE 182
 QY 121 SENFELPQIKKNGILGLAVATLAKPSSLETFEFDLVTOANIPNVFSMQMGAGLPVAGS 180
 DB 183 SENFELPQIKKNGILGLAVATLAKPSSLETFEFDLVTOANIPNVFSMQMGAGLPVAGS 242
 QY 181 GTNGSGLVGGIEPSLYKGDIMWYPIKEWYQIIBLKLEIGQGLNDCEBYNADKAIY 240
 DB 243 GTNGSGLVGGIEPSLYKGDIMWYPIKEWYQIIBLKLEIGQGLNDCEBYNADKAIY 302
 QY 241 DSGTTLRLPKVPAVVEAVARASLIPEFSDGFWTGSOLACWNTSETPWGFPIKISTYL 300
 DB 303 DSGTTLRLPKVPAVVEAVARASLIPEFSDGFWTGSOLACWNTSETPWGFPIKISTYL 362
 QY 301 RDNSSRSRFRITILPOLYIQPMWAGALNVECYRFGISPTNALVIGATWMEGFYIFDRA 360
 DB 363 RDNSSRSRFRITILPOLYIQPMWAGALNVECYRFGISPTNALVIGATWMEGFYIFDRA 422
 QY 361 QKRVGFASPCAETAGAAVSEISGPFSTEDVANSNCVPAQSLSEPTL 406

Db 423 QKRVGFASPCAETAGAAVSEISGPFSTEDVANSNCVPAQSLSEPTL 468
 RESULT 12
 ID AAB44270 standard; Protein; 518 AA.
 XX AAB44270;
 AC AAB44270;
 XX 08-FEB-2001 (first entry)
 DT 08-FEB-2001 (first entry)
 XX Human PRO852 (UNQ418) protein sequence SEQ ID NO:196.
 DE Human PRO852 (UNQ418) protein sequence SEQ ID NO:196.
 XX
 KW Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
 KW expressed sequence tag; detection; cancer.
 XX
 OS Homo sapiens.
 OS Homo sapiens.
 XX
 PN WO200053756-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 18-FEB-2000; 2000WO-US04341.
 XX
 PR 08-MAR-1999; 99WO-US05028.
 PR 12-MAR-1999; 99US-0123957.
 PR 29-MAR-1999; 99US-0126773.
 PR 21-APR-1999; 99US-0130232.
 PR 28-APR-1999; 99US-0131445.
 PR 14-MAY-1999; 99US-0134287.
 PR 23-JUN-1999; 99US-0141037.
 PR 26-JUL-1999; 99US-0145698.
 PR 29-OCT-1999; 99US-0162506.
 PR 30-NOV-1999; 99WO-US28313.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28565.
 PR 16-DEC-1999; 99WO-US30095.
 PR 30-DEC-1999; 99WO-US31243.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 XX
 XX (GETH) GENENTECH INC.
 PA
 PI Ashkenazi AJ, Baker KP, Botstein D, Deenoyers L, Eaton DL;
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerltzen ME;
 PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
 PI Kijavini IU, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
 PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
 XX
 WPI; 2000-611443/58.
 DR N-PSDB; AAC78500.
 XX
 PT Novel PRO polypeptides and polynucleotides used in detection methods,
 PT to target bioactive molecules to specific cells, and to modulate
 PT cellular activities -
 PS
 PS Claim 12; Fig 73; 636pp; English.
 XX
 XX AACT8458 to AACT8599 represent polynucleotide and EST (expressed
 CC sequence tag) sequences which encode secreted or transmembrane PRO
 CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic
 CC activity. The polynucleotides and polypeptides can be used for detecting
 CC the presence of PRO polypeptides in samples, for linking bioactive
 CC molecules to cells and for modulating biological activities of cells,
 CC using the polypeptides for specific targeting. The polypeptide targeting
 CC can be used to kill the target cells, e.g. for the treatment of cancers.
 CC The polypeptide pairs provide specific targeting of bioactive molecules
 CC to cells. AACT8600 to AACT8897 represent PCR primers and probes used in
 CC the isolation of the PRO polynucleotide sequences.

Seq	Sequence	518 AA;	100.0%;	Score 406;	DB 21;	Length 518;
	Query Match		100.0%;			
	Best Local Similarity		100.0%;	Pred. No. 0;		
	Matches 406; Conservative		0;	Mismatches 0;	Indels 0;	Gaps 0
QY	1 ALEPLASPAQANFLAMWDNLQGDGSGRYYLEMLGTPPQKQLIIVDGSISNFAVAGTP	60				
Db	63 ALEPLASPAQANFLAMWDNLQGDGSGRYYLEMLGTPPQKQLIIVDGSISNFAVAGTP	122				
QY	61 HSYIDTTPDTESSSTRYSKGFVDVYKYTQGSMTGPFGEGLVITPKGFNISFLVNTATIRE	120				
Db	123 HSYIDTTPDTESSSTRYSKGFVDVYKYTQGSMTGPFGEGLVITPKGFNISFLVNTATIRE	182				
QY	121 SENFPLPGIKMNGIIGLAATLAKPSSSLETFEFDLSVLTQANIPNVSQMGCGALPVAQS	180				
Db	183 SENFPLPGIKMNGIIGLAATLAKPSSSLETFEFDLSVLTQANIPNVSQMGCGALPVAQS	242				
QY	181 GTNGSLVIGIIEPSLYKGDIVWTPPIKEWYVOIEILKLEIGQSLINDCREYNADKAV	240				
Db	243 GTNGSLVIGIIEPSLYKGDIVWTPPIKEWYVOIEILKLEIGQSLINDCREYNADKAV	302				
QY	241 DSGTLLRLRPQVPAVVAVVAVARASLIPEPSQGFMTGSQLACTNSETPMSPYPKSIYL	300				
Db	303 DSGTLLRLRPQVPAVVAVVAVARASLIPEPSQGFMTGSQLACTNSETPMSPYPKSIYL	362				
QY	301 RDENSSRSFRITILPOLYIQPMWGAGLNEYCRFGISPSTNALVIGATVMEGFYVIFDRA	360				
Db	363 RDENSSRSFRITILPOLYIQPMWGAGLNEYCRFGISPSTNALVIGATVMEGFYVIFDRA	422				
QY	361 QKRVPFAASPCAEIAGAAVSEISGPSTEDVANSNCVPAQSLSEPLL	406				
Db	423 QKRVPFAASPCAEIAGAAVSEISGPSTEDVANSNCVPAQSLSEPLL	468				

CC	This sequence represents the human aspartyl protease amino acid sequence
XX	The invention relates to a protease capable of cleaving the beta
PS	-
PT	Claim 54; Fig 1; 183pp; English.
XX	New enzyme designated human aspartase useful in research into
XX	Alzheimer's Disease is capable of cleaving amyloid protein precursor at
XX	the beta secretase site to produce amyloid beta peptide -
XX	
XX	DR N-PSDB; AAA15661.
XX	DR MPI; 2000-303209/26.
XX	Gurney ME, Bienkowski MJ, Heintikson RL, Parodi LA, Yan R;
PI	(PHAA) PHARMACIA & UPJOHN CO.
PA	24-SEP-1998; 98US-0101594.
XX	
XX	PR 23-SEP-1999; 99WO-US20881.
PE	
XX	PD 30-MAR-2000.
PN	WO200017369-A2.
XX	
OS	Homo sapiens.
XX	
KM	Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 1;
KW	Alzheimer's disease; beta secretase site.
XX	
DE	Human aspartyl protease 1 (Asp1) amino acid sequence.
XX	
DT	03-AUG-2000 (first entry)
XX	
AC	AAV89424;
XX	
ID	AAV89424 standard; Protein; 518 AA.
RESULT 13	
AAV89424	

secretase site of amyloid precursor protein (APP). The protease contains a sequence encoding the amino acid sequence DFG and a sequence encoding DSG or DFG separated by 100-300 amino acids. When mutated the APP gene causes an autosomal dominant form of Alzheimer's disease. APP localises to the cell surface membrane and have a single C-terminal transmembrane domain. Proteolytic processing of APP produces the amyloid beta protein, which is possibly very important in Alzheimer's disease. The invention includes a nucleotide sequence encoding the protease, a vector containing the nucleotide sequence, and a cell line comprising the vector. Methods for screening for inhibitors of beta secretase activity are also given in the invention. The human aspartase protein and nucleotide sequences and the methods for identifying inhibitors of the protease, are useful in the treatment of and research in to Alzheimer's disease.

	Query Match	Similarity	100.0%	Score	406	DB 21	Length	518
	Best Local	Similarity	100.0%	Pred.	No.	0		
	Matches	406	Conservative	0	Mismatches	0	Indels	0
							Gaps	0
Qy	1	ALEPALASPA	ANFLAVNDNLQGD	SGRYYLEMLIGTP	PKQLI	LVDTGSSN	PAVAGTP	60
Db	63	ALEPALASPA	ANFLAVNDNLQGD	SGRYYLEMLIGTP	PKQLI	LVDTGSSN	PAVAGTP	122
Qy	61	HSYIDYVDT	RRSSSTYRSKGF	DVYKTYQSG	MTGVS	GVGDVLTIP	IKGFNTSL	120
Db	123	HSYIDYVDT	RRSSSTYRSKGF	DVYKTYQSG	MTGVS	GVGDVLTIP	IKGFNTSL	182
Qy	121	SENFPLP	CIKKNNGILGL	VAATLAKP	SSLEFP	PSDLVYQANI	PNVFS	180
Db	183	SENFPLP	CIKKNNGILGL	VAATLAKP	SSLEFP	PSDLVYQANI	PNVFS	242
Qy	181	GTNGGSL	VLGGIEB	SLYKGD	IWYTP	IKKEWYQ	IEILKLE	240
Db	243	GTNGGSL	VLGGIEB	SLYKGD	IWYTP	IKKEWYQ	IEILKLE	302
Qy	241	DSGTLT	LTPKQV	PAVVEAVAR	ASLIEP	SFDSG	FWTSQ	300
Db	303	DSGTLT	LTPKQV	PAVVEAVAR	ASLIEP	SFDSG	FWTSQ	362
Qy	301	RDENSSRS	FRITILLPOL	YIQPM	GAGLNYECY	RFGIS	PSNAL	360
Db	363	RDENSSRS	FRITILLPOL	YIQPM	GAGLNYECY	RFGIS	PSNAL	422
Qy	361	QKRV	EFAASPCAE	IAGA	AVSEISG	FSF	EDV	406
Db	423	QKRV	EFAASPCAE	IAGA	AVSEISG	FSF	EDV	468

Accession	Protein	Gene	Organism	Location/Qualifiers
AAE10628	AAE10628 standard; Protein; 518 AA.			
FT	Domain			1..20
FT	Protein			/label= Signal_peptide
FT				21..518
FT				/note= "Mature human aspartyl protease 1"
FT				469..492
FT				/label= Transmembrane_domain


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XX  GB2357767-A.
XX  |
XX  04-JUL-2001.
XX  |
XX  22-SEP-2000; 2000GB-0023315.
XX  |
XX  23-SEP-1999; 99US-0155493.
XX  23-SEP-1999; 99US-0404133.
XX  23-SEP-1999; 99WO-US20881.
XX  13-OCT-1999; 99US-0416901.
XX  06-DEC-1999; 99US-0169232.
XX  (PRAA ) PHARMACIA & UPJOHN CO.
XX  |
XX  Bienkowski MJ, Gurney M;
XX  WPI: 2001-444208/48.
XX  N-PSDB; AAD17864.
XX  |
XX  Polypeptide comprising fragments of human aspartyl protease with
XX  amyloid precursor protein processing activity and alpha-secretase
XX  PT activity, for identifying modulators useful in treating Alzheimer's
XX  PT disease -
XX  |
XX  Claim 36; Fig 1; 187pp; English.
XX  |
XX  The patent discloses human aspartyl protease 1 (hu-Asp1) or modified
XX  CC Asp1 proteins which lack transmembrane domain or amino terminal
XX  CC domain or cytoplasmic domain and retains alpha-secretase activity
XX  CC and amyloid protein precursor (APP) processing activity. The proteins
XX  CC of the invention are useful for assaying hu-Asp1 alpha-secretase
XX  CC activity, which in turn is useful for identifying modulators of
XX  CC hu-Asp1 alpha-secretase activity, where modulators that increase
XX  CC hu-Asp1 alpha-secretase activity are useful for treating Alzheimer's
XX  CC disease (AD) which causes progressive dementia with consequent
XX  CC formation of amyloid plaques, neurofibrillary tangles, gliosis and
XX  CC neuronal loss. Hu-Asp1 protease substrate is useful for assaying
XX  CC hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein with
XX  CC the substrate under acidic conditions and determining the level of
XX  CC hu-Asp1 proteolytic activity. The present sequence is Asp1 protein
XX  CC from human. Asp1 gene is localised on chromosome 21.
XX  |
XX  Sequence 518 AA;
XX  |
XX  Query Match 100.0%; Score 406; DB 22; Length 518;
XX  Best Local Similarity 100.0%; Pred. No. 0;
XX  Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX  |
XX  1 ALEPALASPAGANFLAMVDNLQDSDGRGYLEMLIGTPPOKLQILVDTGSSNFAVAGTP 60
XX  |
XX  63 ALEPALASPAGANFLAMVDNLQDSDGRGYLEMLIGTPPOKLQILVDTGSSNFAVAGTP 122
XX  |
XX  61 HSYIDTYDTERSSSTYRSKGFVDVTVKYTGSGWTGFGVEDLVITPKGFMTSLVNIATIFE 120
XX  |
XX  123 HSYIDTYDTERSSSTYRSKGFVDVTVKYTGSGWTGFGVEDLVITPKGFMTSLVNIATIFE 182
XX  |
XX  121 SENFPLPQIKXNGILGLAVATLAKSSSLFFPDSLVNQANIPNVFSMQCAGIPVAGS 180
XX  |
XX  183 SENFPLPQIKXNGILGLAVATLAKSSSLFFPDSLVNQANIPNVFSMQCAGIPVAGS 242
XX  |
XX  181 GTNGGSLVAGIEPSLVKGDIVYTPIKEWYQIILKLEIGQSLNDCREYNADKAIIV 240
XX  |
XX  243 GTNGGSLVAGIEPSLVKGDIVYTPIKEWYQIILKLEIGQSLNDCREYNADKAIIV 302
XX  |
XX  241 DSGTTLRLPQKVPDVAEVAARASLIPEFSDGFMTGSQLACWTNSETPMWYFKISITL 300
XX  |
XX  303 DSGTTLRLPQKVPDVAEVAARASLIPEFSDGFMTGSQLACWTNSETPMWYFKISITL 362
XX  |
XX  301 RDENSRSFRITITLPOLYIQPMWGAGLVYECRRGISPTNALVIGATVMEGFYIIPDRA 360
XX  |
XX  363 RDENSRSFRITITLPOLYIQPMWGAGLVYECRRGISPTNALVIGATVMEGFYIIPDRA 422

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XX  361 QKRVGFASPQAEIAGAAVSEISGPFSTEDVANSNCVPAQSIUSEPIL 406
XX  |
XX  423 QKRVGFASPQAEIAGAAVSEISGPFSTEDVANSNCVPAQSIUSEPIL 468
XX  |
XX  RESULT 15
XX  ID AAE10656 standard; Protein; 518 AA.
XX  AC AAE10656;
XX  DT 10-DEC-2001 (first entry)
XX  |
XX  Human-Asp 1 protein lacking TM domain and containing (His)6 tag.
XX  |
XX  Human; aspartyl protease 1; Asp1; amyloid precursor protein; APP;
XX  KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
XX  KM amyloid plaque; neuronal loss; proteolytic; neurotrophic; neuroprotective.
XX  |
XX  Homo sapiens.
XX  OS Synthetic.
XX  |
XX  GB2357767-A.
XX  |
XX  04-JUL-2001.
XX  |
XX  22-SEP-2000; 2000GB-0023315.
XX  |
XX  23-SEP-1999; 99US-0155493.
XX  23-SEP-1999; 99US-0404133.
XX  23-SEP-1999; 99WO-US20881.
XX  13-OCT-1999; 99US-0416901.
XX  06-DEC-1999; 99US-0169232.
XX  |
XX  (PRAA ) PHARMACIA & UPJOHN CO.
XX  |
XX  Bienkowski MJ, Gurney M;
XX  WPI: 2001-444208/48.
XX  |
XX  Polypeptide comprising fragments of human aspartyl protease with
XX  PT amyloid precursor protein processing activity and alpha-secretase
XX  PT activity, for identifying modulators useful in treating Alzheimer's
XX  PT disease -
XX  |
XX  Example 14; Page 155-156; 187pp; English.
XX  |
XX  The patent discloses human aspartyl protease 1 (hu-Asp1) or modified
XX  CC Asp1 proteins which lack transmembrane domain or amino terminal
XX  CC domain or cytoplasmic domain and retains alpha-secretase activity
XX  CC and amyloid protein precursor (APP) processing activity. The proteins
XX  CC of the invention are useful for assaying hu-Asp1 alpha-secretase
XX  CC activity, which in turn is useful for identifying modulators of
XX  CC hu-Asp1 alpha-secretase activity, where modulators that increase
XX  CC hu-Asp1 alpha-secretase activity are useful for treating Alzheimer's
XX  CC disease (AD) which causes progressive dementia with consequent
XX  CC formation of amyloid plaques, neurofibrillary tangles, gliosis and
XX  CC neuronal loss. Hu-Asp1 protease substrate is useful for assaying
XX  CC hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein with
XX  CC the substrate under acidic conditions and determining the level of
XX  CC hu-Asp1 proteolytic activity. The present sequence is human Asp 1
XX  CC protein lacking a transmembrane (TM) domain and containing (His)6
XX  CC tag. This sequence is generated from human Asp 1 protein by the
XX  CC deletion of its C-terminal TM domain and addition of hexa-histidine
XX  CC tag at its C-terminus.
XX  |
XX  Sequence 518 AA;
XX  |
XX  Query Match 100.0%; Score 406; DB 22; Length 518;
XX  Best Local Similarity 100.0%; Pred. No. 0;
XX  Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX  |
XX  1 ALEPALASPAGANFLAMVDNLQDSDGRGYLEMLIGTPPOKLQILVDTGSSNFAVAGTP 60

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```
Db 63 ALEPALASPAGANFLAMVDNLQGDSSGRGYLHMLIGTPQKLQILVDTGSSNFAVAGTP 122
QY 61 HSYIDTYFDTERSSSTYRSGKGPVYVYKTQGSWTGFVGEDLVTI PKGFNTSPLVNIATIFE 120
Db 123 HSYIDTYFDTERSSSTYRSGKGPVYVYKTQGSWTGFVGEDLVTI PKGFNTSPLVNIATIFE 182
QY 121 SENFPLPGIKWNGILGLAVATLAKPSSLETFFDSLVTQANIPNVFSMQMGAGLPVAGS 180
Db 183 SENFPLPGIKWNGILGLAVATLAKPSSLETFFDSLVTQANIPNVFSMQMGAGLPVAGS 242
QY 181 GTNGSLVLGGIEPSLYKGDIMWTFPIKEWYQIEILKLEIGGSLNLDCREYNADKAIV 240
Db 243 GTNGSLVLGGIEPSLYKGDIMWTFPIKEWYQIEILKLEIGGSLNLDCREYNADKAIV 302
QY 241 DSGITLLRLPQVFDVAVVAVARASLIPEFSDGFMTGSQLACWTNSETPMWSYFPKISITL 300
Db 303 DSGITLLRLPQVFDVAVVAVARASLIPEFSDGFMTGSQLACWTNSETPMWSYFPKISITL 362
QY 301 RDESSRSFRITILPOLYIQPMWAGLNEYECYRFGISPSSTNALVIGATMEGFYVIFDRA 360
Db 363 RDESSRSFRITILPOLYIQPMWAGLNEYECYRFGISPSSTNALVIGATMEGFYVIFDRA 422
QY 361 QKRVGFPAASPCAEIAGAASVSEISGPFSTEDVASNCVPAQSISEPIL 406
Db 423 QKRVGFPAASPCAEIAGAASVSEISGPFSTEDVASNCVPAQSISEPIL 468
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Search completed: April 1, 2003, 11:51:27
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OM protein - protein search, using sw model

Run on: April 1, 2003, 11:50:50 ; Search time 18 Seconds
(without alignments)
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	406	100.0	518	3	US-08-999-723-2
2	406	100.0	518	4	US-09-434-427-2
3	406	100.0	518	4	US-09-548-372D-2
4	406	100.0	518	4	US-09-548-367D-2
5	59	14.5	514	4	US-09-717-432-2
6	59	14.5	514	4	US-09-912-484-2
7	12	3.0	425	4	US-09-548-372D-28
8	12	3.0	425	4	US-09-548-367D-28
9	12	3.0	428	4	US-09-548-372D-51
10	12	3.0	428	4	US-09-548-367D-51
11	12	3.0	433	4	US-09-548-372D-26
12	12	3.0	433	4	US-09-548-367D-26
13	12	3.0	434	4	US-09-548-372D-53
14	12	3.0	434	4	US-09-548-367D-53
15	12	3.0	446	4	US-09-548-372D-22
16	12	3.0	446	4	US-09-548-367D-22
17	12	3.0	453	4	US-09-548-372D-30
18	12	3.0	453	4	US-09-548-367D-30
19	12	3.0	459	4	US-09-548-372D-24
20	12	3.0	459	4	US-09-548-372D-32
21	12	3.0	459	4	US-09-548-367D-32
22	12	3.0	476	4	US-09-548-372D-6
23	12	3.0	476	4	US-09-548-367D-6
24	12	3.0	476	4	US-09-548-372D-73
25	12	3.0	476	4	US-09-548-367D-73
26	12	3.0	476	4	US-09-548-367D-73
27	12	3.0	501	4	US-09-009-191-2

28	12	3.0	501	4	US-09-713-158-2	Sequence 2, Appli
29	12	3.0	501	4	US-09-548-372D-8	Sequence 4, Appli
30	12	3.0	501	4	US-09-548-372D-8	Sequence 8, Appli
31	12	3.0	501	4	US-09-548-367D-4	Sequence 4, Appli
32	12	3.0	501	4	US-09-548-367D-8	Sequence 8, Appli
33	12	3.0	774	4	US-09-009-191-4	Sequence 4, Appli
34	12	3.0	774	4	US-09-009-191-4	Sequence 4, Appli
35	12	1.7	60	1	US-08-362-739-7	Sequence 7, Appli
36	12	1.7	140	3	US-09-211-631-13	Sequence 13, Appli
37	12	1.7	140	4	US-09-265-628-13	Sequence 11, Appli
38	7	1.7	140	4	US-09-001-141-11	Sequence 11, Appli
39	7	1.7	140	4	US-09-532-803-6	Sequence 6, Appli
40	7	1.7	140	4	US-09-653-403-14	Sequence 14, Appli
41	7	1.7	140	4	US-10-013-784-14	Sequence 14, Appli
42	7	1.7	268	4	US-09-651-556-29	Sequence 29, Appli
43	7	1.7	268	4	US-09-650-855-29	Sequence 29, Appli
44	7	1.7	279	2	US-08-326-886-8	Sequence 8, Appli
45	7	1.7	306	2	US-08-454-196-11	Sequence 11, Appli
46	7	1.7	306	2	US-08-286-819A-33	Sequence 33, Appli
47	7	1.7	306	3	US-08-980-357-33	Sequence 33, Appli
48	7	1.7	320	3	US-09-064-033-11	Sequence 11, Appli
49	7	1.7	354	1	US-08-362-739-2	Sequence 2, Appli
50	7	1.7	363	2	US-08-222-289-2	Sequence 2, Appli
51	7	1.7	363	4	US-08-646-590B-36	Sequence 36, Appli
52	7	1.7	363	4	US-09-412-184-36	Sequence 36, Appli
53	7	1.7	397	3	US-09-079-415-2	Sequence 2, Appli
54	7	1.7	409	1	US-09-640-305-6	Sequence 6, Appli
55	7	1.7	410	1	US-08-360-673-6	Sequence 6, Appli
56	7	1.7	410	1	US-08-088-633-2	Sequence 2, Appli
57	7	1.7	410	1	US-08-245-756-2	Sequence 2, Appli
58	7	1.7	410	1	US-08-441-750-2	Sequence 2, Appli
59	7	1.7	410	2	US-08-441-751-2	Sequence 2, Appli
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61	7	1.7	802	1	US-08-261-465-2	Sequence 2, Appli
62	7	1.7	802	1	US-08-405-254-6	Sequence 6, Appli
63	6	1.5	802	2	US-08-326-286-4	Sequence 4, Appli
64	6	1.5	12	4	US-08-469-260A-446	Sequence 46, App
65	6	1.5	14	4	US-09-369-364A-28	Sequence 28, Appli
66	6	1.5	19	4	US-09-369-364A-24	Sequence 24, Appli
67	6	1.5	21	1	US-08-672-571A-9	Sequence 9, Appli
68	6	1.5	24	2	US-08-480-190-249	Sequence 249, App
69	6	1.5	24	2	US-08-488-379-249	Sequence 249, App
70	6	1.5	24	5	PCT-US93-07545-249	Sequence 249, App
71	6	1.5	29	2	US-07-746-705A-2	Sequence 2, Appli
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73	6	1.5	40	2	US-08-727-688-19	Sequence 19, Appli
74	6	1.5	41	2	US-08-640-847C-39	Sequence 39, Appli
75	6	1.5	43	4	US-09-149-476-524	Sequence 524, App
76	6	1.5	50	4	US-09-586-563C-8	Sequence 8, Appli
77	6	1.5	51	4	US-09-586-562C-8	Sequence 8, Appli
78	6	1.5	55	1	US-08-927-219-49	Sequence 49, Appli
79	6	1.5	55	1	US-08-309-147-10	Sequence 10, Appli
80	6	1.5	55	1	US-08-458-298-10	Sequence 10, Appli
81	6	1.5	59	1	US-08-313-050-16	Sequence 16, Appli
82	6	1.5	60	1	US-08-117-083-20	Sequence 20, Appli
83	6	1.5	68	4	US-09-220-528-50	Sequence 50, Appli
84	6	1.5	73	2	US-08-530-569B-5	Sequence 5, Appli
85	6	1.5	79	4	US-08-817-811-19	Sequence 19, Appli
86	6	1.5	85	7	US-09-220-528-115	Sequence 115, App
87	6	1.5	91	1	US-08-591-498-3	Sequence 3, Appli
88	6	1.5	107	4	US-09-220-528-52	Sequence 52, Appli
89	6	1.5	108	4	US-09-149-476-552	Sequence 552, App
90	6	1.5	117	5	PCT-US96-08730-11	Sequence 11, Appli
91	6	1.5	131	2	US-08-647-860-9	Sequence 9, Appli
92	6	1.5	136	4	US-08-905-223-287	Sequence 287, App
93	6	1.5	137	4	US-09-149-476-350	Sequence 350, App
94	6	1.5	144	4	US-08-858-407A-502	Sequence 502, App
95	6	1.5	173	1	US-09-134-001C-5205	Sequence 5205, Ap
96	6	1.5	173	1	US-08-157-005-8	Sequence 8, Appli
97	6	1.5	173	2	US-08-799-464A-24	Sequence 24, Appli
98	6	1.5	173	4	US-08-747-863-8	Sequence 8, Appli
99	6	1.5	173	4	US-09-565-864-8	Sequence 8, Appli
100	6	1.5	173	5	PCT-US95-09927-24	Sequence 24, Appli
					PCT-US95-10904-24	Sequence 24, Appli

101	6	1.5	174	1	US-08-131-625B-14	Sequence 14, Appl	174	6	1.5	337	3	US-09-116-115-17	Sequence 17, Appl
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103	6	1.5	174	4	US-09-113-750A-41	Sequence 41, Appl	176	6	1.5	358	2	US-08-824-878-3	Sequence 3, Appl
104	6	1.5	174	5	PCT-US95-10927-11	Sequence 11, Appl	177	6	1.5	358	4	US-09-353-688-3	Sequence 3, Appl
105	6	1.5	174	5	PCT-US95-10904-17	Sequence 17, Appl	178	6	1.5	359	1	US-08-700-359-21	Sequence 21, Appl
106	6	1.5	174	5	PCT-US95-10904-43	Sequence 43, Appl	179	6	1.5	373	2	US-08-824-878-1	Sequence 1, Appl
107	6	1.5	174	5	PCT-US95-10904-45	Sequence 45, Appl	180	6	1.5	373	4	US-09-353-688-1	Sequence 1, Appl
108	6	1.5	174	5	PCT-US95-10904-47	Sequence 47, Appl	181	6	1.5	374	4	US-08-821-994-68	Sequence 68, Appl
109	6	1.5	174	5	PCT-US95-10904-49	Sequence 49, Appl	182	6	1.5	377	2	US-08-227-108-17	Sequence 17, Appl
110	6	1.5	174	5	PCT-US95-10904-51	Sequence 51, Appl	183	6	1.5	377	2	US-08-553-3678-4	Sequence 4, Appl
111	6	1.5	175	4	US-08-887-534A-14	Sequence 14, Appl	184	6	1.5	377	2	US-09-073-674-17	Sequence 17, Appl
112	6	1.5	177	4	US-09-263-933-25	Sequence 25, Appl	185	6	1.5	377	4	US-09-295-306-4	Sequence 4, Appl
113	6	1.5	181	4	US-09-220-528-10	Sequence 40, Appl	186	6	1.5	377	4	US-09-734-719-4	Sequence 4, Appl
114	6	1.5	184	2	US-08-737-825-10	Sequence 10, Appl	187	6	1.5	381	2	US-08-667-057-3	Sequence 3, Appl
115	6	1.5	184	3	US-08-741-411-7	Sequence 7, Appl	188	6	1.5	381	2	US-09-128-369-3	Sequence 3, Appl
116	6	1.5	185	3	US-08-984-295-1	Sequence 1, Appl	189	6	1.5	382	4	US-09-542-733-2	Sequence 2, Appl
117	6	1.5	186	3	US-09-149-476-394	Sequence 394, App	190	6	1.5	383	1	US-08-196-8989-4	Sequence 4, Appl
118	6	1.5	186	3	US-08-855-511D-37	Sequence 37, Appl	191	6	1.5	383	2	US-08-760-836-4	Sequence 4, Appl
119	6	1.5	188	4	US-08-855-526B-37	Sequence 37, Appl	192	6	1.5	387	4	US-09-457-302-1	Sequence 1, Appl
120	6	1.5	188	4	US-09-134-001C-3152	Sequence 3152, Ap	193	6	1.5	384	4	US-09-385-928-8	Sequence 8, Appl
121	6	1.5	192	1	US-08-086-428B-64	Sequence 64, Appl	194	6	1.5	395	1	US-08-723-938-3	Sequence 3, Appl
122	6	1.5	192	2	US-08-468-570-64	Sequence 64, Appl	195	6	1.5	395	2	US-09-080-538-3	Sequence 3, Appl
123	6	1.5	192	2	US-08-290-665A-64	Sequence 64, Appl	196	6	1.5	396	1	US-08-208-007A-13	Sequence 9, Appl
124	6	1.5	192	5	PCT-US95-10398-64	Sequence 64, Appl	197	6	1.5	396	4	US-09-032-523-9	Sequence 9, Appl
125	6	1.5	220	4	US-09-220-528-26	Sequence 26, Appl	198	6	1.5	396	4	US-08-915-095A-13	Sequence 13, Appl
126	6	1.5	223	4	US-09-124-238A-34	Sequence 34, Appl	199	6	1.5	396	4	US-08-798-096-13	Sequence 13, Appl
127	6	1.5	223	4	US-09-721-975-34	Sequence 34, Appl	200	6	1.5	396	4	US-08-798-095A-13	Sequence 13, Appl
128	6	1.5	225	1	US-07-991-867B-3	Sequence 3, Appl	201	6	1.5	398	1	US-08-091-519-2	Sequence 2, Appl
129	6	1.5	225	1	US-08-107-755A-3	Sequence 3, Appl	202	6	1.5	398	1	US-08-176-413-5	Sequence 5, Appl
130	6	1.5	225	2	US-08-544-332-3	Sequence 3, Appl	203	6	1.5	398	1	US-08-328-314-2	Sequence 2, Appl
131	6	1.5	225	3	US-09-248-335-40	Sequence 40, Appl	204	6	1.5	398	1	US-08-507-431-2	Sequence 2, Appl
132	6	1.5	225	4	US-08-821-994-49	Sequence 49, Appl	205	6	1.5	398	1	US-08-731-045-2	Sequence 2, Appl
133	6	1.5	225	4	US-09-370-861A-3	Sequence 3, Appl	206	6	1.5	398	1	US-08-442-043A-2	Sequence 2, Appl
134	6	1.5	226	6	5498600-2	Patent No. 5498600	207	6	1.5	398	2	US-08-371-377-17	Sequence 17, Appl
135	6	1.5	230	4	US-08-821-994-50	Sequence 50, Appl	208	6	1.5	398	2	US-08-902-655A-2	Sequence 2, Appl
136	6	1.5	237	4	US-09-220-528-32	Sequence 32, Appl	209	6	1.5	398	3	US-09-116-622-2	Sequence 2, Appl
137	6	1.5	237	4	US-09-227-357-154	Sequence 154, App	210	6	1.5	398	4	US-09-219-377-2	Sequence 2, Appl
138	6	1.5	241	4	US-08-634-475-7	Sequence 7, Appl	211	6	1.5	398	4	US-09-599-661-2	Sequence 2, Appl
139	6	1.5	241	4	US-09-709-791-7	Sequence 7, Appl	212	6	1.5	398	4	US-09-173-151A-26	Sequence 26, Appl
140	6	1.5	241	4	US-09-153-599A-5	Sequence 5, Appl	213	6	1.5	398	4	US-09-347-878-14	Sequence 14, Appl
141	6	1.5	241	6	5175255-2	Patent No. 5175255	214	6	1.5	398	5	PCT-US91-03478-2	Sequence 2, Appl
142	6	1.5	241	6	5175255-8	Patent No. 5175255	215	6	1.5	398	5	PCT-US94-14931-5	Sequence 5, Appl
143	6	1.5	244	1	US-08-910-973-22	Sequence 22, Appl	216	6	1.5	405	5	PCT-US93-11404-2	Sequence 5, Appl
144	6	1.5	244	3	US-09-003-287-6	Sequence 6, Appl	217	6	1.5	408	1	US-07-841-646-7	Sequence 7, Appl
145	6	1.5	244	3	US-09-003-287-8	Sequence 8, Appl	218	6	1.5	408	1	US-07-718-273A-16	Sequence 6, Appl
146	6	1.5	244	4	US-09-518-988-2	Sequence 2, Appl	219	6	1.5	408	1	US-07-901-703-19	Sequence 19, Appl
147	6	1.5	244	4	US-09-499-227-22	Sequence 22, Appl	220	6	1.5	408	1	US-08-149-106-6	Sequence 6, Appl
148	6	1.5	247	1	US-08-324-977-44	Sequence 44, Appl	221	6	1.5	408	1	US-08-147-023-7	Sequence 7, Appl
149	6	1.5	247	2	US-08-384-616-44	Sequence 44, Appl	222	6	1.5	408	1	US-08-298-021-6	Sequence 6, Appl
150	6	1.5	247	2	US-08-904-686A-44	Sequence 44, Appl	223	6	1.5	408	1	US-08-050-132A-4	Sequence 4, Appl
151	6	1.5	247	4	US-09-315-850-44	Sequence 44, Appl	224	6	1.5	408	1	US-08-447-570-7	Sequence 7, Appl
152	6	1.5	247	4	US-09-724-864-49	Sequence 49, Appl	225	6	1.5	408	2	US-08-459-346-11	Sequence 11, Appl
153	6	1.5	258	4	US-09-134-001C-3536	Sequence 3536, Ap	226	6	1.5	408	2	US-08-449-700-7	Sequence 7, Appl
154	6	1.5	258	4	US-09-632-947B-3	Sequence 3, Appl	227	6	1.5	408	2	US-07-989-847-4	Sequence 4, Appl
155	6	1.5	264	4	US-08-469-260A-76	Sequence 76, Appl	228	6	1.5	408	2	US-08-449-699A-7	Sequence 7, Appl
156	6	1.5	266	4	US-08-904-234-3	Sequence 3, Appl	229	6	1.5	408	3	US-08-750-222A-4	Sequence 4, Appl
157	6	1.5	270	4	US-09-403-768-2	Sequence 2, Appl	230	6	1.5	408	3	US-08-815-552B-4	Sequence 4, Appl
158	6	1.5	281	2	US-09-013-881-6	Sequence 6, Appl	231	6	1.5	408	3	US-08-889-419-11	Sequence 11, Appl
159	6	1.5	281	2	US-08-822-701-9	Sequence 9, Appl	232	6	1.5	408	3	US-08-889-419-11	Sequence 11, Appl
160	6	1.5	281	3	US-08-935-855-9	Sequence 9, Appl	233	6	1.5	408	4	US-07-721-847A-6	Sequence 6, Appl
161	6	1.5	282	1	US-08-445-847A-1	Sequence 1, Appl	234	6	1.5	408	4	US-08-469-411-4	Sequence 4, Appl
162	6	1.5	307	4	US-08-858-207A-481	Sequence 481, App	235	6	1.5	408	4	US-08-925-779-6	Sequence 6, Appl
163	6	1.5	314	4	US-09-134-001C-2983	Sequence 2983, Ap	236	6	1.5	408	4	US-08-284-353A-4	Sequence 4, Appl
164	6	1.5	317	2	US-08-864-799-4	Sequence 4, Appl	237	6	1.5	408	4	US-08-462-542-11	Sequence 11, Appl
165	6	1.5	317	2	US-08-864-799-5	Sequence 5, Appl	238	6	1.5	408	5	PCT-US91-03540A-9	Sequence 9, Appl
166	6	1.5	320	1	US-07-613-083B-1	Sequence 1, Appl	239	6	1.5	408	5	PCT-US92-05374A-4	Sequence 4, Appl
167	6	1.5	333	4	US-09-117-710-2	Sequence 2, Appl	240	6	1.5	408	5	PCT-US93-05446-19	Sequence 19, Appl
168	6	1.5	340	1	PCT-US93-08528-49	Sequence 49, Appl	241	6	1.5	408	5	PCT-US93-07189-11	Sequence 11, Appl
169	6	1.5	340	5	US-08-469-260A-608	Sequence 608, App	242	6	1.5	408	6	5166058-6	Patent No. 5166058
170	6	1.5	343	4	US-09-032-523-3	Sequence 3, Appl	243	6	1.5	409	6	5168050-4	Patent No. 5168050
171	6	1.5	349	4	US-09-134-001C-4004	Sequence 4004, Ap	244	6	1.5	412	1	US-08-208-007A-12	Sequence 12, Appl
172	6	1.5	355	4	US-09-330-611-16	Sequence 16, Appl	245	6	1.5	412	4	US-08-974-691-4	Sequence 4, Appl

247	6	1.5	412	4	US-08-915-095A-12	Sequence 12, Appl	320	6	1.5	511	4	US-09-305-681-4	Sequence 4, Appl
248	6	1.5	412	4	US-08-798-096-12	Sequence 12, Appl	321	6	1.5	511	4	US-09-305-681-6	Sequence 6, Appl
249	6	1.5	412	4	US-08-798-095A-12	Sequence 12, Appl	322	6	1.5	525	1	US-08-681-129-2	Sequence 2, Appl
250	6	1.5	416	1	US-08-117-083-62	Sequence 62, Appl	323	6	1.5	525	4	US-09-369-664A-21	Sequence 21, Appl
251	6	1.5	419	4	US-08-974-691-3	Sequence 3, Appl	324	6	1.5	533	1	US-08-368-071-10	Sequence 10, Appl
252	6	1.5	419	4	US-09-705-448-10	Sequence 10, Appl	325	6	1.5	533	1	US-08-458-181-10	Sequence 10, Appl
253	6	1.5	420	4	US-09-008-271A-4	Sequence 4, Appl	326	6	1.5	533	5	PCT-US93-02172-10	Sequence 10, Appl
254	6	1.5	420	4	US-08-974-691-8	Sequence 8, Appl	327	6	1.5	544	1	US-08-264-002-7	Sequence 7, Appl
255	6	1.5	420	4	US-09-705-448-1	Sequence 1, Appl	328	6	1.5	544	4	US-09-457-440B-15	Sequence 15, Appl
256	6	1.5	427	4	US-08-065-844A-2	Sequence 2, Appl	329	6	1.5	555	4	US-09-027-169-2	Sequence 2, Appl
257	6	1.5	429	1	US-08-745-977-4	Sequence 4, Appl	330	6	1.5	559	4	US-09-271-637-4	Sequence 4, Appl
258	6	1.5	429	3	US-09-040-699A-4	Sequence 4, Appl	331	6	1.5	566	4	US-09-134-001C-3431	Sequence 331, Ap
259	6	1.5	431	1	US-08-090-523-2	Sequence 2, Appl	332	6	1.5	572	2	US-09-032-315-7	Sequence 7, Appl
260	6	1.5	431	1	US-08-090-523-4	Sequence 4, Appl	333	6	1.5	572	2	US-08-993-318A-7	Sequence 7, Appl
261	6	1.5	431	1	US-08-398-627-2	Sequence 2, Appl	334	6	1.5	572	4	US-09-399-886-7	Sequence 7, Appl
262	6	1.5	431	1	US-08-398-627-4	Sequence 4, Appl	335	6	1.5	572	4	US-09-396-660-7	Sequence 7, Appl
263	6	1.5	431	1	US-08-406-858-2	Sequence 2, Appl	336	6	1.5	572	4	US-09-576-281-7	Sequence 7, Appl
264	6	1.5	431	1	US-08-406-858-4	Sequence 4, Appl	337	6	1.5	573	4	US-09-134-001C-4813	Sequence 4813, Ap
265	6	1.5	431	1	US-08-469-202-14	Sequence 14, Appl	338	6	1.5	574	1	US-08-354-618-2	Sequence 2, Appl
266	6	1.5	431	2	US-08-484-434C-14	Sequence 14, Appl	339	6	1.5	579	4	US-09-171-710-6	Sequence 4, Appl
267	6	1.5	431	5	PCT-US91-04036-2	Sequence 2, Appl	340	6	1.5	579	4	US-09-171-710-6	Sequence 6, Appl
268	6	1.5	431	5	PCT-US91-04036-2	Sequence 4, Appl	341	6	1.5	581	2	US-08-989-386-7	Sequence 7, Appl
269	6	1.5	431	5	PCT-US94-05275-2	Sequence 2, Appl	342	6	1.5	584	2	US-08-928-692-13	Sequence 13, Appl
270	6	1.5	431	5	PCT-US94-05275-4	Sequence 4, Appl	343	6	1.5	584	4	US-09-339-972-13	Sequence 13, Appl
271	6	1.5	433	4	US-09-705-448-3	Sequence 3, Appl	344	6	1.5	586	4	US-09-504-358-20	Sequence 20, Appl
272	6	1.5	437	4	US-09-353-332-2	Sequence 2, Appl	345	6	1.5	586	4	US-09-354-314-20	Sequence 44, Appl
273	6	1.5	445	4	US-08-974-691-6	Sequence 6, Appl	346	6	1.5	591	4	US-09-352-159-4	Sequence 46, Appl
274	6	1.5	451	4	US-08-974-691-2	Sequence 2, Appl	347	6	1.5	591	4	US-09-352-159-46	Sequence 46, Appl
275	6	1.5	452	1	US-08-275-488A-2	Sequence 2, Appl	348	6	1.5	598	4	US-09-352-159-42	Sequence 42, Appl
276	6	1.5	452	1	US-08-275-490-2	Sequence 2, Appl	349	6	1.5	600	4	US-09-352-159-36	Sequence 36, Appl
277	6	1.5	452	1	US-08-446-380-2	Sequence 2, Appl	350	6	1.5	600	4	US-09-352-159-38	Sequence 38, Appl
278	6	1.5	452	1	US-08-446-374-2	Sequence 2, Appl	351	6	1.5	600	4	US-09-423-468A-13	Sequence 13, Appl
279	6	1.5	452	1	US-08-446-382-2	Sequence 2, Appl	352	6	1.5	601	4	US-09-398-995A-42	Sequence 42, Appl
280	6	1.5	452	1	US-08-445-801-2	Sequence 2, Appl	353	6	1.5	604	1	US-08-224-657-95	Sequence 84, Appl
281	6	1.5	452	1	US-08-275-487-2	Sequence 2, Appl	354	6	1.5	604	1	US-08-224-657-95	Sequence 95, Appl
282	6	1.5	452	4	US-09-323-872A-15	Sequence 15, Appl	355	6	1.5	604	1	US-08-224-657-98	Sequence 98, Appl
283	6	1.5	452	5	PCT-US95-08919-2	Sequence 2, Appl	356	6	1.5	604	4	US-09-354-138-98	Sequence 98, Appl
284	6	1.5	453	1	US-08-275-488A-12	Sequence 12, Appl	357	6	1.5	604	4	US-09-354-138-95	Sequence 95, Appl
285	6	1.5	453	1	US-08-275-490-12	Sequence 12, Appl	358	6	1.5	604	4	US-09-354-138-98	Sequence 98, Appl
286	6	1.5	453	1	US-08-446-380-12	Sequence 12, Appl	359	6	1.5	604	2	US-08-472-534-5	Sequence 5, Appl
287	6	1.5	453	1	US-08-446-374-12	Sequence 12, Appl	360	6	1.5	609	4	US-09-271-778-1	Sequence 1, Appl
288	6	1.5	453	1	US-08-446-382-12	Sequence 12, Appl	361	6	1.5	609	4	US-09-788-871-1	Sequence 1, Appl
289	6	1.5	453	1	US-08-445-801-12	Sequence 12, Appl	362	6	1.5	610	1	US-07-821-717B-6	Sequence 6, Appl
290	6	1.5	453	1	US-08-275-487-12	Sequence 12, Appl	363	6	1.5	610	1	US-08-119-262B-6	Sequence 6, Appl
291	6	1.5	453	5	PCT-US95-08919-12	Sequence 12, Appl	364	6	1.5	610	1	US-08-135-929A-11	Sequence 11, Appl
292	6	1.5	457	4	US-09-124-238A-1	Sequence 1, Appl	365	6	1.5	612	4	US-08-234-265A-11	Sequence 11, Appl
293	6	1.5	457	4	US-09-124-238A-10	Sequence 10, Appl	366	6	1.5	612	4	US-09-516-914-5	Sequence 5, Appl
294	6	1.5	457	4	US-09-134-001C-3838	Sequence 3838, Ap	367	6	1.5	629	1	US-08-250-740-33	Sequence 33, Appl
295	6	1.5	457	4	US-09-721-975-1	Sequence 1, Appl	368	6	1.5	629	1	US-07-695-472B-2	Sequence 2, Appl
296	6	1.5	457	4	US-09-721-975-10	Sequence 10, Appl	369	6	1.5	668	1	US-08-530-950-13	Sequence 13, Appl
297	6	1.5	461	1	US-08-672-571A-3	Sequence 3, Appl	370	6	1.5	668	4	US-09-149-879-13	Sequence 13, Appl
298	6	1.5	462	4	US-09-102-528-35	Sequence 25, Appl	371	6	1.5	669	4	US-09-071-035-264	Sequence 264, App
299	6	1.5	462	1	US-08-289-351-1	Sequence 1, Appl	372	6	1.5	672	1	US-07-841-651-2	Sequence 2, Appl
300	6	1.5	462	2	US-08-371-977-18	Sequence 18, Appl	373	6	1.5	672	1	US-07-841-651-3	Sequence 3, Appl
301	6	1.5	462	1	US-09-309-572-10	Sequence 10, Appl	374	6	1.5	687	1	US-08-204-656B-10	Sequence 10, Appl
302	6	1.5	462	6	5225348-1	Patent No. 5225348	375	6	1.5	687	1	US-08-470-702-11	Sequence 10, Appl
303	6	1.5	470	1	US-08-471-996-2	Sequence 2, Appl	376	6	1.5	687	3	US-08-467-831-10	Sequence 10, Appl
304	6	1.5	470	2	US-08-894-840-2	Sequence 2, Appl	377	6	1.5	687	3	US-08-947-965-75	Sequence 75, Appl
305	6	1.5	470	3	US-09-139-675-2	Sequence 2, Appl	378	6	1.5	718	2	US-08-560-398-12	Sequence 12, Appl
306	6	1.5	479	1	US-08-583-318-5	Sequence 5, Appl	379	6	1.5	718	2	US-09-097-053-12	Sequence 12, Appl
307	6	1.5	480	4	US-09-305-681-2	Sequence 2, Appl	380	6	1.5	795	1	US-09-308-1179B-1	Sequence 1, Appl
308	6	1.5	488	4	US-09-444-728-2	Sequence 2, Appl	381	6	1.5	820	2	US-07-716-827C-5	Sequence 5, Appl
309	6	1.5	489	4	US-09-986-536-2	Sequence 2, Appl	382	6	1.5	820	2	US-08-380-182-23	Sequence 23, Appl
310	6	1.5	490	1	US-08-672-571A-1	Sequence 1, Appl	383	6	1.5	831	2	US-08-677-734A-11	Sequence 11, Appl
311	6	1.5	494	1	US-08-275-488A-4	Sequence 4, Appl	384	6	1.5	831	4	US-09-097-053-11	Sequence 11, Appl
312	6	1.5	494	1	US-08-275-490-4	Sequence 4, Appl	385	6	1.5	832	2	US-08-677-734A-12	Sequence 12, Appl
313	6	1.5	494	1	US-08-446-380-4	Sequence 4, Appl	386	6	1.5	832	4	US-09-097-053-13	Sequence 13, Appl
314	6	1.5	494	1	US-08-446-374-4	Sequence 4, Appl	387	6	1.5	834	2	US-08-677-734A-9	Sequence 9, Appl
315	6	1.5	494	1	US-08-446-382-4	Sequence 4, Appl	388	6	1.5	834	4	US-09-097-053-9	Sequence 9, Appl
316	6	1.5	494	1	US-08-445-801-4	Sequence 4, Appl	389	6	1.5	834	4	US-09-097-053-10	Sequence 10, Appl
317	6	1.5	494	1	US-08-275-487-4	Sequence 4, Appl	390	6	1.5	849	2	US-08-867-129-2	Sequence 2, Appl
318	6	1.5	494	5	PCT-US95-08919-4	Sequence 4, Appl	391	6	1.5	849	1	US-08-405-392-18	Sequence 18, Appl
319	6	1.5	500	4	US-08-960-190A-25	Sequence 25, Appl	392	6	1.5	849	3	US-08-487-691-18	Sequence 18, Appl

393	6	1.5	853	3	US-08-699-103B-10	Sequence 10, Appl	466	6	1.5	2048	4	US-09-268-347-48	Sequence 48, Appl
394	6	1.5	853	4	US-09-229-059-10	Sequence 10, Appl	467	6	1.5	2123	4	US-08-968-685A-10	Sequence 10, Appl
395	6	1.5	856	4	US-09-134-001C-5438	Sequence 5438, Ap	468	6	1.5	2183	4	US-08-348-891A-7	Sequence 7, Appl
396	6	1.5	866	1	US-08-405-382-17	Sequence 17, Appl	469	6	1.5	2183	2	US-08-905-817-7	Sequence 7, Appl
397	6	1.5	866	3	US-08-487-691-17	Sequence 6, Appl	470	6	1.5	2201	4	US-08-952-981A-2	Sequence 2, Appl
398	6	1.5	873	1	US-08-571-758-6	Sequence 6, Appl	471	6	1.5	2307	4	US-09-263-933-2	Sequence 2, Appl
399	6	1.5	873	1	US-08-909-984A-6	Sequence 6, Appl	472	6	1.5	2307	4	US-09-263-933-9	Sequence 9, Appl
400	6	1.5	873	1	US-08-909-984A-6	Sequence 6, Appl	473	6	1.5	2307	4	US-09-263-933-16	Sequence 16, Appl
401	6	1.5	897	3	US-08-975-703-6	Sequence 6, Appl	474	6	1.5	2314	4	US-09-268-347-49	Sequence 49, Appl
402	6	1.5	897	4	US-08-515-88A-6	Sequence 6, Appl	475	6	1.5	2584	3	US-08-936-135-4	Sequence 4, Appl
403	6	1.5	905	1	US-08-405-382-2	Sequence 2, Appl	476	6	1.5	2588	3	US-08-936-135-2	Sequence 2, Appl
404	6	1.5	905	3	US-08-487-691-2	Sequence 2, Appl	477	6	1.5	2620	1	US-08-324-977-32	Sequence 32, Appl
405	6	1.5	905	4	US-08-666-221B-4	Sequence 4, Appl	478	6	1.5	2620	2	US-08-384-616-32	Sequence 32, Appl
406	6	1.5	905	4	US-08-666-221B-10	Sequence 10, Appl	479	6	1.5	2620	2	US-08-304-686A-32	Sequence 32, Appl
407	6	1.5	908	3	US-08-699-103B-12	Sequence 12, Appl	480	6	1.5	2621	1	US-09-315-850-32	Sequence 32, Appl
408	6	1.5	908	4	US-09-229-059-12	Sequence 12, Appl	481	6	1.5	2621	1	US-08-324-977-36	Sequence 36, Appl
409	6	1.5	920	1	US-07-718-575-10	Sequence 10, Appl	482	6	1.5	2621	2	US-08-384-616-36	Sequence 36, Appl
410	6	1.5	920	1	US-08-481-206-10	Sequence 10, Appl	483	6	1.5	2621	2	US-08-904-686A-36	Sequence 36, Appl
411	6	1.5	920	2	US-08-486-269A-10	Sequence 10, Appl	484	6	1.5	2621	4	US-09-315-850-36	Sequence 36, Appl
412	6	1.5	933	1	US-08-370-193A-8	Sequence 8, Appl	485	6	1.5	2802	4	US-09-510-791-1	Sequence 1, Appl
413	6	1.5	933	4	US-09-271-438A-9	Sequence 9, Appl	486	6	1.5	2887	4	US-08-462-667B-2	Sequence 2, Appl
414	6	1.5	935	4	US-09-271-438A-3	Sequence 3, Appl	487	6	1.5	2887	4	US-08-462-667B-8	Sequence 8, Appl
415	6	1.5	935	4	US-09-271-438A-8	Sequence 8, Appl	488	6	1.5	2972	4	US-08-469-260A-387	Sequence 387, App
416	6	1.5	979	4	US-09-323-872A-55	Sequence 55, Appl	489	6	1.5	3010	1	US-08-324-977-2	Sequence 2, Appl
417	6	1.5	997	4	US-09-369-364A-7	Sequence 7, Appl	490	6	1.5	3010	1	US-08-324-977-14	Sequence 14, Appl
418	6	1.5	999	2	US-08-473-553A-5	Sequence 5, Appl	491	6	1.5	3010	2	US-08-384-616-2	Sequence 2, Appl
419	6	1.5	1048	3	US-09-356-952-5	Sequence 5, Appl	492	6	1.5	3010	2	US-08-384-616-2	Sequence 2, Appl
420	6	1.5	1070	4	US-09-091-042A-2	Sequence 2, Appl	493	6	1.5	3010	2	US-08-384-616-14	Sequence 14, Appl
421	6	1.5	1090	4	US-09-346-237-5	Sequence 5, Appl	494	6	1.5	3010	2	US-08-904-686A-14	Sequence 2, Appl
422	6	1.5	1093	5	PCT-US93-03077-1	Sequence 1, Appl	495	6	1.5	3010	2	US-08-904-686A-14	Sequence 14, Appl
423	6	1.5	1097	2	US-08-680-326-39	Sequence 39, Appl	496	6	1.5	3010	4	US-09-014-616-3	Sequence 3, Appl
424	6	1.5	1114	2	US-08-576-626A-31	Sequence 31, Appl	497	6	1.5	3010	4	US-09-315-850-2	Sequence 2, Appl
425	6	1.5	1137	1	US-08-369-043-2	Sequence 2, Appl	498	6	1.5	3010	4	US-09-315-850-14	Sequence 14, Appl
426	6	1.5	1156	4	US-09-001-982-10	Sequence 10, Appl	499	6	1.5	7257	3	US-09-335-409-5	Sequence 5, Appl
427	6	1.5	1156	4	US-09-002-285-70	Sequence 70, Appl	500	6	1.5	7257	4	US-09-568-102-5	Sequence 5, Appl
428	6	1.5	1220	2	US-08-843-530B-36	Sequence 36, Appl	501	6	1.5	7257	4	US-09-568-969-5	Sequence 5, Appl
429	6	1.5	1242	4	US-09-001-982-12	Sequence 12, Appl	502	6	1.5	7257	4	US-09-568-180-5	Sequence 5, Appl
430	6	1.5	1265	4	US-09-347-878-5	Sequence 5, Appl	503	6	1.5	7257	4	US-09-568-486-5	Sequence 5, Appl
431	6	1.5	1265	4	US-09-347-878-7	Sequence 7, Appl	504	6	1.5	7257	4	US-09-568-472-5	Sequence 5, Appl
432	6	1.5	1274	4	US-09-095-443-2	Sequence 2, Appl	505	6	1.5	7257	4	US-09-567-899-5	Sequence 5, Appl
433	6	1.5	1290	1	US-08-138-641-2	Sequence 2, Appl	506	6	1.5	15281	2	US-08-471-119A-2	Sequence 2, Appl
434	6	1.5	1290	1	US-08-138-133-2	Sequence 2, Appl	507	5	1.2	5276016-9	6	5276016-9	Patent No. 5276016
435	6	1.5	1356	4	US-09-098-707A-2	Sequence 2, Appl	508	5	1.2	5276016-12	5	5276016-12	Patent No. 5276016
436	6	1.5	1356	4	US-09-483-539-2	Sequence 2, Appl	509	5	1.2	5276016-15	5	5276016-15	Patent No. 5276016
437	6	1.5	1358	1	US-08-404-665-4	Sequence 4, Appl	510	5	1.2	5276016-17	5	5276016-17	Patent No. 5276016
438	6	1.5	1358	1	US-08-404-671-4	Sequence 4, Appl	511	5	1.2	5276016-17	5	5276016-17	Patent No. 5276016
439	6	1.5	1358	1	US-08-404-781-4	Sequence 4, Appl	512	5	1.2	5276016-17	5	5276016-17	Patent No. 5276016
440	6	1.5	1367	1	US-07-813-593-4	Sequence 4, Appl	513	5	1.2	5276016-17	5	5276016-17	Patent No. 5276016
441	6	1.5	1367	1	US-07-977-451-6	Sequence 6, Appl	514	5	1.2	5276016-17	5	5276016-17	Patent No. 5276016
442	6	1.5	1367	1	US-07-946-507-6	Sequence 6, Appl	515	5	1.2	5276016-17	5	5276016-17	Patent No. 5276016
443	6	1.5	1367	1	US-08-252-517-6	Sequence 6, Appl	516	5	1.2	5276016-17	5	5276016-17	Patent No. 5276016
444	6	1.5	1367	1	US-07-906-397A-6	Sequence 6, Appl	517	5	1.2	5276016-17	5	5276016-17	Patent No. 5276016
445	6	1.5	1367	1	US-08-601-891-6	Sequence 6, Appl	518	5	1.2	5276016-17	5	5276016-17	Patent No. 5276016
446	6	1.5	1367	2	US-08-443-861-2	Sequence 2, Appl	519	5	1.2	5276016-17	5	5276016-17	Patent No. 5276016
447	6	1.5	1367	2	US-09-021-324-6	Sequence 2, Appl	520	5	1.2	5276016-17	5	5276016-17	Patent No. 5276016
448	6	1.5	1367	2	US-08-193-829B-2	Sequence 2, Appl	521	5	1.2	5276016-17	5	5276016-17	Patent No. 5276016
449	6	1.5	1367	5	PCT-US92-02750-8	Sequence 8, Appl	522	5	1.2	5276016-17	5	5276016-17	Patent No. 5276016
450	6	1.5	1367	5	PCT-US92-05401-6	Sequence 6, Appl	523	5	1.2	5276016-17	5	5276016-17	Patent No. 5276016
451	6	1.5	1367	5	PCT-US92-09893-6	Sequence 6, Appl	524	5	1.2	5276016-17	5	5276016-17	Patent No. 5276016
452	6	1.5	1395	4	US-09-540-245A-15	Sequence 15, Appl	525	5	1.2	5276016-17	5	5276016-17	Patent No. 5276016
453	6	1.5	1455	2	US-08-726-012B-2	Sequence 2, Appl	526	5	1.2	5276016-17	5	5276016-17	Patent No. 5276016
454	6	1.5	1487	3	US-08-840-062-7	Sequence 7, Appl	527	5	1.2	5276016-17	5	5276016-17	Patent No. 5276016
455	6	1.5	1611	2	US-08-804-227C-5	Sequence 5, Appl	528	5	1.2	5276016-17	5	5276016-17	Patent No. 5276016
456	6	1.5	1611	2	US-08-804-227C-5	Sequence 5, Appl	529	5	1.2	5276016-17	5	5276016-17	Patent No. 5276016
457	6	1.5	1638	4	US-09-071-035-258	Sequence 258, App	530	5	1.2	5276016-17	5	5276016-17	Patent No. 5276016
458	6	1.5	1638	4	US-09-071-035-262	Sequence 262, App	531	5	1.2	5276016-17	5	5276016-17	Patent No. 5276016
459	6	1.5	1638	4	US-09-071-035-266	Sequence 266, App	532	5	1.2	5276016-17	5	5276016-17	Patent No. 5276016
460	6	1.5	1692	4	US-09-263-933-4	Sequence 4, Appl	533	5	1.2	5276016-17	5	5276016-17	Patent No. 5276016
461	6	1.5	1692	4	US-09-263-933-11	Sequence 11, Appl	534	5	1.2	5276016-17	5	5276016-17	Patent No. 5276016
462	6	1.5	1692	4	US-09-263-933-18	Sequence 18, Appl	535	5	1.2	5276016-17	5	5276016-17	Patent No. 5276016
463	6	1.5	2013	1	US-08-324-977-12	Sequence 12, Appl	536	5	1.2	5276016-17	5	5276016-17	Patent No. 5276016
464	6	1.5	2013	2	US-08-384-616-12	Sequence 12, Appl	537	5	1.2	5276016-17	5	5276016-17	Patent No. 5276016
465	6	1.5	2013	2	US-08-904-686A-12	Sequence 12, Appl	538	5	1.2	5276016-17	5	5276016-17	Patent No. 5276016
					US-09-315-850-12	Sequence 12, Appl							

539	5	1.2	9	2	US-08-934-222-81	Sequence 81, Appl	612	5	1.2	14	1	US-08-321-668-21	Sequence 21, Appl
540	5	1.2	9	2	US-08-933-402-81	Sequence 81, Appl	613	5	1.2	14	1	US-08-321-668-22	Sequence 22, Appl
541	5	1.2	9	2	US-09-207-621-81	Sequence 81, Appl	614	5	1.2	14	1	US-08-321-668-23	Sequence 23, Appl
542	5	1.2	9	2	US-08-533-818-81	Sequence 81, Appl	615	5	1.2	14	1	US-08-321-668-24	Sequence 24, Appl
543	5	1.2	9	3	US-09-231-797-81	Sequence 81, Appl	616	5	1.2	14	1	US-08-321-668-25	Sequence 25, Appl
544	5	1.2	9	3	US-08-422-093-20	Sequence 20, Appl	617	5	1.2	14	1	US-08-321-668-26	Sequence 26, Appl
545	5	1.2	9	3	US-08-934-224-81	Sequence 81, Appl	618	5	1.2	14	1	US-08-321-668-27	Sequence 27, Appl
546	5	1.2	9	3	US-08-933-843-81	Sequence 81, Appl	619	5	1.2	14	1	US-08-321-668-28	Sequence 28, Appl
547	5	1.2	9	3	US-08-422-112-20	Sequence 20, Appl	620	5	1.2	14	1	US-08-321-668-29	Sequence 29, Appl
548	5	1.2	9	4	US-08-934-223-81	Sequence 81, Appl	621	5	1.2	14	1	US-08-321-668-30	Sequence 30, Appl
549	5	1.2	9	4	US-09-413-492-81	Sequence 81, Appl	622	5	1.2	14	1	US-08-321-668-31	Sequence 31, Appl
550	5	1.2	9	4	US-08-981-392-67	Sequence 67, Appl	623	5	1.2	14	1	US-08-321-668-32	Sequence 32, Appl
551	5	1.2	9	4	US-09-510-738A-163	Sequence 163, App	624	5	1.2	14	1	US-08-321-668-33	Sequence 33, Appl
552	5	1.2	9	4	US-09-518-046-58	Sequence 58, Appl	625	5	1.2	14	1	US-08-321-668-34	Sequence 34, Appl
553	5	1.2	9	5	PCT-US93-00325-5	Sequence 5, Appl	626	5	1.2	14	1	US-08-321-668-35	Sequence 35, Appl
554	5	1.2	9	5	PCT-US95-09262-163	Sequence 163, App	627	5	1.2	14	1	US-08-321-668-36	Sequence 36, Appl
555	5	1.2	10	1	US-08-462-949-14	Sequence 14, Appl	628	5	1.2	14	1	US-08-321-668-37	Sequence 37, Appl
556	5	1.2	10	1	US-08-462-949-33	Sequence 33, Appl	629	5	1.2	14	1	US-08-321-668-38	Sequence 38, Appl
557	5	1.2	10	1	US-08-023-764B-14	Sequence 14, Appl	630	5	1.2	14	1	US-08-321-668-39	Sequence 39, Appl
558	5	1.2	10	1	US-08-023-764B-33	Sequence 33, Appl	631	5	1.2	14	1	US-08-321-668-40	Sequence 40, Appl
559	5	1.2	10	3	US-08-823-586-10	Sequence 10, Appl	632	5	1.2	14	1	US-08-321-668-41	Sequence 41, Appl
560	5	1.2	10	3	US-08-159-339A-325	Sequence 325, App	633	5	1.2	14	1	US-08-321-668-42	Sequence 42, Appl
561	5	1.2	10	3	US-08-159-339A-958	Sequence 958, App	634	5	1.2	14	1	US-08-837-941-21	Sequence 21, Appl
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563	5	1.2	10	6	5223391-2	Sequence 11, Appl	636	5	1.2	14	1	US-08-837-941-23	Sequence 23, Appl
564	5	1.2	11	4	US-08-875-309-12	Sequence 12, Appl	637	5	1.2	14	1	US-08-837-941-24	Sequence 24, Appl
565	5	1.2	11	4	US-09-001-984C-67	Sequence 67, Appl	638	5	1.2	14	1	US-08-837-941-25	Sequence 25, Appl
566	5	1.2	11	5	PCT-US96-00310-12	Sequence 12, Appl	639	5	1.2	14	1	US-08-837-941-26	Sequence 26, Appl
567	5	1.2	12	1	US-08-031-148-16	Sequence 16, Appl	640	5	1.2	14	1	US-08-837-941-27	Sequence 27, Appl
568	5	1.2	12	1	US-08-031-148-17	Sequence 17, Appl	641	5	1.2	14	1	US-08-837-941-28	Sequence 28, Appl
569	5	1.2	12	1	US-08-031-148-18	Sequence 18, Appl	642	5	1.2	14	1	US-08-837-941-29	Sequence 29, Appl
570	5	1.2	12	1	US-08-196-989B-8	Sequence 8, Appl	643	5	1.2	14	1	US-08-837-941-30	Sequence 30, Appl
571	5	1.2	12	1	US-08-383-743A-11	Sequence 11, Appl	644	5	1.2	14	1	US-08-837-941-31	Sequence 31, Appl
572	5	1.2	12	1	US-08-321-668-11	Sequence 11, Appl	645	5	1.2	14	1	US-08-837-941-32	Sequence 32, Appl
573	5	1.2	12	1	US-08-321-668-12	Sequence 12, Appl	646	5	1.2	14	1	US-08-837-941-33	Sequence 33, Appl
574	5	1.2	12	1	US-08-321-668-13	Sequence 13, Appl	647	5	1.2	14	1	US-08-837-941-34	Sequence 34, Appl
575	5	1.2	12	1	US-08-321-668-14	Sequence 14, Appl	648	5	1.2	14	1	US-08-837-941-35	Sequence 35, Appl
576	5	1.2	12	1	US-08-321-668-15	Sequence 15, Appl	649	5	1.2	14	1	US-08-837-941-36	Sequence 36, Appl
577	5	1.2	12	1	US-08-321-668-16	Sequence 16, Appl	650	5	1.2	14	1	US-08-837-941-37	Sequence 37, Appl
578	5	1.2	12	1	US-08-837-941-11	Sequence 11, Appl	651	5	1.2	14	1	US-08-837-941-38	Sequence 38, Appl
579	5	1.2	12	1	US-08-837-941-12	Sequence 12, Appl	652	5	1.2	14	1	US-08-837-941-39	Sequence 39, Appl
580	5	1.2	12	1	US-08-837-941-13	Sequence 13, Appl	653	5	1.2	14	1	US-08-837-941-40	Sequence 40, Appl
581	5	1.2	12	1	US-08-837-941-14	Sequence 14, Appl	654	5	1.2	14	1	US-08-837-941-41	Sequence 41, Appl
582	5	1.2	12	1	US-08-837-941-15	Sequence 15, Appl	655	5	1.2	14	1	US-08-837-941-42	Sequence 42, Appl
583	5	1.2	12	1	US-08-837-941-16	Sequence 16, Appl	656	5	1.2	14	3	US-08-825-669A-2	Sequence 2, Appl
584	5	1.2	12	2	US-08-950-866-8	Sequence 8, Appl	657	5	1.2	15	1	US-08-221-683-23	Sequence 23, Appl
585	5	1.2	12	2	US-08-760-926-8	Sequence 8, Appl	658	5	1.2	15	1	US-08-383-753-48	Sequence 48, Appl
586	5	1.2	12	2	US-08-729-152-11	Sequence 11, Appl	659	5	1.2	15	2	US-08-586-772-48	Sequence 48, Appl
587	5	1.2	12	3	US-08-415-838-16	Sequence 16, Appl	660	5	1.2	15	2	US-08-476-662A-22	Sequence 22, Appl
588	5	1.2	12	3	US-08-415-838-17	Sequence 17, Appl	661	5	1.2	15	2	US-08-522-669B-8	Sequence 8, Appl
589	5	1.2	12	3	US-08-415-838-18	Sequence 18, Appl	662	5	1.2	15	2	US-08-959-512-48	Sequence 48, Appl
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591	5	1.2	12	3	US-08-825-369A-1	Sequence 1, Appl	664	5	1.2	15	4	US-09-294-923-8	Sequence 8, Appl
592	5	1.2	12	3	US-08-599-226-33	Sequence 33, Appl	665	5	1.2	15	4	US-09-512-883-48	Sequence 48, Appl
593	5	1.2	12	3	US-09-188-579-15	Sequence 15, Appl	666	5	1.2	15	5	PCT-US95-04018-23	Sequence 23, Appl
594	5	1.2	12	3	US-09-188-579-21	Sequence 21, Appl	667	5	1.2	15	5	PCT-US96-01314-22	Sequence 22, Appl
595	5	1.2	12	4	US-09-315-444-15	Sequence 15, Appl	668	5	1.2	16	1	US-07-987-272A-23	Sequence 23, Appl
596	5	1.2	12	4	US-09-315-444-21	Sequence 21, Appl	669	5	1.2	16	1	US-08-418-444A-9	Sequence 9, Appl
597	5	1.2	12	4	US-09-125-098-33	Sequence 33, Appl	670	5	1.2	16	2	US-08-207-481-6	Sequence 6, Appl
598	5	1.2	12	4	US-09-205-169-16	Sequence 16, Appl	671	5	1.2	16	2	US-08-839-008-3	Sequence 3, Appl
599	5	1.2	12	4	US-09-205-169-17	Sequence 17, Appl	672	5	1.2	16	2	US-08-360-606B-8	Sequence 8, Appl
600	5	1.2	12	4	US-09-205-169-18	Sequence 18, Appl	673	5	1.2	16	5	PCT-US95-02689-8	Sequence 6, Appl
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602	5	1.2	12	4	US-09-721-362-21	Sequence 21, Appl	675	5	1.2	17	2	US-08-464-438-31	Sequence 31, Appl
603	5	1.2	12	4	US-09-752-165-17	Sequence 17, Appl	676	5	1.2	17	3	US-08-782-997A-12	Sequence 12, Appl
604	5	1.2	12	4	US-09-752-165-23	Sequence 23, Appl	677	5	1.2	17	4	US-09-308-022-3	Sequence 3, Appl
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608	5	1.2	13	2	US-08-803-899-13	Sequence 13, Appl	681	5	1.2	18	1	US-08-383-743A-2	Sequence 6, Appl
609	5	1.2	13	2	US-08-803-899-16	Sequence 16, Appl	682	5	1.2	18	2	US-08-705-660-6	Sequence 6, Appl
610	5	1.2	13	3	US-08-725-459B-11	Sequence 11, Appl	683	5	1.2	18	2	US-08-945-168-100	Sequence 100, App
611	5	1.2	13	4	US-08-469-260A-445	Sequence 445, App	684	5	1.2	18	3	US-08-989-045-6	Sequence 6, Appl

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688	5	1.2	18	5	PCT-US93-07116-2	Sequence 2, Appli	761	5	1.2	28	1	US-08-053-131-98	Sequence 98, Appli
689	5	1.2	18	5	PCT-US94-05387-5	Sequence 5, Appli	762	5	1.2	28	1	US-08-645-641-98	Sequence 98, Appli
690	5	1.2	19	1	US-08-180-572-3	Sequence 3, Appli	763	5	1.2	28	1	US-07-853-408B-98	Sequence 98, Appli
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695	5	1.2	19	2	US-08-478-572-18	Sequence 12, Appli	768	5	1.2	28	4	US-09-135-166-34	Sequence 34, Appli
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705	5	1.2	21	3	US-09-413-452-21	Sequence 21, Appli	778	5	1.2	29	2	US-08-622-720A-15	Sequence 15, Appli
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714	5	1.2	22	3	US-09-330-945-31	Sequence 31, Appli	787	5	1.2	31	4	US-08-477-346-159	Sequence 159, App
715	5	1.2	22	3	US-08-725-459B-13	Sequence 13, Appli	788	5	1.2	31	4	US-08-473-089-159	Sequence 159, App
716	5	1.2	22	3	US-09-138-056-16	Sequence 16, Appli	789	5	1.2	31	4	US-08-487-072A-159	Sequence 159, App
717	5	1.2	22	4	US-08-484-296-19	Sequence 19, Appli	790	5	1.2	32	1	US-08-190-802A-184	Sequence 184, App
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719	5	1.2	22	5	PCT-US94-01768-11	Sequence 11, Appli	792	5	1.2	32	1	US-08-645-641-92	Sequence 92, Appli
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722	5	1.2	23	1	US-07-952-817-15	Sequence 15, Appli	795	5	1.2	32	2	US-08-518-667-10	Sequence 10, Appli
723	5	1.2	23	1	US-08-086-428B-151	Sequence 151, App	796	5	1.2	32	2	US-08-308-665-92	Sequence 92, Appli
724	5	1.2	23	1	US-08-423-399B-31	Sequence 31, Appli	797	5	1.2	32	3	US-08-484-322-14	Sequence 14, App
725	5	1.2	23	2	US-08-468-570-151	Sequence 151, App	798	5	1.2	32	3	US-08-649-100-14	Sequence 10, Appli
726	5	1.2	23	2	US-08-290-665A-255	Sequence 255, App	799	5	1.2	32	3	US-08-649-100-30	Sequence 30, Appli
727	5	1.2	23	2	US-08-609-236-3	Sequence 3, Appli	800	5	1.2	32	4	US-09-042-353-289	Sequence 289, App
728	5	1.2	23	3	PCT-US95-10398-255	Sequence 255, App	801	5	1.2	32	4	US-08-477-346-184	Sequence 184, App
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730	5	1.2	24	1	US-08-031-148-5	Sequence 5, Appli	803	5	1.2	32	4	US-08-758-417A-137	Sequence 137, App
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735	5	1.2	24	1	US-08-434-198-5	Sequence 5, Appli	808	5	1.2	33	2	US-08-468-570-147	Sequence 147, App
736	5	1.2	24	2	US-08-306-078-2	Sequence 2, Appli	809	5	1.2	33	2	US-08-290-665A-251	Sequence 251, App
737	5	1.2	24	3	US-08-415-838-5	Sequence 5, Appli	810	5	1.2	33	5	PCT-US95-10398-251	Sequence 251, App
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744	5	1.2	24	5	PCT-US94-01768-6	Sequence 6, Appli	817	5	1.2	34	1	US-08-443-863-23	Sequence 23, Appli
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754	5	1.2	27	4	US-09-153-586-6	Sequence 6, Appli	827	5	1.2	34	1	US-08-488-105-9	Sequence 9, Appli
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757	5	1.2	27	4	US-09-448-867-9	Sequence 9, Appli	830	5	1.2	34	1	US-08-488-105-14	Sequence 14, Appli

831	5	1.2	34	1	US-08-488-105-15	Sequence 15, Appl	904	5	1.2	37	4	US-09-153-586-4	Sequence 4, Appl
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833	5	1.2	34	1	US-08-488-105-18	Sequence 18, Appl	906	5	1.2	38	1	US-08-471-052A-109	Sequence 109, App
834	5	1.2	34	1	US-08-433-854-12	Sequence 12, Appl	907	5	1.2	38	1	US-08-220-606B-56	Sequence 56, Appl
835	5	1.2	34	1	US-08-174-745A-12	Sequence 12, Appl	908	5	1.2	38	1	US-08-189-331-109	Sequence 109, App
836	5	1.2	34	1	US-08-449-500-2	Sequence 2, Appl	909	5	1.2	38	2	US-08-471-939-109	Sequence 109, App
837	5	1.2	34	1	US-08-449-500-23	Sequence 23, Appl	910	5	1.2	38	2	US-08-471-600-109	Sequence 109, App
838	5	1.2	34	1	US-08-449-500-24	Sequence 24, Appl	911	5	1.2	38	2	US-08-471-068-109	Sequence 109, App
839	5	1.2	34	1	US-08-449-500-35	Sequence 35, Appl	912	5	1.2	38	2	US-08-378-548-13	Sequence 13, App
840	5	1.2	34	1	US-08-449-500-36	Sequence 36, Appl	913	5	1.2	39	4	US-09-149-476-538	Sequence 538, App
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847	5	1.2	34	1	US-08-449-317A-35	Sequence 35, Appl	920	5	1.2	41	5	PCT-US93-087744-3	Sequence 254, App
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ALIGNMENTS

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; GENERAL INFORMATION:
; APPLICANT: Powell, David J.
; APPLICANT: Southan, Christopher
; APPLICANT: Chapman, Conrad G.
; APPLICANT: Evans, Joanne R.
; TITLE OF INVENTION: ASPI
; FILE REFERENCE: GH/70262
; CURRENT APPLICATION NUMBER: US/08/999,723A
; CURRENT FILING DATE: 1997-10-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
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US-08-999-723-2
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; Patent No. 6162630
; GENERAL INFORMATION:
; APPLICANT: POWELL, DAVID J.
; APPLICANT: SOUTHAN, CHRISTOPHER
; APPLICANT: CHAPMAN, CONRAD G.
; APPLICANT: EVANS, JOANNE R.
; TITLE OF INVENTION: ASPI
; FILE REFERENCE: GH-70262-D1
; CURRENT APPLICATION NUMBER: US/09/434,427
; CURRENT FILING DATE: 1999-11-04
; EARLIER APPLICATION NUMBER: US 08/999,723
; EARLIER FILING DATE: 1997-10-06
; EARLIER APPLICATION NUMBER: UK 9626022.9
; EARLIER FILING DATE: 1996-12-14
; NUMBER OF SEQ ID NOS: 2
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US-09-434-427-2
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; Patent No. 6420534
; GENERAL INFORMATION:
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; APPLICANT: GURNEY ET AL.
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; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; PRIORITY FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; NUMBER OF SEQ ID NOS: 73
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US-09-548-372D-2

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; Patent No. 6440698
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; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
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; PRIOR FILING DATE: 1998-09-24
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US-09-548-367D-2

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; GENERAL INFORMATION:
; APPLICANT: ZHU, YUAN
; APPLICANT: LI, XIAOTONG
; APPLICANT: CHRISTIE, GARY
; APPLICANT: POWELL, DAVID J.
; TITLE OF INVENTION: Mouse Aspartic Secretase-1 (mAsp1)
; FILE REFERENCE: GP-70663
; CURRENT APPLICATION NUMBER: US/09/717,432
; CURRENT FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/166,974
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QY 166 FSNMOMGAGLPVAGSGTNGSLVLGGIIEPSLYKGDIMWYPIKEWYQIIEILKLEIGGO 224
DB 224 FSNMOMGAGLPVAGSGTNGSLVLGGIIEPSLYKGDIMWYPIKEWYQIIEILKLEIGGO 282

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RESULT 6
US-09-912-484-2
; Sequence 2, Application US/09912484
; Patent No. 6358725
; GENERAL INFORMATION:
; APPLICANT: Christie, Gary
; APPLICANT: Li, Xiaotong
; APPLICANT: Powell, David J.
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: Mouse Aspartic Secretase-1 (MASP1)
; FILE REFERENCE: GP-70663-D1
; CURRENT APPLICATION NUMBER: US/09/912,484
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/166,974
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 09/717,432
; PRIOR FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 514
; TYPE: PRT
; ORGANISM: MUS MUSCULUS
US-09-912-484-2

Query Match 14.5%; Score 59; DB 4; Length 514;
Best Local Similarity 100.0%; Pred. No. 14e-49;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 166 FSMOMCGAGLPVAGSGTNGSLVLCGIEPSLYKGD1WYTP1KEWYQ1EIKLEIGGQ 224
Db 224 FSMOMCGAGLPVAGSGTNGSLVLCGIEPSLYKGD1WYTP1KEWYQ1EIKLEIGGQ 282

RESULT 7
US-09-548-372D-28
; Sequence 28, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-28

Query Match 3.0%; Score 12; DB 4; Length 425;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 45 ILVDTGSSNFAY 56
Db 62 ILVDTGSSNFAY 73

RESULT 8
US-09-548-367D-28

; Sequence 28, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-28

Query Match 3.0%; Score 12; DB 4; Length 425;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 45 ILVDTGSSNFAY 56
Db 62 ILVDTGSSNFAY 73

RESULT 9
US-09-548-372D-51
; Sequence 51, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Artificial sequence
; OTHER INFORMATION: Hu-Aep2(b) delta TM
US-09-548-372D-51

Query Match 3.0%; Score 12; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 45 ILVDTGSSNFAY 56
Db 90 ILVDTGSSNFAY 101

RESULT 10

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US-09-548-367D-51
; Sequence 51, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hu-Asp2(b) delta TM
US-09-548-367D-51

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Query Match
Best Local Similarity 3.0%; Score 12; DB 4; Length 428;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 45 ILVDTGSSNFAV 56
Db 90 ILVDTGSSNFAV 101

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RESULT 11
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; Sequence 26, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280I
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Hu-Asp2(b) delta TM
US-09-548-372D-26

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Query Match
Best Local Similarity 3.0%; Score 12; DB 4; Length 433;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 45 ILVDTGSSNFAV 56
Db 70 ILVDTGSSNFAV 81

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RESULT 12
US-09-548-367D-26
; Sequence 26, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Hu-Asp2(b) delta TM
US-09-548-367D-26

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Query Match
Best Local Similarity 3.0%; Score 12; DB 4; Length 433;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 45 ILVDTGSSNFAV 56
Db 70 ILVDTGSSNFAV 81

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RESULT 13
US-09-548-372D-53
; Sequence 53, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280I
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hu-Asp2(b) delta TM
US-09-548-372D-53

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Query Match
Best Local Similarity 3.0%; Score 12; DB 4; Length 434;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 45 ILVDTGSSNFAV 56
Db 90 ILVDTGSSNFAV 101

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RESULT 14
US-09-548-367D-53
; Sequence 53, Application US/09548372D

; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
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; SEQ ID NO 53
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hu-Asp2(b) delta TM
US-09-548-367D-53

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Best Local Similarity 100.0%; Pred.No.0.0015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 ILVDTGSSNFAV 56
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Db 90 ILVDTGSSNFAV 101

RESULT 15
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; Sequence 22, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280I
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-22

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Best Local Similarity 100.0%; Pred.No.0.0016;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 ILVDTGSSNFAV 56
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Db 83 ILVDTGSSNFAV 94

Search completed: April 1, 2003, 11:54:09
Job time : 27 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 1, 2003, 11:53:31 ; Search time 36 Seconds
(without alignments)
689.479 Million cell updates/sec

Title: US-09-668-314C-2_COPY_63_468
Perfect score: 406
Sequence: 1 ALEPALSPPAGANFLAMVD.....STEDVANSVCVPAQSLSEPTL 406

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Word size : 0

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0

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Post-processing: Listing first 1000 summaries

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Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	406	100.0	518	9	US-09-886-143-2
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4	406	100.0	518	9	US-09-978-192A-196
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8	406	100.0	518	9	US-10-176-758-72
9	406	100.0	518	9	US-10-175-737-72
10	406	100.0	518	9	US-10-173-706-72
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23	406	100.0	518	9	US-10-175-729-72	Sequence 72, Appl
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25	406	100.0	518	9	US-10-175-743-72	Sequence 72, Appl
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85	406	100.0	518	9	US-10-180-999-72	Sequence 72, Appl
86	406	100.0	518	9	US-10-183-013-72	Sequence 72, Appl
87	406	100.0	518	9	US-10-184-612-72	Sequence 72, Appl
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90	406	100.0	518	9	US-10-184-622-72	Sequence 72, Appl
91	406	100.0	518	9	US-10-184-628-72	Sequence 72, Appl
92	406	100.0	518	9	US-10-184-629-72	Sequence 72, Appl

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99	406	100.0	518	9	US-10-187-588-72	Sequence 72, App1	172	406	100.0	518	9	US-10-195-894-72	Sequence 72, App1
100	406	100.0	518	9	US-10-187-597-72	Sequence 72, App1	173	406	100.0	518	9	US-10-205-908-72	Sequence 72, App1
101	406	100.0	518	9	US-10-187-598-72	Sequence 72, App1	174	406	100.0	518	9	US-09-978-191A-196	Sequence 196, App
102	406	100.0	518	9	US-10-187-600-72	Sequence 72, App1	175	406	100.0	518	9	US-09-978-403A-196	Sequence 196, App
103	406	100.0	518	9	US-10-187-601-72	Sequence 72, App1	176	406	100.0	518	9	US-09-978-564A-196	Sequence 196, App
104	406	100.0	518	9	US-10-187-602-72	Sequence 72, App1	177	406	100.0	518	9	US-09-978-585A-196	Sequence 196, App
105	406	100.0	518	9	US-10-187-603-72	Sequence 72, App1	178	406	100.0	518	9	US-10-017-081A-196	Sequence 196, App
106	406	100.0	518	9	US-10-187-741-72	Sequence 72, App1	179	406	100.0	518	9	US-10-184-619-72	Sequence 72, App1
107	406	100.0	518	9	US-10-187-743-72	Sequence 72, App1	180	406	100.0	518	9	US-10-186-855-72	Sequence 72, App1
108	406	100.0	518	9	US-10-187-746-72	Sequence 72, App1	181	406	100.0	518	9	US-10-187-599-72	Sequence 72, App1
109	406	100.0	518	9	US-10-187-747-72	Sequence 72, App1	182	406	100.0	518	9	US-10-187-750-72	Sequence 72, App1
110	406	100.0	518	9	US-10-187-751-72	Sequence 72, App1	183	406	100.0	518	9	US-10-188-780-72	Sequence 72, App1
111	406	100.0	518	9	US-10-187-753-72	Sequence 72, App1	184	406	100.0	518	9	US-10-192-015-72	Sequence 72, App1
112	406	100.0	518	9	US-10-187-754-72	Sequence 72, App1	185	406	100.0	518	9	US-10-194-394-72	Sequence 72, App1
113	406	100.0	518	9	US-10-187-757-72	Sequence 72, App1	186	406	100.0	518	9	US-10-194-425-72	Sequence 72, App1
114	406	100.0	518	9	US-10-187-884-72	Sequence 72, App1	187	406	100.0	518	9	US-10-194-485-72	Sequence 72, App1
115	406	100.0	518	9	US-10-188-767-72	Sequence 72, App1	188	406	100.0	518	9	US-10-195-885-72	Sequence 72, App1
116	406	100.0	518	9	US-10-188-769-72	Sequence 72, App1	189	406	100.0	518	9	US-10-195-890-72	Sequence 72, App1
117	406	100.0	518	9	US-10-188-770-72	Sequence 72, App1	190	406	100.0	518	9	US-10-195-899-72	Sequence 72, App1
118	406	100.0	518	9	US-10-188-773-72	Sequence 72, App1	191	406	100.0	518	9	US-10-196-748-72	Sequence 72, App1
119	406	100.0	518	9	US-10-188-781-72	Sequence 72, App1	192	406	100.0	518	9	US-10-196-750-72	Sequence 72, App1
120	406	100.0	518	9	US-10-194-361-72	Sequence 72, App1	193	406	100.0	518	9	US-10-197-699-72	Sequence 72, App1
121	406	100.0	518	9	US-10-194-423-72	Sequence 72, App1	194	406	100.0	518	9	US-10-197-700-72	Sequence 72, App1
122	406	100.0	518	9	US-10-195-897-72	Sequence 72, App1	195	406	100.0	518	9	US-10-197-705-72	Sequence 72, App1
123	406	100.0	518	9	US-10-195-901-72	Sequence 72, App1	196	406	100.0	518	9	US-10-197-708-72	Sequence 72, App1
124	406	100.0	518	9	US-10-196-756-72	Sequence 72, App1	197	406	100.0	518	9	US-10-198-764-72	Sequence 72, App1
125	406	100.0	518	9	US-10-173-708-72	Sequence 72, App1	198	406	100.0	518	9	US-10-198-765-72	Sequence 72, App1
126	406	100.0	518	9	US-10-176-479-72	Sequence 72, App1	199	406	100.0	518	9	US-10-198-768-72	Sequence 72, App1
127	406	100.0	518	9	US-10-176-748-72	Sequence 72, App1	200	406	100.0	518	9	US-10-198-769-72	Sequence 72, App1
128	406	100.0	518	9	US-10-176-916-72	Sequence 72, App1	201	406	100.0	518	9	US-10-199-305-72	Sequence 72, App1
129	406	100.0	518	9	US-10-179-507-72	Sequence 72, App1	202	406	100.0	518	9	US-10-199-306-72	Sequence 72, App1
130	406	100.0	518	9	US-10-179-516-72	Sequence 72, App1	203	406	100.0	518	9	US-10-199-310-72	Sequence 72, App1
131	406	100.0	518	9	US-10-179-519-72	Sequence 72, App1	204	406	100.0	518	9	US-10-199-311-72	Sequence 72, App1
132	406	100.0	518	9	US-10-179-525-72	Sequence 72, App1	205	406	100.0	518	9	US-10-199-314-72	Sequence 72, App1
133	406	100.0	518	9	US-10-180-540-72	Sequence 72, App1	206	406	100.0	518	9	US-10-199-317-72	Sequence 72, App1
134	406	100.0	518	9	US-10-180-545-72	Sequence 72, App1	207	406	100.0	518	9	US-10-199-665-72	Sequence 72, App1
135	406	100.0	518	9	US-10-183-006-72	Sequence 72, App1	208	406	100.0	518	9	US-10-199-666-72	Sequence 72, App1
136	406	100.0	518	9	US-10-183-008-72	Sequence 72, App1	209	406	100.0	518	9	US-10-199-669-72	Sequence 72, App1
137	406	100.0	518	9	US-10-183-017-72	Sequence 72, App1	210	406	100.0	518	9	US-10-201-534-72	Sequence 72, App1
138	406	100.0	518	9	US-10-183-019-72	Sequence 72, App1	211	406	100.0	518	9	US-10-201-570-72	Sequence 72, App1
139	406	100.0	518	9	US-10-184-618-72	Sequence 72, App1	212	406	100.0	518	9	US-10-201-855-72	Sequence 72, App1
140	406	100.0	518	9	US-10-184-625-72	Sequence 72, App1	213	406	100.0	518	9	US-10-201-856-72	Sequence 72, App1
141	406	100.0	518	9	US-10-184-626-72	Sequence 72, App1	214	406	100.0	518	9	US-10-202-469-72	Sequence 72, App1
142	406	100.0	518	9	US-10-184-627-72	Sequence 72, App1	215	406	100.0	518	9	US-10-202-470-72	Sequence 72, App1
143	406	100.0	518	9	US-10-184-645-72	Sequence 72, App1	216	406	100.0	518	9	US-10-202-476-72	Sequence 72, App1
144	406	100.0	518	9	US-10-184-654-72	Sequence 72, App1	217	406	100.0	518	9	US-10-202-934-72	Sequence 72, App1
145	406	100.0	518	9	US-10-184-655-72	Sequence 72, App1	218	406	100.0	518	9	US-10-202-935-72	Sequence 72, App1
146	406	100.0	518	9	US-10-188-774-72	Sequence 72, App1	219	406	100.0	518	9	US-10-202-936-72	Sequence 72, App1
147	406	100.0	518	9	US-10-188-775-72	Sequence 72, App1	220	406	100.0	518	9	US-10-202-939-72	Sequence 72, App1
148	406	100.0	518	9	US-10-194-462-72	Sequence 72, App1	221	406	100.0	518	9	US-10-205-504-72	Sequence 72, App1
149	406	100.0	518	9	US-10-195-902-72	Sequence 72, App1	222	406	100.0	518	9	US-10-205-509-72	Sequence 72, App1
150	406	100.0	518	9	US-10-196-743-72	Sequence 72, App1	223	406	100.0	518	9	US-10-205-895-72	Sequence 72, App1
151	406	100.0	518	9	US-10-196-745-72	Sequence 72, App1	224	406	100.0	518	9	US-10-205-899-72	Sequence 72, App1
152	406	100.0	518	9	US-10-196-760-72	Sequence 72, App1	225	406	100.0	518	9	US-10-205-900-72	Sequence 72, App1
153	406	100.0	518	9	US-10-196-762-72	Sequence 72, App1	226	406	100.0	518	9	US-10-205-909-72	Sequence 72, App1
154	406	100.0	518	9	US-10-197-695-72	Sequence 72, App1	227	406	100.0	518	9	US-09-978-824-196	Sequence 196, App
155	406	100.0	518	9	US-09-978-695A-196	Sequence 196, App	228	406	100.0	518	9	US-09-981-915A-196	Sequence 196, App
156	406	100.0	518	9	US-10-176-484-72	Sequence 72, App1	229	406	100.0	518	9	US-09-999-833A-196	Sequence 196, App
157	406	100.0	518	9	US-10-176-753-72	Sequence 72, App1	230	406	100.0	518	9	US-10-167-749-196	Sequence 196, App
158	406	100.0	518	9	US-10-176-917-72	Sequence 72, App1	231	406	100.0	518	9	US-10-183-002-72	Sequence 72, App1
159	406	100.0	518	9	US-10-176-982-72	Sequence 72, App1	232	406	100.0	518	9	US-10-184-621-72	Sequence 72, App1
160	406	100.0	518	9	US-10-179-506-72	Sequence 72, App1	233	406	100.0	518	9	US-10-184-628-72	Sequence 72, App1
161	406	100.0	518	9	US-10-179-513-72	Sequence 72, App1	234	406	100.0	518	9	US-10-187-852-72	Sequence 72, App1
162	406	100.0	518	9	US-10-179-514-72	Sequence 72, App1	235	406	100.0	518	9	US-10-187-887-72	Sequence 72, App1
163	406	100.0	518	9	US-10-179-522-72	Sequence 72, App1	236	406	100.0	518	9	US-10-194-461-72	Sequence 72, App1
164	406	100.0	518	9	US-10-180-556-72	Sequence 72, App1	237	406	100.0	518	9	US-10-195-892-72	Sequence 72, App1
165	406	100.0	518	9	US-10-180-560-72	Sequence 72, App1	238	406	100.0	518	9	US-10-196-751-72	Sequence 72, App1

239	406	100.0	518	9	US-10-197-694-72	Sequence 72, Appl	312	12	3.0	453	10	US-09-794-748-30	Sequence 30, Appl
240	406	100.0	518	9	US-10-197-697-72	Sequence 72, Appl	313	12	3.0	453	10	US-09-794-925-30	Sequence 30, Appl
241	406	100.0	518	9	US-10-197-707-72	Sequence 72, Appl	314	12	3.0	453	10	US-09-681-442-30	Sequence 30, Appl
242	406	100.0	518	9	US-10-199-303-72	Sequence 72, Appl	315	12	3.0	459	10	US-09-794-927-24	Sequence 24, Appl
243	406	100.0	518	9	US-10-199-318-72	Sequence 72, Appl	316	12	3.0	459	10	US-09-794-927-32	Sequence 32, Appl
244	406	100.0	518	9	US-10-199-458-72	Sequence 72, Appl	317	12	3.0	459	10	US-09-795-847-24	Sequence 24, Appl
245	406	100.0	518	9	US-10-199-462-72	Sequence 72, Appl	318	12	3.0	459	10	US-09-795-847-32	Sequence 32, Appl
246	406	100.0	518	9	US-10-201-324-72	Sequence 72, Appl	319	12	3.0	459	10	US-09-794-743-24	Sequence 24, Appl
247	406	100.0	518	9	US-10-201-338-72	Sequence 72, Appl	320	12	3.0	459	10	US-09-794-743-32	Sequence 32, Appl
248	406	100.0	518	9	US-10-201-527-72	Sequence 72, Appl	321	12	3.0	459	10	US-09-794-748-24	Sequence 24, Appl
249	406	100.0	518	9	US-10-201-528-72	Sequence 72, Appl	322	12	3.0	459	10	US-09-794-748-32	Sequence 32, Appl
250	406	100.0	518	9	US-10-201-529-72	Sequence 72, Appl	323	12	3.0	459	10	US-09-794-925-24	Sequence 24, Appl
251	406	100.0	518	9	US-10-201-530-72	Sequence 72, Appl	324	12	3.0	459	10	US-09-794-925-32	Sequence 32, Appl
252	406	100.0	518	9	US-10-202-408-72	Sequence 72, Appl	325	12	3.0	459	10	US-09-681-442-32	Sequence 32, Appl
253	406	100.0	518	9	US-10-202-409-72	Sequence 72, Appl	326	12	3.0	459	10	US-09-681-442-32	Sequence 32, Appl
254	406	100.0	518	9	US-10-202-411-72	Sequence 72, Appl	327	12	3.0	459	10	US-09-794-927-6	Sequence 6, Appl
255	406	100.0	518	9	US-10-202-472-72	Sequence 72, Appl	328	12	3.0	459	10	US-09-795-847-6	Sequence 6, Appl
256	406	100.0	518	9	US-10-205-502-72	Sequence 72, Appl	329	12	3.0	459	10	US-09-794-743-6	Sequence 6, Appl
257	406	100.0	518	9	US-10-205-507-72	Sequence 72, Appl	330	12	3.0	459	10	US-09-794-748-6	Sequence 6, Appl
258	406	100.0	518	9	US-10-205-511-72	Sequence 72, Appl	331	12	3.0	459	10	US-09-794-925-6	Sequence 6, Appl
259	406	100.0	518	9	US-10-205-902-72	Sequence 72, Appl	332	12	3.0	459	10	US-09-681-442-6	Sequence 6, Appl
260	406	100.0	518	9	US-10-205-907-72	Sequence 72, Appl	333	12	3.0	459	10	US-09-795-903A-2	Sequence 2, Appl
261	406	100.0	518	9	US-09-918-585A-196	Sequence 196, App	334	12	3.0	459	10	US-09-795-903A-2	Sequence 2, Appl
262	406	100.0	518	9	US-10-194-456-72	Sequence 72, Appl	335	12	3.0	459	10	US-09-845-226-2	Sequence 2, Appl
263	406	100.0	518	9	US-10-196-758-72	Sequence 72, Appl	336	12	3.0	501	9	US-09-969-671A-2	Sequence 2, Appl
264	406	100.0	518	9	US-10-198-770-72	Sequence 72, Appl	337	12	3.0	501	10	US-09-794-927-8	Sequence 8, Appl
265	406	100.0	518	9	US-10-199-308-72	Sequence 72, Appl	338	12	3.0	501	10	US-09-794-927-8	Sequence 8, Appl
266	406	100.0	518	9	US-10-200-617-72	Sequence 72, Appl	339	12	3.0	501	10	US-09-795-847-8	Sequence 8, Appl
267	406	100.0	518	9	US-10-205-893-72	Sequence 72, Appl	340	12	3.0	501	10	US-09-795-847-8	Sequence 8, Appl
268	406	100.0	518	9	US-10-205-897-72	Sequence 72, Appl	341	12	3.0	501	10	US-09-794-743-4	Sequence 4, Appl
269	406	100.0	518	10	US-09-794-927-2	Sequence 2, Appl	342	12	3.0	501	10	US-09-794-743-8	Sequence 8, Appl
270	406	100.0	518	10	US-09-795-847-2	Sequence 2, Appl	343	12	3.0	501	10	US-09-794-748-4	Sequence 4, Appl
271	406	100.0	518	10	US-09-794-743-2	Sequence 2, Appl	344	12	3.0	501	10	US-09-794-748-8	Sequence 8, Appl
272	406	100.0	518	10	US-09-794-748-2	Sequence 2, Appl	345	12	3.0	501	10	US-09-794-925-4	Sequence 4, Appl
273	406	100.0	518	10	US-09-794-925-2	Sequence 2, Appl	346	12	3.0	501	10	US-09-794-925-8	Sequence 8, Appl
274	406	100.0	518	10	US-09-215-450-19	Sequence 19, Appl	347	12	3.0	501	10	US-09-681-442-4	Sequence 4, Appl
275	406	100.0	518	10	US-09-681-442-2	Sequence 2, Appl	348	12	3.0	501	10	US-09-681-442-8	Sequence 8, Appl
276	406	100.0	518	12	US-10-052-586-72	Sequence 72, Appl	349	12	3.0	503	9	US-09-795-903A-3	Sequence 3, Appl
277	373	91.9	423	9	US-09-470-954A-46	Sequence 46, Appl	350	12	3.0	503	10	US-09-796-264-3	Sequence 3, Appl
278	50	12.3	50	10	US-09-864-761-49075	Sequence 49075, A	351	12	3.0	503	10	US-09-845-226-3	Sequence 3, Appl
279	12	3.0	425	10	US-09-794-927-28	Sequence 28, Appl	352	12	3.0	774	9	US-09-969-671A-4	Sequence 4, Appl
280	12	3.0	425	10	US-09-795-847-28	Sequence 28, Appl	353	9	2.2	322	9	US-09-470-954A-47	Sequence 47, Appl
281	12	3.0	425	10	US-09-794-743-28	Sequence 28, Appl	354	9	2.2	401	9	US-09-924-340-24	Sequence 24, Appl
282	12	3.0	425	10	US-09-794-748-28	Sequence 28, Appl	355	9	2.2	401	9	US-09-992-600A-24	Sequence 24, Appl
283	12	3.0	425	10	US-09-794-925-28	Sequence 28, Appl	356	8	2.0	504	10	US-09-919-497-67	Sequence 67, App
284	12	3.0	425	10	US-09-681-442-28	Sequence 28, Appl	357	8	2.0	548	10	US-09-741-669-413	Sequence 413, App
285	12	3.0	428	10	US-09-794-927-51	Sequence 51, Appl	358	7	1.7	21	9	US-09-974-879-293	Sequence 293, App
286	12	3.0	428	10	US-09-795-847-51	Sequence 51, Appl	359	7	1.7	25	10	US-09-864-761-45398	Sequence 45398, A
287	12	3.0	428	10	US-09-794-743-51	Sequence 51, Appl	360	7	1.7	34	9	US-09-948-820-94	Sequence 94, Appl
288	12	3.0	428	10	US-09-794-748-51	Sequence 51, Appl	361	7	1.7	50	9	US-09-974-879-291	Sequence 291, App
289	12	3.0	428	10	US-09-794-925-51	Sequence 51, Appl	362	7	1.7	60	8	US-08-914-350-7	Sequence 7, Appl
290	12	3.0	428	10	US-09-681-442-51	Sequence 51, Appl	363	7	1.7	95	10	US-09-734-569-52	Sequence 52, Appl
291	12	3.0	433	10	US-09-794-927-26	Sequence 26, Appl	364	7	1.7	175	10	US-09-864-761-46612	Sequence 46612, A
292	12	3.0	433	10	US-09-795-847-26	Sequence 26, Appl	365	7	1.7	262	10	US-09-925-302-522	Sequence 522, App
293	12	3.0	433	10	US-09-794-743-26	Sequence 26, Appl	366	7	1.7	265	9	US-09-866-050A-655	Sequence 655, App
294	12	3.0	433	10	US-09-794-748-26	Sequence 26, Appl	367	7	1.7	306	10	US-09-741-669-456	Sequence 456, App
295	12	3.0	433	10	US-09-794-925-26	Sequence 26, Appl	368	7	1.7	320	8	US-08-914-350-2	Sequence 2, Appl
296	12	3.0	433	10	US-09-681-442-26	Sequence 26, Appl	369	7	1.7	323	9	US-09-948-820-85	Sequence 85, Appl
297	12	3.0	434	10	US-09-794-927-53	Sequence 53, Appl	370	7	1.7	326	9	US-09-795-903A-31	Sequence 31, Appl
298	12	3.0	434	10	US-09-795-847-53	Sequence 53, Appl	371	7	1.7	326	10	US-09-796-264-31	Sequence 31, Appl
299	12	3.0	434	10	US-09-794-743-53	Sequence 53, Appl	372	7	1.7	336	10	US-09-845-226-31	Sequence 31, Appl
300	12	3.0	434	10	US-09-794-748-53	Sequence 53, Appl	373	7	1.7	337	10	US-09-734-569-156	Sequence 156, App
301	12	3.0	434	10	US-09-794-925-53	Sequence 53, Appl	374	7	1.7	353	10	US-09-905-173-36	Sequence 36, Appl
302	12	3.0	434	10	US-09-681-442-53	Sequence 53, Appl	375	7	1.7	388	10	US-09-215-450-23	Sequence 23, Appl
303	12	3.0	446	10	US-09-794-927-22	Sequence 22, Appl	376	7	1.7	451	9	US-10-042-431-43	Sequence 43, Appl
304	12	3.0	446	10	US-09-795-847-22	Sequence 22, Appl	377	7	1.7	451	9	US-09-759-130B-413	Sequence 413, App
305	12	3.0	446	10	US-09-794-743-22	Sequence 22, Appl	378	7	1.7	470	9	US-10-042-431-69	Sequence 69, App
306	12	3.0	446	10	US-09-794-748-22	Sequence 22, Appl	379	7	1.7	490	9	US-09-759-130B-439	Sequence 439, App
307	12	3.0	446	10	US-09-794-925-22	Sequence 22, Appl	380	7	1.7	615	10	US-09-862-027-49	Sequence 49, Appl
308	12	3.0	446	10	US-09-681-442-22	Sequence 22, Appl	381	7	1.7	1429	9	US-09-953-407-1	Sequence 1, Appl
309	12	3.0	453	10	US-09-794-927-30	Sequence 30, Appl	382	6	1.5	12	8	US-08-424-550B-446	Sequence 446, App
310	12	3.0	453	10	US-09-795-847-30	Sequence 30, Appl	383	6	1.5	14	10	US-09-918-171A-28	Sequence 28, Appl
311	12	3.0	453	10	US-09-794-743-30	Sequence 30, Appl	384	6	1.5	19	10	US-09-918-171A-24	Sequence 24, Appl

385	6	1.5	31	9	US-09-996-069-12	Sequence 12, Appl	458	6	1.5	207	9	US-10-230-414-76	Sequence 76, Appl
386	6	1.5	32	10	US-09-864-761-41359	Sequence 41359, A	459	6	1.5	210	9	US-10-060-765-2	Sequence 2, Appl1
387	6	1.5	35	10	US-09-864-761-36036	Sequence 36036, A	460	6	1.5	210	9	US-10-090-983-7	Sequence 7, Appl1
388	6	1.5	35	10	US-09-864-761-39580	Sequence 39580, A	461	6	1.5	211	9	US-10-222-577-5	Sequence 5, Appl1
389	6	1.5	36	10	US-09-764-877-1258	Sequence 1258, Ap	462	6	1.5	211	9	US-10-232-578-5	Sequence 5, Appl1
390	6	1.5	38	10	US-09-873-106B-16	Sequence 16, Appl	463	6	1.5	211	10	US-09-790-045-5	Sequence 5, Appl1
391	6	1.5	43	9	US-09-809-391-524	Sequence 524, App	464	6	1.5	214	10	US-09-925-299-864	Sequence 864, App
392	6	1.5	47	10	US-09-864-761-43013	Sequence 43013, A	465	6	1.5	214	10	US-09-925-299-864	Sequence 864, App
393	6	1.5	48	10	US-09-864-761-48227	Sequence 48227, A	466	6	1.5	218	9	US-09-738-626-4670	Sequence 4670, App
394	6	1.5	49	10	US-09-864-761-35532	Sequence 35532, A	467	6	1.5	220	9	US-10-001-054-56	Sequence 56, Appl
395	6	1.5	55	10	US-09-908-711-80	Sequence 80, Appl	468	6	1.5	220	10	US-09-220-920-26	Sequence 26, Appl
396	6	1.5	55	10	US-09-864-761-39275	Sequence 39275, A	469	6	1.5	220	10	US-09-804-615-9	Sequence 9, Appl1
397	6	1.5	55	10	US-09-864-761-40066	Sequence 40066, A	470	6	1.5	222	10	US-09-815-242-10768	Sequence 10768, A
398	6	1.5	57	10	US-09-864-761-41100	Sequence 41100, A	471	6	1.5	234	12	US-10-081-281-119	Sequence 119, App
399	6	1.5	58	10	US-09-854-191	Sequence 191, App	472	6	1.5	237	9	US-09-992-998-295	Sequence 295, App
400	6	1.5	58	10	US-09-764-878-191	Sequence 191, App	473	6	1.5	237	9	US-09-989-2934-295	Sequence 295, App
401	6	1.5	59	9	US-09-848-616-141	Sequence 141, App	474	6	1.5	237	9	US-09-989-735-295	Sequence 295, App
402	6	1.5	62	9	US-10-012-542-191	Sequence 191, App	475	6	1.5	237	9	US-09-990-444-295	Sequence 295, App
403	6	1.5	67	10	US-09-864-761-36500	Sequence 36500, A	476	6	1.5	237	9	US-09-989-730-295	Sequence 295, App
404	6	1.5	68	10	US-09-220-920-50	Sequence 50, Appl	477	6	1.5	237	9	US-09-990-436-295	Sequence 295, App
405	6	1.5	68	10	US-09-864-761-37739	Sequence 37739, A	478	6	1.5	237	9	US-09-991-181-295	Sequence 295, App
406	6	1.5	78	10	US-09-881-752A-120	Sequence 120, App	479	6	1.5	237	9	US-09-993-687-295	Sequence 295, App
407	6	1.5	82	10	US-09-864-761-37785	Sequence 37785, A	480	6	1.5	237	9	US-09-989-734-295	Sequence 295, App
408	6	1.5	87	10	US-09-220-920-115	Sequence 115, App	481	6	1.5	237	9	US-09-997-653-295	Sequence 295, App
409	6	1.5	91	9	US-09-989-920-205	Sequence 205, App	482	6	1.5	237	9	US-10-174-590-222	Sequence 222, App
410	6	1.5	97	9	US-09-925-299-1071	Sequence 1071, Ap	483	6	1.5	237	9	US-10-176-758-222	Sequence 222, App
411	6	1.5	97	10	US-09-925-299-1071	Sequence 1071, Ap	484	6	1.5	237	9	US-10-175-737-222	Sequence 222, App
412	6	1.5	107	10	US-09-230-920-52	Sequence 52, Appl	485	6	1.5	237	9	US-09-983-602-154	Sequence 154, App
413	6	1.5	108	9	US-09-809-391-552	Sequence 552, App	486	6	1.5	237	9	US-09-993-667-295	Sequence 295, App
414	6	1.5	110	10	US-09-867-550-298	Sequence 298, App	487	6	1.5	237	9	US-10-173-706-222	Sequence 222, App
415	6	1.5	113	9	US-10-092-154-974	Sequence 974, App	488	6	1.5	237	9	US-10-175-738-222	Sequence 222, App
416	6	1.5	113	10	US-09-764-847-974	Sequence 974, App	489	6	1.5	237	9	US-10-175-752-222	Sequence 222, App
417	6	1.5	114	9	US-09-738-626-3786	Sequence 3786, Ap	490	6	1.5	237	9	US-10-176-482-222	Sequence 222, App
418	6	1.5	115	9	US-09-738-626-5389	Sequence 5389, Ap	491	6	1.5	237	9	US-10-176-757-222	Sequence 222, App
419	6	1.5	126	9	US-09-764-868-1053	Sequence 1053, Ap	492	6	1.5	237	9	US-10-176-913-222	Sequence 222, App
420	6	1.5	130	9	US-10-101-464A-496	Sequence 496, App	493	6	1.5	237	9	US-10-180-552-222	Sequence 222, App
421	6	1.5	138	10	US-09-912-020-300	Sequence 300, App	494	6	1.5	237	9	US-10-180-557-222	Sequence 222, App
422	6	1.5	142	9	US-09-839-894-38	Sequence 38, Appl	495	6	1.5	237	9	US-09-990-438-295	Sequence 295, App
423	6	1.5	144	9	US-10-076-785-50	Sequence 50, Appl	496	6	1.5	237	9	US-09-990-662-295	Sequence 295, App
424	6	1.5	145	10	US-09-915-582-88	Sequence 88, Appl	497	6	1.5	237	9	US-09-997-428-295	Sequence 295, App
425	6	1.5	154	10	US-09-867-550-646	Sequence 646, App	498	6	1.5	237	9	US-09-997-666-295	Sequence 295, App
426	6	1.5	157	9	US-09-981-286A-1	Sequence 1, Appl1	499	6	1.5	237	9	US-10-173-700-222	Sequence 222, App
427	6	1.5	157	9	US-09-809-391-350	Sequence 350, App	500	6	1.5	237	9	US-10-174-572-222	Sequence 222, App
428	6	1.5	163	10	US-09-867-550-522	Sequence 522, App	501	6	1.5	237	9	US-10-174-579-222	Sequence 222, App
429	6	1.5	165	9	US-09-839-894-33	Sequence 33, Appl	502	6	1.5	237	9	US-10-174-582-222	Sequence 222, App
430	6	1.5	165	9	US-09-981-286A-33	Sequence 33, Appl	503	6	1.5	237	9	US-10-174-588-222	Sequence 222, App
431	6	1.5	165	9	US-09-981-286A-34	Sequence 34, Appl	504	6	1.5	237	9	US-10-175-739-222	Sequence 222, App
432	6	1.5	167	9	US-09-764-868-953	Sequence 953, App	505	6	1.5	237	9	US-10-175-740-222	Sequence 222, App
433	6	1.5	167	9	US-09-839-894-4	Sequence 4, Appl1	506	6	1.5	237	9	US-10-175-743-222	Sequence 222, App
434	6	1.5	168	9	US-09-831-894-37	Sequence 37, Appl	507	6	1.5	237	9	US-10-176-488-222	Sequence 222, App
435	6	1.5	169	9	US-09-981-286A-7	Sequence 7, Appl1	508	6	1.5	237	9	US-10-176-492-222	Sequence 222, App
436	6	1.5	173	9	US-09-738-626-6034	Sequence 6034, Ap	509	6	1.5	237	9	US-10-176-747-222	Sequence 222, App
437	6	1.5	173	10	US-09-925-301-425	Sequence 1425, Ap	510	6	1.5	237	9	US-10-176-750-222	Sequence 222, App
438	6	1.5	174	9	US-09-738-626-4376	Sequence 4376, Ap	511	6	1.5	237	9	US-10-176-985-222	Sequence 222, App
439	6	1.5	174	10	US-09-764-864-904	Sequence 904, App	512	6	1.5	237	9	US-10-176-987-222	Sequence 222, App
440	6	1.5	181	10	US-09-220-920-40	Sequence 40, Appl	513	6	1.5	237	9	US-10-176-991-222	Sequence 222, App
441	6	1.5	184	10	US-09-925-297-737	Sequence 737, App	514	6	1.5	237	9	US-10-176-992-222	Sequence 222, App
442	6	1.5	185	9	US-10-078-770-178	Sequence 178, App	515	6	1.5	237	9	US-10-176-993-222	Sequence 222, App
443	6	1.5	186	9	US-09-809-391-394	Sequence 394, App	516	6	1.5	237	9	US-10-184-558-222	Sequence 222, App
444	6	1.5	187	10	US-09-864-761-35716	Sequence 35716, A	517	6	1.5	237	9	US-09-990-711-295	Sequence 295, App
445	6	1.5	187	10	US-09-864-761-36056	Sequence 36056, A	518	6	1.5	237	9	US-10-173-695-222	Sequence 222, App
446	6	1.5	188	9	US-09-974-879-508	Sequence 508, App	519	6	1.5	237	9	US-10-173-697-222	Sequence 222, App
447	6	1.5	193	10	US-09-764-898-214	Sequence 214, App	520	6	1.5	237	9	US-10-173-705-222	Sequence 222, App
448	6	1.5	196	9	US-09-957-187-8	Sequence 8, Appl1	521	6	1.5	237	9	US-10-174-576-222	Sequence 222, App
449	6	1.5	196	12	US-10-081-281-109	Sequence 109, App	522	6	1.5	237	9	US-10-174-585-222	Sequence 222, App
450	6	1.5	196	12	US-10-081-281-117	Sequence 117, App	523	6	1.5	237	9	US-10-174-586-222	Sequence 222, App
451	6	1.5	200	9	US-09-738-626-4692	Sequence 4692, Ap	524	6	1.5	237	9	US-10-175-747-222	Sequence 222, App
452	6	1.5	200	10	US-09-804-615-2	Sequence 2, Appl1	525	6	1.5	237	9	US-10-176-481-222	Sequence 222, App
453	6	1.5	207	9	US-10-227-884-76	Sequence 76, Appl	526	6	1.5	237	9	US-10-176-485-222	Sequence 222, App
454	6	1.5	207	9	US-10-230-163-76	Sequence 16, Appl	527	6	1.5	237	9	US-10-176-487-222	Sequence 222, App
455	6	1.5	207	9	US-10-149-819-19	Sequence 19, Appl	528	6	1.5	237	9	US-10-176-493-222	Sequence 222, App
456	6	1.5	207	9	US-10-218-631-76	Sequence 76, Appl	529	6	1.5	237	9	US-10-176-756-222	Sequence 222, App
457	6	1.5	207	9	US-10-230-338-76	Sequence 76, Appl	530	6	1.5	237	9	US-10-176-911-222	Sequence 222, App

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586	6	1.5	237	9	US-10-187-602-222	Sequence 222	App	659	6	1.5	237	9	US-09-991-172-995	Sequence 295	App
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594	6	1.5	237	9	US-10-187-754-222	Sequence 222	App	667	6	1.5	237	9	US-10-192-015-222	Sequence 222	App
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603	6	1.5	237	9	US-10-194-421-222	Sequence 222	App	676	6	1.5	237	9	US-10-197-699-222	Sequence 222	App

677	6	1.5	237	9	US-10-197-700-222	Sequence 222, App	750	6	1.5	237	9	US-09-997-683-295	Sequence 295, App
678	6	1.5	237	9	US-10-197-705-222	Sequence 222, App	751	6	1.5	237	9	US-10-194-456-222	Sequence 222, App
679	6	1.5	237	9	US-10-197-708-222	Sequence 222, App	752	6	1.5	237	9	US-10-196-758-222	Sequence 222, App
680	6	1.5	237	9	US-10-198-764-222	Sequence 222, App	753	6	1.5	237	9	US-10-198-770-222	Sequence 222, App
681	6	1.5	237	9	US-10-198-765-222	Sequence 222, App	754	6	1.5	237	9	US-10-199-308-222	Sequence 222, App
682	6	1.5	237	9	US-10-198-768-222	Sequence 222, App	755	6	1.5	237	9	US-10-200-617-222	Sequence 222, App
683	6	1.5	237	9	US-10-198-769-222	Sequence 222, App	756	6	1.5	237	9	US-10-205-893-222	Sequence 222, App
684	6	1.5	237	9	US-10-198-769-222	Sequence 222, App	757	6	1.5	237	9	US-10-205-897-222	Sequence 222, App
685	6	1.5	237	9	US-10-199-306-222	Sequence 222, App	758	6	1.5	237	10	US-09-220-920-32	Sequence 32, App
686	6	1.5	237	9	US-10-199-310-222	Sequence 222, App	759	6	1.5	237	10	US-09-804-615-4	Sequence 4, App
687	6	1.5	237	9	US-10-199-311-222	Sequence 222, App	760	6	1.5	237	10	US-09-989-722-295	Sequence 295, App
688	6	1.5	237	9	US-10-199-314-222	Sequence 222, App	761	6	1.5	237	10	US-09-989-723-295	Sequence 295, App
689	6	1.5	237	9	US-10-199-317-222	Sequence 222, App	762	6	1.5	237	10	US-09-989-279-295	Sequence 295, App
690	6	1.5	237	9	US-10-199-665-222	Sequence 222, App	763	6	1.5	237	10	US-09-989-727-295	Sequence 295, App
691	6	1.5	237	9	US-10-199-666-222	Sequence 222, App	764	6	1.5	237	10	US-09-989-731-295	Sequence 295, App
692	6	1.5	237	9	US-10-199-669-222	Sequence 222, App	765	6	1.5	237	10	US-09-989-732-295	Sequence 295, App
693	6	1.5	237	9	US-10-201-534-222	Sequence 222, App	766	6	1.5	237	10	US-09-991-073-295	Sequence 295, App
694	6	1.5	237	9	US-10-201-770-222	Sequence 222, App	767	6	1.5	237	10	US-09-990-442-295	Sequence 295, App
695	6	1.5	237	9	US-10-201-855-222	Sequence 222, App	768	6	1.5	237	10	US-09-991-163-295	Sequence 295, App
696	6	1.5	237	9	US-10-201-856-222	Sequence 222, App	769	6	1.5	237	10	US-09-993-604-295	Sequence 295, App
697	6	1.5	237	9	US-10-202-469-222	Sequence 222, App	770	6	1.5	237	10	US-09-990-456-295	Sequence 295, App
698	6	1.5	237	9	US-10-202-470-222	Sequence 222, App	771	6	1.5	237	10	US-09-989-721-295	Sequence 295, App
699	6	1.5	237	9	US-10-202-476-222	Sequence 222, App	772	6	1.5	237	12	US-10-052-586-222	Sequence 222, App
700	6	1.5	237	9	US-10-202-934-222	Sequence 222, App	773	6	1.5	238	9	US-09-813-398-40	Sequence 40, App
701	6	1.5	237	9	US-10-202-935-222	Sequence 222, App	774	6	1.5	240	9	US-09-908-193-43	Sequence 43, App
702	6	1.5	237	9	US-10-202-936-222	Sequence 222, App	775	6	1.5	240	9	US-09-860-636B-15	Sequence 15, App
703	6	1.5	237	9	US-10-202-939-222	Sequence 222, App	776	6	1.5	241	10	US-09-925-297-542	Sequence 542, App
704	6	1.5	237	9	US-10-205-504-222	Sequence 222, App	777	6	1.5	242	9	US-10-042-141-101	Sequence 101, App
705	6	1.5	237	9	US-10-205-509-222	Sequence 222, App	778	6	1.5	242	10	US-09-726-643-101	Sequence 101, App
706	6	1.5	237	9	US-10-205-895-222	Sequence 222, App	779	6	1.5	244	1	US-08-722-570-1	Sequence 1, App
707	6	1.5	237	9	US-10-205-899-222	Sequence 222, App	780	6	1.5	247	9	US-09-866-050A-687	Sequence 687, App
708	6	1.5	237	9	US-10-205-900-222	Sequence 222, App	781	6	1.5	248	10	US-09-791-171-60	Sequence 60, App
709	6	1.5	237	9	US-10-205-909-222	Sequence 222, App	782	6	1.5	256	9	US-09-738-626-6299	Sequence 6299, App
710	6	1.5	237	9	US-09-990-443-295	Sequence 295, App	783	6	1.5	259	9	US-09-991-211-3	Sequence 3, App
711	6	1.5	237	9	US-09-990-726-295	Sequence 295, App	784	6	1.5	259	10	US-09-815-242-11603	Sequence 11603, A
712	6	1.5	237	9	US-09-997-559-295	Sequence 295, App	785	6	1.5	260	9	US-09-764-868-992	Sequence 992, App
713	6	1.5	237	9	US-09-997-601-295	Sequence 295, App	786	6	1.5	262	10	US-09-915-582-66	Sequence 66, App
714	6	1.5	237	9	US-10-183-002-222	Sequence 222, App	787	6	1.5	264	8	US-08-424-550B-76	Sequence 76, App
715	6	1.5	237	9	US-10-184-621-222	Sequence 222, App	788	6	1.5	266	9	US-09-738-626-3657	Sequence 3657, App
716	6	1.5	237	9	US-10-184-638-222	Sequence 222, App	789	6	1.5	266	12	US-10-007-693-66	Sequence 66, App
717	6	1.5	237	9	US-10-187-752-222	Sequence 222, App	790	6	1.5	273	9	US-09-738-626-4392	Sequence 4392, App
718	6	1.5	237	9	US-10-187-887-222	Sequence 222, App	791	6	1.5	274	9	US-09-738-626-6741	Sequence 6741, App
719	6	1.5	237	9	US-10-194-461-222	Sequence 222, App	792	6	1.5	276	10	US-09-925-300-164	Sequence 1624, App
720	6	1.5	237	9	US-10-195-892-222	Sequence 222, App	793	6	1.5	277	10	US-09-925-300-1169	Sequence 1169, App
721	6	1.5	237	9	US-10-196-751-222	Sequence 222, App	794	6	1.5	281	10	US-09-801-368-278	Sequence 278, App
722	6	1.5	237	9	US-10-197-694-222	Sequence 222, App	795	6	1.5	283	10	US-09-908-711-95	Sequence 95, App
723	6	1.5	237	9	US-10-197-697-222	Sequence 222, App	796	6	1.5	284	9	US-09-738-626-3667	Sequence 3667, App
724	6	1.5	237	9	US-10-197-707-222	Sequence 222, App	797	6	1.5	289	9	US-10-151-832-6	Sequence 6, App
725	6	1.5	237	9	US-10-199-303-222	Sequence 222, App	798	6	1.5	289	9	US-10-151-832-8	Sequence 8, App
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727	6	1.5	237	9	US-10-199-458-222	Sequence 222, App	800	6	1.5	302	9	US-10-125-540-421	Sequence 421, App
728	6	1.5	237	9	US-10-199-462-222	Sequence 222, App	801	6	1.5	302	10	US-09-764-870-421	Sequence 421, App
729	6	1.5	237	9	US-10-201-324-222	Sequence 222, App	802	6	1.5	303	10	US-09-854-122-48	Sequence 48, App
730	6	1.5	237	9	US-10-201-328-222	Sequence 222, App	803	6	1.5	303	10	US-09-733-569B-15	Sequence 15, App
731	6	1.5	237	9	US-10-201-527-222	Sequence 222, App	804	6	1.5	303	10	US-09-882-837-2	Sequence 2, App
732	6	1.5	237	9	US-10-201-528-222	Sequence 222, App	805	6	1.5	304	9	US-09-738-626-3743	Sequence 3743, App
733	6	1.5	237	9	US-10-201-529-222	Sequence 222, App	806	6	1.5	304	10	US-09-854-122-47	Sequence 47, App
734	6	1.5	237	9	US-10-201-530-222	Sequence 222, App	807	6	1.5	309	10	US-09-886-055-149	Sequence 149, App
735	6	1.5	237	9	US-10-202-408-222	Sequence 222, App	808	6	1.5	310	9	US-10-147-761-2	Sequence 2, App
736	6	1.5	237	9	US-10-202-409-222	Sequence 222, App	809	6	1.5	310	9	US-10-151-832-3	Sequence 3, App
737	6	1.5	237	9	US-10-202-411-222	Sequence 222, App	810	6	1.5	312	9	US-10-151-832-9	Sequence 9, App
738	6	1.5	237	9	US-10-202-472-222	Sequence 222, App	811	6	1.5	317	9	US-10-151-832-5	Sequence 5, App
739	6	1.5	237	9	US-10-205-502-222	Sequence 222, App	812	6	1.5	324	1	US-08-781-986A-5209	Sequence 5209, App
740	6	1.5	237	9	US-10-205-507-222	Sequence 222, App	813	6	1.5	324	10	US-09-854-122-18	Sequence 18, App
741	6	1.5	237	9	US-10-205-511-222	Sequence 222, App	814	6	1.5	324	10	US-09-815-242-5392	Sequence 5392, App
742	6	1.5	237	9	US-10-205-902-222	Sequence 222, App	815	6	1.5	326	10	US-09-815-242-12264	Sequence 12264, A
743	6	1.5	237	9	US-10-205-907-222	Sequence 222, App	816	6	1.5	328	9	US-09-738-626-5059	Sequence 5059, App
744	6	1.5	237	9	US-09-989-729A-295	Sequence 295, App	817	6	1.5	330	10	US-09-815-837-94	Sequence 94, App
745	6	1.5	237	9	US-09-990-440-295	Sequence 295, App	818	6	1.5	341	9	US-09-974-879-465	Sequence 465, App
746	6	1.5	237	9	US-09-991-854-295	Sequence 295, App	819	6	1.5	341	10	US-09-873-106B-2	Sequence 2, App
747	6	1.5	237	9	US-09-997-349-295	Sequence 295, App	820	6	1.5	342	10	US-09-991-258-10	Sequence 10, App
748	6	1.5	237	9	US-09-997-440-295	Sequence 295, App	821	6	1.5	343	8	US-08-424-550B-608	Sequence 608, App
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823	6	1.5	345	10	US-09-815-242-5103	Sequence 5103, Ap	896	6	1.5	419	10	US-09-784-911-2	Sequence 2, Appli
824	6	1.5	347	10	US-09-815-242-10754	Sequence 11054, A	897	6	1.5	420	10	US-09-815-0742-11001	Sequence 11001, A
825	6	1.5	349	10	US-09-815-242-116955	Sequence 11695, A	898	6	1.5	420	10	US-09-804-073-2	Sequence 2, Appli
826	6	1.5	349	9	US-09-361-630-2	Sequence 2, Appli	899	6	1.5	427	10	US-09-826-508-32	Sequence 32, Appli
827	6	1.5	349	9	US-10-028-072-170	Sequence 170, App	900	6	1.5	427	10	US-09-826-508-32	Sequence 6, Appli
828	6	1.5	349	9	US-10-121-049-170	Sequence 170, App	901	6	1.5	427	10	US-09-942-447-4	Sequence 4, Appli
829	6	1.5	349	9	US-10-123-904-170	Sequence 170, App	902	6	1.5	427	12	US-10-002-278-2	Sequence 2, Appli
830	6	1.5	349	9	US-10-140-470-170	Sequence 170, App	903	6	1.5	433	9	US-09-964-899-11	Sequence 11, Appli
831	6	1.5	349	9	US-10-175-746-170	Sequence 170, App	904	6	1.5	436	9	US-09-712-263-258	Sequence 258, App
832	6	1.5	349	9	US-10-176-918-170	Sequence 170, App	905	6	1.5	436	10	US-09-815-242-5800	Sequence 5800, Ap
833	6	1.5	349	9	US-10-176-921-170	Sequence 170, App	906	6	1.5	436	10	US-09-815-242-11846	Sequence 11846, A
834	6	1.5	349	9	US-10-137-865-170	Sequence 170, App	907	6	1.5	437	9	US-09-738-626-3992	Sequence 3992, Ap
835	6	1.5	349	9	US-10-140-474-170	Sequence 170, App	908	6	1.5	437	10	US-09-784-911-4	Sequence 4, Appli
836	6	1.5	349	9	US-10-143-431-170	Sequence 170, App	909	6	1.5	437	12	US-10-016-358-2	Sequence 2, Appli
837	6	1.5	349	9	US-10-143-114-170	Sequence 170, App	910	6	1.5	438	9	US-10-078-770-182	Sequence 182, Appli
838	6	1.5	349	9	US-10-140-002-170	Sequence 170, App	911	6	1.5	441	9	US-09-738-626-5156	Sequence 5156, Ap
839	6	1.5	349	9	US-10-142-419-170	Sequence 170, App	912	6	1.5	441	12	US-10-081-281-115	Sequence 115, App
840	6	1.5	349	9	US-10-123-262-170	Sequence 170, App	913	6	1.5	444	10	US-09-815-242-12376	Sequence 12376, A
841	6	1.5	349	9	US-10-142-423-170	Sequence 170, App	914	6	1.5	448	12	US-10-081-281-111	Sequence 111, App
842	6	1.5	349	9	US-10-121-050-170	Sequence 170, App	915	6	1.5	454	10	US-09-767-041-30	Sequence 30, Appli
843	6	1.5	349	9	US-10-141-755-170	Sequence 170, App	916	6	1.5	459	10	US-09-767-041-16	Sequence 16, Appli
844	6	1.5	349	9	US-10-143-032-170	Sequence 170, App	917	6	1.5	459	10	US-09-815-242-11954	Sequence 11954, A
845	6	1.5	353	9	US-09-971-228-9	Sequence 9, Appli	918	6	1.5	471	10	US-09-912-020-284	Sequence 284, App
846	6	1.5	353	9	US-10-084-507B-17	Sequence 17, Appli	919	6	1.5	485	9	US-10-191-598A-5	Sequence 5, Appli
847	6	1.5	353	9	US-10-084-507B-22	Sequence 22, Appli	920	6	1.5	487	9	US-09-796-753-54	Sequence 54, Appli
848	6	1.5	353	10	US-09-771-063-2	Sequence 2, Appli	921	6	1.5	488	9	US-09-796-753-52	Sequence 52, Appli
849	6	1.5	353	10	US-09-771-063-4	Sequence 4, Appli	922	6	1.5	488	10	US-09-815-242-5040	Sequence 5040, Ap
850	6	1.5	353	10	US-09-842-316-8	Sequence 8, Appli	923	6	1.5	485	10	US-09-815-242-10315	Sequence 10315, A
851	6	1.5	353	10	US-09-731-030A-19	Sequence 23, Appli	924	6	1.5	495	10	US-09-925-302-475	Sequence 11716, A
852	6	1.5	353	12	US-10-037-616-23	Sequence 16, Appli	925	6	1.5	498	10	US-09-925-302-475	Sequence 475, App
853	6	1.5	355	9	US-09-847-010-16	Sequence 16, Appli	926	6	1.5	499	10	US-09-735-169A-2	Sequence 2, Appli
854	6	1.5	355	10	US-09-815-242-113830	Sequence 13830, A	927	6	1.5	499	10	US-09-735-171A-2	Sequence 2, Appli
855	6	1.5	357	10	US-09-952-663-17	Sequence 17, Appli	928	6	1.5	500	10	US-09-815-242-13764	Sequence 13764, A
856	6	1.5	361	9	US-10-114-893-88	Sequence 88, Appli	929	6	1.5	504	10	US-09-766-378A-25	Sequence 25, Appli
857	6	1.5	365	9	US-09-738-626-336	Sequence 6336, Ap	930	6	1.5	504	10	US-09-801-368-208	Sequence 208, App
858	6	1.5	376	10	US-09-815-242-10160	Sequence 10160, Ap	931	6	1.5	510	9	US-09-738-626-3754	Sequence 3754, App
859	6	1.5	378	10	US-09-925-301-1208	Sequence 1208, Ap	932	6	1.5	510	9	US-10-228-806-6	Sequence 6, Appli
860	6	1.5	382	10	US-09-738-626-5949	Sequence 5949, Ap	933	6	1.5	513	9	US-09-738-626-6073	Sequence 6073, Ap
861	6	1.5	382	10	US-09-969-711-2	Sequence 2, Appli	934	6	1.5	514	9	US-09-833-745-44	Sequence 44, Appli
862	6	1.5	386	9	US-09-975-901-4	Sequence 4, Appli	935	6	1.5	514	9	US-09-738-626-5869	Sequence 5869, Ap
863	6	1.5	388	9	US-09-470-954A-48	Sequence 48, Appli	936	6	1.5	522	9	US-09-764-868-1138	Sequence 1138, Ap
864	6	1.5	388	10	US-09-815-242-10684	Sequence 10684, A	937	6	1.5	524	9	US-09-764-868-761	Sequence 761, App
865	6	1.5	388	10	US-09-215-450-24	Sequence 24, Appli	938	6	1.5	525	9	US-09-978-295A-301	Sequence 301, App
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867	6	1.5	395	9	US-10-094-080-3	Sequence 3, Appli	940	6	1.5	525	9	US-09-978-697-301	Sequence 301, App
868	6	1.5	396	9	US-09-470-954A-49	Sequence 49, Appli	941	6	1.5	525	9	US-09-978-192A-301	Sequence 301, App
869	6	1.5	396	10	US-09-215-450-22	Sequence 22, Appli	942	6	1.5	525	9	US-09-978-189-301	Sequence 301, App
870	6	1.5	396	10	US-09-953-956-13	Sequence 13, Appli	943	6	1.5	525	9	US-10-174-590-436	Sequence 436, App
871	6	1.5	396	12	US-10-114-464-13	Sequence 13, Appli	944	6	1.5	525	9	US-10-176-758-436	Sequence 436, App
872	6	1.5	398	9	US-10-215-211-2	Sequence 2, Appli	945	6	1.5	525	9	US-10-175-737-436	Sequence 436, App
873	6	1.5	398	9	US-10-011-548-26	Sequence 26, Appli	946	6	1.5	525	9	US-10-173-706-436	Sequence 436, App
874	6	1.5	398	9	US-10-199-209-2	Sequence 2, Appli	947	6	1.5	525	9	US-10-175-738-436	Sequence 436, App
875	6	1.5	398	10	US-09-854-162-2	Sequence 2, Appli	948	6	1.5	525	9	US-10-175-738-436	Sequence 436, App
876	6	1.5	398	10	US-09-912-020-304	Sequence 304, App	949	6	1.5	525	9	US-10-176-482-436	Sequence 436, App
877	6	1.5	398	10	US-09-921-667-8	Sequence 8, Appli	950	6	1.5	525	9	US-10-176-482-436	Sequence 436, App
878	6	1.5	398	10	US-09-840-107A-4	Sequence 4, Appli	951	6	1.5	525	9	US-10-176-913-436	Sequence 436, App
879	6	1.5	403	9	US-09-976-059-23	Sequence 23, Appli	952	6	1.5	525	9	US-10-180-552-436	Sequence 436, App
880	6	1.5	403	9	US-09-738-626-5159	Sequence 5159, Ap	953	6	1.5	525	9	US-10-180-552-436	Sequence 436, App
881	6	1.5	403	10	US-09-826-508-30	Sequence 30, Appli	954	6	1.5	525	9	US-10-173-700-436	Sequence 436, App
882	6	1.5	403	10	US-09-895-686-5	Sequence 5, Appli	955	6	1.5	525	9	US-10-174-572-436	Sequence 436, App
883	6	1.5	404	10	US-09-864-761-36208	Sequence 36208, A	956	6	1.5	525	9	US-10-174-579-436	Sequence 436, App
884	6	1.5	405	10	US-09-768-781-6	Sequence 6, Appli	957	6	1.5	525	9	US-10-174-582-436	Sequence 436, App
885	6	1.5	406	10	US-09-215-450-26	Sequence 26, Appli	958	6	1.5	525	9	US-10-174-582-436	Sequence 436, App
886	6	1.5	407	10	US-09-815-242-5348	Sequence 5348, Ap	959	6	1.5	525	9	US-10-175-739-436	Sequence 436, App
887	6	1.5	408	9	US-09-804-625-6	Sequence 6, Appli	960	6	1.5	525	9	US-10-175-740-436	Sequence 436, App
888	6	1.5	408	10	US-09-749-1288-69	Sequence 69, Appli	961	6	1.5	525	9	US-10-175-743-436	Sequence 436, App
889	6	1.5	409	9	US-09-813-398-27	Sequence 27, Appli	962	6	1.5	525	9	US-10-176-492-436	Sequence 436, App
890	6	1.5	409	9	US-10-081-051-18	Sequence 18, Appli	963	6	1.5	525	9	US-10-176-492-436	Sequence 436, App
891	6	1.5	411	9	US-10-015-536-17	Sequence 17, Appli	964	6	1.5	525	9	US-10-176-747-436	Sequence 436, App
892	6	1.5	412	10	US-09-215-450-25	Sequence 25, Appli	965	6	1.5	525	9	US-10-176-750-436	Sequence 436, App
893	6	1.5	412	10	US-09-953-956-12	Sequence 12, Appli	966	6	1.5	525	9	US-10-176-985-436	Sequence 436, App
894	6	1.5	412	12	US-10-114-464-12	Sequence 12, Appli	967	6	1.5	525	9	US-10-176-987-436	Sequence 436, App
895	6	1.5	419	10	US-09-789-919-44	Sequence 44, Appli	968	6	1.5	525	9	US-10-176-991-436	Sequence 436, App

969	6	1.5	525	9	US-10-176-992-436	Sequence 436, App
970	6	1.5	525	9	US-10-176-993-436	Sequence 436, App
971	6	1.5	525	9	US-10-184-658-436	Sequence 436, App
972	6	1.5	525	9	US-10-227-884-154	Sequence 154, App
973	6	1.5	525	9	US-10-173-695-436	Sequence 436, App
974	6	1.5	525	9	US-10-173-697-436	Sequence 436, App
975	6	1.5	525	9	US-10-173-705-436	Sequence 436, App
976	6	1.5	525	9	US-10-174-576-436	Sequence 436, App
977	6	1.5	525	9	US-10-174-585-436	Sequence 436, App
978	6	1.5	525	9	US-10-174-586-436	Sequence 436, App
979	6	1.5	525	9	US-10-175-747-436	Sequence 436, App
980	6	1.5	525	9	US-10-176-481-436	Sequence 436, App
981	6	1.5	525	9	US-10-176-485-436	Sequence 436, App
982	6	1.5	525	9	US-10-176-487-436	Sequence 436, App
983	6	1.5	525	9	US-10-176-493-436	Sequence 436, App
984	6	1.5	525	9	US-10-176-756-436	Sequence 436, App
985	6	1.5	525	9	US-10-176-911-436	Sequence 436, App
986	6	1.5	525	9	US-10-176-919-436	Sequence 436, App
987	6	1.5	525	9	US-10-176-925-436	Sequence 436, App
988	6	1.5	525	9	US-10-176-978-436	Sequence 436, App
989	6	1.5	525	9	US-10-179-510-436	Sequence 436, App
990	6	1.5	525	9	US-10-180-543-436	Sequence 436, App
991	6	1.5	525	9	US-10-180-544-436	Sequence 436, App
992	6	1.5	525	9	US-10-180-546-436	Sequence 436, App
993	6	1.5	525	9	US-10-180-547-436	Sequence 436, App
994	6	1.5	525	9	US-10-180-549-436	Sequence 436, App
995	6	1.5	525	9	US-10-180-555-436	Sequence 436, App
996	6	1.5	525	9	US-10-180-559-436	Sequence 436, App
997	6	1.5	525	9	US-10-181-000-436	Sequence 436, App
998	6	1.5	525	9	US-10-183-010-436	Sequence 436, App
999	6	1.5	525	9	US-10-183-012-436	Sequence 436, App
1000	6	1.5	525	9	US-10-184-614-436	Sequence 436, App

ALIGNMENTS

RESULT 1

US-09-978-295A-196

Sequence 196, Application US/09978295A

Patent No. US20020156006A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottlieb, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumias, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PRC11
CURRENT APPLICATION NUMBER: US/09/978, 295A

CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 406; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALEPALASPAGANFLAMVDNLQGDGGRGYLLEMLIGTPPKLQTLVDTGSSNFAVAGTP 60
DB 63 ALEPALASPAGANFLAMVDNLQGDGGRGYLLEMLIGTPPKLQTLVDTGSSNFAVAGTP 122
QY 61 HSYIDTYDTERSSSTYRSKGFVDVTVKTYQSGWTGFGEDLVITPKGFNTSLVNIAITFE 120
DB 123 HSYIDTYDTERSSSTYRSKGFVDVTVKTYQSGWTGFGEDLVITPKGFNTSLVNIAITFE 182
QY 121 SENFPLGIKXNGILGLAYATLAKPSSLETFPPSLVQANIPNVFSMOMGAGLPVAGS 180
DB 193 SENFPLGIKXNGILGLAYATLAKPSSLETFPPSLVQANIPNVFSMOMGAGLPVAGS 242
QY 181 GTNGSLVLGGIIEPSLYKGDIMYTPIKEWYVYQIETLKEIGOSLNDCEYNADKAIV 240
DB 243 GTNGSLVLGGIIEPSLYKGDIMYTPIKEWYVYQIETLKEIGOSLNDCEYNADKAIV 302
QY 241 DSGTTLRLPKQVPDAVEAVARASLIPEFSDGFWTGSQLAQWNTSETPMSYFPKISITYL 300
DB 303 DSGTTLRLPKQVPDAVEAVARASLIPEFSDGFWTGSQLAQWNTSETPMSYFPKISITYL 362
QY 301 RDENSRSRFRITLIPOLYIQPMMGAGLNECYRGISPTNALVYGATVMEGFYIIPRA 360
DB 363 RDENSRSRFRITLIPOLYIQPMMGAGLNECYRGISPTNALVYGATVMEGFYIIPRA 422
QY 361 QKRVGFASPCAETAGAAVSEISGPFSTEDVANSNCVPAQSISEPII 406
DB 423 QKRVGFASPCAETAGAAVSEISGPFSTEDVANSNCVPAQSISEPII 468

RESULT 2
US-09-886-143-2
Sequence 2, Application US/09886143
Patent No. US2002015991A1
GENERAL INFORMATION:
APPLICANT: Cordell, Barbara
APPLICANT: Schimmoller, Frauke
APPLICANT: Liu, Yu-Wang
APPLICANT: Quon, Diana Hom
TITLE OF INVENTION: Modulation of A Levels by
FILE OF INVENTION: Secretase BACE2
FILE REFERENCE: SCIOS.022A
CURRENT APPLICATION NUMBER: US/09/886,143
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/215,729
PRIOR FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2

LENGTH: 518
TYPE: PRT
ORGANISM: Homo sapiens
US-09-886-143-2

Query Match 100.0%; Score 406; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALEPLASPAAGANFLAVNDNQSGSGRGYEMILGIPPOKQILVDPGSSNFAVAGTP 60
DB 63 ALEPLASPAAGANFLAVNDNQSGSGRGYEMILGIPPOKQILVDPGSSNFAVAGTP 122
QY 61 HSYIDTYEDTERSSYTRSGKPDVTWKYTOGSWTGVGEDLVITIPKGFMTPLVNIATTFE 120
DB 123 HSYIDTYEDTERSSYTRSGKPDVTWKYTOGSWTGVGEDLVITIPKGFMTPLVNIATTFE 182
QY 121 SENFPLPGIKWNGILGLAVATLAKPSSSLETFPDSLVTQANIPNVFSMQMCGAGLPVAGS 180
DB 183 SENFPLPGIKWNGILGLAVATLAKPSSSLETFPDSLVTQANIPNVFSMQMCGAGLPVAGS 242
QY 181 GINGSLVGGIEPSLYKGDIVYTPIKEWYQIEILKLEIGQSUNLDCREYNADKAIY 240
DB 243 GINGSLVGGIEPSLYKGDIVYTPIKEWYQIEILKLEIGQSUNLDCREYNADKAIY 302
QY 241 DSGTLLRLPKQVFDPAVEAVARASLIPEFSDGFWTGSOLACMTSSETPMSYFPKISITL 300
DB 303 DSGTLLRLPKQVFDPAVEAVARASLIPEFSDGFWTGSOLACMTSSETPMSYFPKISITL 362
QY 301 RDENSSRSFRITILPOLYIQPMMGAGLNECYRFGISPTNALVYGATVMEGFYIIPDRA 360
DB 363 RDENSSRSFRITILPOLYIQPMMGAGLNECYRFGISPTNALVYGATVMEGFYIIPDRA 422
QY 361 OKRVGFASPCAETIGAANVSEISGPSTEDVASCNPQSLSEPII 406
DB 423 OKRVGFASPCAETIGAANVSEISGPSTEDVASCNPQSLSEPII 468

RESULT 3

US-09-978-697-196
Sequence 196, Application US/09978697
Patent No. US20020169284A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deemoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kiljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C27

CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
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Query Match 100.0%; Score 406; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ALPELASPAGANFLAVNDUJGDSGGRYLEMLIGTPPOKLIUVDTGSSNFAVAGTP 60
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Oy 61 HSYIDYPTDTERSSSTYRSKGFDTVKYTGSGWTGPGEDLVITIRKGPNTSFLVNIATIFE 120
Db 123 HSYIDYPTDTERSSSTYRSKGFDTVKYTGSGWTGPGEDLVITIRKGPNTSFLVNIATIFE 182
Oy 121 SENFPLPGIKNNGLGLAYATLAKPSSLEFFPFSLYTQANIPIVFSNOMGAGLPVAGS 180
Db 183 SENFPLPGIKNNGLGLAYATLAKPSSLEFFPFSLYTQANIPIVFSNOMGAGLPVAGS 242
Oy 181 GTNGSLVLGGIPEPSLVKGDIMWTPIKEEMYYQIEILKEIGQSLNDCREYNADRAIV 240
Db 243 GTNGSLVLGGIPEPSLVKGDIMWTPIKEEMYYQIEILKEIGQSLNDCREYNADRAIV 302
Oy 241 DSGTTLRLPQKVDVAEVAARASLIPEPSDGFWTGSQLACWTNSETPMSPKISITL 300
Db 303 DSGTTLRLPQKVDVAEVAARASLIPEPSDGFWTGSQLACWTNSETPMSPKISITL 362
Oy 301 RDNSSRSFRITTIIPOLYIOPMAGALNECYRFGISPTALVIGATWEGFYVIFDRA 360
Db 363 RDNSSRSFRITTIIPOLYIOPMAGALNECYRFGISPTALVIGATWEGFYVIFDRA 422
Oy 361 QKRVGFAASPCAFIAGAASEISGPFSTEDVASNCVPAQSLSEPTL 406
Db 423 QKRVGFAASPCAFIAGAASEISGPFSTEDVASNCVPAQSLSEPTL 468

RESULT 4

US-09-978-192A-196
Sequence 196, Application US/09978192A

Patent No. US2002017553A1
GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Denoyers, Luc
APPLICANT: Baton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottlieb, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 406; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 63 ALBPALSPAGANFLAMVDNLQDSDGRGYLEMLIGTPPKQLQILVDTGSSNFAVAGTP 122
QY 61 HSYIDTYFDTERSSSTYRSKGFDTVYKYTGSGWTGFGEDLVITPKGNTSFLVNIAITFE 120
DB 123 HSYIDTYFDTERSSSTYRSKGFDTVYKYTGSGWTGFGEDLVITPKGNTSFLVNIAITFE 182
QY 121 SENFPLPKIKNGILGLAVATLAKRSSLETFPDSLVTOANIPNVFSMOMCGAGLPAVGS 180
DB 183 SENFPLPKIKNGILGLAVATLAKRSSLETFPDSLVTOANIPNVFSMOMCGAGLPAVGS 242
QY 181 GTNGSGLVAGIEPSLYKGDIMYTPIKEWYQIETLKEIGGSLNDCEHYNDKAIIV 240
DB 243 GTNGSGLVAGIEPSLYKGDIMYTPIKEWYQIETLKEIGGSLNDCEHYNDKAIIV 302
QY 241 DSGTTLRLPKQVPDAVVAVARASLIPEFSDGFWTGSQALCWNSETPMWSPFKISITL 300
DB 303 DSGTTLRLPKQVPDAVVAVARASLIPEFSDGFWTGSQALCWNSETPMWSPFKISITL 362
QY 301 RDENSSRFRITLIPOLYIOPMGAGLVYECRFGISPTALVIGATVMGFPYIIPRA 360
DB 363 RDENSSRFRITLIPOLYIOPMGAGLVYECRFGISPTALVIGATVMGFPYIIPRA 422
QY 361 QKRVGFASPCAEIAGAIVSEISGPFSTEDVASNCVPAQSLSEPTL 406
DB 423 QKRVGFASPCAEIAGAIVSEISGPFSTEDVASNCVPAQSLSEPTL 468

RESULT 5

US-09-999-832A-196
;; Sequence 196, Application US/09999832A
;; Publication No. US20020192706A1
;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi
;; APPLICANT: Baker Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan
;; APPLICANT: Ferrara, Napoleon
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gao, Wei-Qiang
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;; APPLICANT: Hillan, Kenneth J.
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;; APPLICANT: Kuo, Sophia S.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James J.
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Shelton, David L.
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2630PIC63
;; CURRENT APPLICATION NUMBER: US/09/999,832A
;; PRIOR FILING DATE: 2001-10-24
;; PRIOR APPLICATION NUMBER: 09/918585
;; PRIOR FILING DATE: 2001-07-30
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Query Match 100.0%; Score 406; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALEPALASPAAGANFLAVNDVILQDSDGRGYLLEMLIGTPPOKQILVDTGSSNFAVACTP 60
Db 63 ALEPLASPAAGANFLAVNDVILQDSDGRGYLLEMLIGTPPOKQILVDTGSSNFAVACTP 122
Qy 61 HSYIDTYDTERSSSTYRSKGFVTVKTYTQGSWTGFGEDLVTTIPKGFNTSLVNIATTFE 120
Db 123 HSYIDTYDTERSSSTYRSKGFVTVKTYTQGSWTGFGEDLVTTIPKGFNTSLVNIATTFE 182
Qy 121 SENFPLPGIKNGGILGLAVATLAKPSSLETFPDSLVYQANIPVFSQMGAGLPVAGS 180
Db 183 SENFPLPGIKNGGILGLAVATLAKPSSLETFPDSLVYQANIPVFSQMGAGLPVAGS 242
Qy 181 GTNGGSILVGLGIEPSLYKGDITWYTIKIEWYQIEILKLEIGQSLNLDCREYNADKAIV 240

Db 243 GTNGSLVLGGIEBLYGDIWYTPKEEWYQIEILLEIGGOSLNDCEBYNDKAIv 302
Qy 241 DSGTLLRLPKVFDVAVEAVARASLIPEFSDGFWTGSQLAQWTSFTPMGYFPKISYL 300
Db 303 DSGTLLRLPKVFDVAVEAVARASLIPEFSDGFWTGSQLAQWTSFTPMGYFPKISYL 362
Qy 301 RDENSSRSFRITLLPOLYIQPMGAGLNYECYRFGISPSSTNALVIGATWMEGFYIFDRA 360
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RESULT 6
US-09-978-189-196
; Sequence 196, Application US/09978189
; Publication No. US2003004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
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; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C7
; CURRENT APPLICATION NUMBER: US/09/978, 189
; PRIOR APPLICATION NUMBER: 09/918585
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; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080328
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080334
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081071
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081952
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082804

PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-5-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 406; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALEPALASPAGANFLAMVNDLQDSDGRGYYLEMLIGTPPOKQIIVDTGSSNFAVAGTP 60
DB 63 ALEPALASPAGANFLAMVNDLQDSDGRGYYLEMLIGTPPOKQIIVDTGSSNFAVAGTP 122
QY 61 HSYIDYFPTDERSSTYRSKGFVTVKYGQSWTGFVGEDVLTIPKGFNTSFLVNIATIFE 120
DB 123 HSYIDYFPTDERSSTYRSKGFVTVKYGQSWTGFVGEDVLTIPKGFNTSFLVNIATIFE 182
QY 121 SENFPLGKIKWNGILGLAYATLAKPSSLETFFPSLVTQANIPVFSMOMCGALPTVAGS 180
DB 183 SENFPLGKIKWNGILGLAYATLAKPSSLETFFPSLVTQANIPVFSMOMCGALPTVAGS 242
QY 181 GTNGSLVIGIIEPSLYKGDHWTPRIKEEMYYOIEILKEIGGOSLMDCREYNADAIY 240
DB 243 GTNGSLVIGIIEPSLYKGDHWTPRIKEEMYYOIEILKEIGGOSLMDCREYNADAIY 302
QY 241 DSGTTLRLPKQVDAVVEAVARASLIPEFSDGFWTSQOLACWTNSETPMSYFPKISITL 300
DB 303 DSGTTLRLPKQVDAVVEAVARASLIPEFSDGFWTSQOLACWTNSETPMSYFPKISITL 362
QY 301 RDNSSRSFRTITLPIQYIOPMGAGLNYECYRGISPTNALYIGATNMEGFVITDRA 360
DB 363 RDNSSRSFRTITLPIQYIOPMGAGLNYECYRGISPTNALYIGATNMEGFVITDRA 422
QY 361 QKRVGPAASPCAETAGAAVSEISGPFSTEDVASCVPAOSISEPIL 406
DB 423 QKRVGPAASPCAETAGAAVSEISGPFSTEDVASCVPAOSISEPIL 468

RESULT 7

US-10-174-590-72
Sequence 72, Application US/10174590
Publication No. US20030008352A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C42
CURRENT APPLICATION NUMBER: US/10/174,590
CURRENT FILING DATE: 2002-06-18
Prior application removed - See file wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 72
LENGTH: 518
TYPE: PRT
ORGANISM: Homo Sapien
US-10-174-590-72

Query Match 100.0%; Score 406; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALEPALASPAGANFLAMVNDLQDSDGRGYYLEMLIGTPPOKQIIVDTGSSNFAVAGTP 60
DB 63 ALEPALASPAGANFLAMVNDLQDSDGRGYYLEMLIGTPPOKQIIVDTGSSNFAVAGTP 122
QY 61 HSYIDYFPTDERSSTYRSKGFVTVKYGQSWTGFVGEDVLTIPKGFNTSFLVNIATIFE 120
DB 123 HSYIDYFPTDERSSTYRSKGFVTVKYGQSWTGFVGEDVLTIPKGFNTSFLVNIATIFE 182

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QY 121 SENFLLPGIKKNGILGLAVATLAKBSSSLETFPDSLVTQANIPNVFSMOMCAGLPVAGS 180
DB 183 SENFLLPGIKKNGILGLAVATLAKBSSSLETFPDSLVTQANIPNVFSMOMCAGLPVAGS 242
QY 181 GTNGSLVVGIEPSLYKGDIVWTPPIKEWYQIEILKLEIGGOSLNDCEYNADKAIY 240
DB 243 GTNGSLVVGIEPSLYKGDIVWTPPIKEWYQIEILKLEIGGOSLNDCEYNADKAIY 302
QY 241 DSGTLLRLPKQVDAVEAVARASLIPEFSDGFWTGSOLACWNSSETPMWSYFPKISITL 300
DB 303 DSGTLLRLPKQVDAVEAVARASLIPEFSDGFWTGSOLACWNSSETPMWSYFPKISITL 362
QY 301 RDNSSRSFRITILPOLYIQPMGAGLNECYRFGISPSSTNALVIGATVMEGFYIIPDRA 360
DB 363 RDNSSRSFRITILPOLYIQPMGAGLNECYRFGISPSSTNALVIGATVMEGFYIIPDRA 422
QY 361 QKRVGFPAASPCAEIAGAAVSEISGPFSTEDVANSNCVPAQSLSEPIIL 406
DB 423 QKRVGFPAASPCAEIAGAAVSEISGPFSTEDVANSNCVPAQSLSEPIIL 468

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RESULT 8

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US-10-176-758-72
; Sequence 72, Application US/10176758
; Publication No. US20030008353A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C104
; CURRENT FILING DATE: 2002-06-21
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-758-72

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Query Match 100.0%; Score 406; DB 9; Length 518;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ALEPLASPAAGANFLAVNDNLQDGSGRGYLEMIGTPQKQLIVDTGSSNFAVAGTP 60
DB 63 ALEPLASPAAGANFLAVNDNLQDGSGRGYLEMIGTPQKQLIVDTGSSNFAVAGTP 122
QY 61 HSYIDTYFDTERSSSTYRSKGPVTVKYTQGSWTGFGVEDLVTPPKGFNTSFLVNIATIFE 120
DB 123 HSYIDTYFDTERSSSTYRSKGPVTVKYTQGSWTGFGVEDLVTPPKGFNTSFLVNIATIFE 182
QY 121 SENFLLPGIKKNGILGLAVATLAKBSSSLETFPDSLVTQANIPNVFSMOMCAGLPVAGS 180
DB 183 SENFLLPGIKKNGILGLAVATLAKBSSSLETFPDSLVTQANIPNVFSMOMCAGLPVAGS 242
QY 181 GTNGSLVVGIEPSLYKGDIVWTPPIKEWYQIEILKLEIGGOSLNDCEYNADKAIY 240
DB 243 GTNGSLVVGIEPSLYKGDIVWTPPIKEWYQIEILKLEIGGOSLNDCEYNADKAIY 302
QY 241 DSGTLLRLPKQVDAVEAVARASLIPEFSDGFWTGSOLACWNSSETPMWSYFPKISITL 300

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DB 303 DSGTLLRLPKQVDAVEAVARASLIPEFSDGFWTGSOLACWNSSETPMWSYFPKISITL 362
QY 301 RDNSSRSFRITILPOLYIQPMGAGLNECYRFGISPSSTNALVIGATVMEGFYIIPDRA 360
DB 363 RDNSSRSFRITILPOLYIQPMGAGLNECYRFGISPSSTNALVIGATVMEGFYIIPDRA 422
QY 361 QKRVGFPAASPCAEIAGAAVSEISGPFSTEDVANSNCVPAQSLSEPIIL 406
DB 423 QKRVGFPAASPCAEIAGAAVSEISGPFSTEDVANSNCVPAQSLSEPIIL 468

```

RESULT 9

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US-10-175-737-72
; Sequence 72, Application US/10175737
; Publication No. US20030013153A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C50
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-737-72

```

Query Match 100.0%; Score 406; DB 9; Length 518;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 ALEPLASPAAGANFLAVNDNLQDGSGRGYLEMIGTPQKQLIVDTGSSNFAVAGTP 60
DB 63 ALEPLASPAAGANFLAVNDNLQDGSGRGYLEMIGTPQKQLIVDTGSSNFAVAGTP 122
QY 61 HSYIDTYFDTERSSSTYRSKGPVTVKYTQGSWTGFGVEDLVTPPKGFNTSFLVNIATIFE 120
DB 123 HSYIDTYFDTERSSSTYRSKGPVTVKYTQGSWTGFGVEDLVTPPKGFNTSFLVNIATIFE 182
QY 121 SENFLLPGIKKNGILGLAVATLAKBSSSLETFPDSLVTQANIPNVFSMOMCAGLPVAGS 180
DB 183 SENFLLPGIKKNGILGLAVATLAKBSSSLETFPDSLVTQANIPNVFSMOMCAGLPVAGS 242
QY 181 GTNGSLVVGIEPSLYKGDIVWTPPIKEWYQIEILKLEIGGOSLNDCEYNADKAIY 240
DB 243 GTNGSLVVGIEPSLYKGDIVWTPPIKEWYQIEILKLEIGGOSLNDCEYNADKAIY 302
QY 241 DSGTLLRLPKQVDAVEAVARASLIPEFSDGFWTGSOLACWNSSETPMWSYFPKISITL 300
DB 303 DSGTLLRLPKQVDAVEAVARASLIPEFSDGFWTGSOLACWNSSETPMWSYFPKISITL 362
QY 301 RDNSSRSFRITILPOLYIQPMGAGLNECYRFGISPSSTNALVIGATVMEGFYIIPDRA 360
DB 363 RDNSSRSFRITILPOLYIQPMGAGLNECYRFGISPSSTNALVIGATVMEGFYIIPDRA 422
QY 361 QKRVGFPAASPCAEIAGAAVSEISGPFSTEDVANSNCVPAQSLSEPIIL 406
DB 423 QKRVGFPAASPCAEIAGAAVSEISGPFSTEDVANSNCVPAQSLSEPIIL 468

```

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RESULT 10
US-10-173-706-72
; Sequence 72, Application US/10173706
; Publication No. US20030022293A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Deenoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C7
; CURRENT APPLICATION NUMBER: US/10/173,706
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-173-706-72

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```

Query Match      100.0%; Score 406; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALEPLASPAAGANFLAMVDNLQSDSGRGYLEMLIGTPQKQLIVDTGSSNFAVAGTP 60
DB 63 ALEPLASPAAGANFLAMVDNLQSDSGRGYLEMLIGTPQKQLIVDTGSSNFAVAGTP 122
QY 61 HSYIDTFDTERSSSTYRSKGFVDVTKYTOGSGWTFVGEDLVITIPKGFNTSLVNIATIFE 120
DB 123 HSYIDTFDTERSSSTYRSKGFVDVTKYTOGSGWTFVGEDLVITIPKGFNTSLVNIATIFE 182
QY 121 SENFLLPGIKKNGILGLAVATLAKPSSSLETFPDSLVTQANIPIVFSMOMCGAGLPVAGS 180
DB 183 SENFLLPGIKKNGILGLAVATLAKPSSSLETFPDSLVTQANIPIVFSMOMCGAGLPVAGS 242
QY 181 GTNGSLVLGGIEPSLVKGDWYTPIKEWYQIEILKLEIGGOSLNDCREYNADKAIY 240
DB 243 GTNGSLVLGGIEPSLVKGDWYTPIKEWYQIEILKLEIGGOSLNDCREYNADKAIY 302
QY 241 DSGTLLRLPKQVDAVEAVARASLIPEFSDGFWTGSQACMTNSETPMSYFPKISITYL 300
DB 303 DSGTLLRLPKQVDAVEAVARASLIPEFSDGFWTGSQACMTNSETPMSYFPKISITYL 362
QY 301 RDENSSRSFRITILPOLYIQPMGAGLNYECYRGISBSTNALVIQATWEGFYIIPDRA 360
DB 363 RDENSSRSFRITILPOLYIQPMGAGLNYECYRGISBSTNALVIQATWEGFYIIPDRA 422
QY 361 QKRVGFASPCAETAGAAVSEISGPFSTEDVASCVPQSLSEPII 406
DB 423 QKRVGFASPCAETAGAAVSEISGPFSTEDVASCVPQSLSEPII 468

```

```

RESULT 11
US-10-175-738-72
; Sequence 72, Application US/10175738
; Publication No. US20030022294A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Deenoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.

```

```

; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C45
; CURRENT APPLICATION NUMBER: US/10/175,738
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-738-72

```

```

Query Match      100.0%; Score 406; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALEPLASPAAGANFLAMVDNLQSDSGRGYLEMLIGTPQKQLIVDTGSSNFAVAGTP 60
DB 63 ALEPLASPAAGANFLAMVDNLQSDSGRGYLEMLIGTPQKQLIVDTGSSNFAVAGTP 122
QY 61 HSYIDTFDTERSSSTYRSKGFVDVTKYTOGSGWTFVGEDLVITIPKGFNTSLVNIATIFE 120
DB 123 HSYIDTFDTERSSSTYRSKGFVDVTKYTOGSGWTFVGEDLVITIPKGFNTSLVNIATIFE 182
QY 121 SENFLLPGIKKNGILGLAVATLAKPSSSLETFPDSLVTQANIPIVFSMOMCGAGLPVAGS 180
DB 183 SENFLLPGIKKNGILGLAVATLAKPSSSLETFPDSLVTQANIPIVFSMOMCGAGLPVAGS 242
QY 181 GTNGSLVLGGIEPSLVKGDWYTPIKEWYQIEILKLEIGGOSLNDCREYNADKAIY 240
DB 243 GTNGSLVLGGIEPSLVKGDWYTPIKEWYQIEILKLEIGGOSLNDCREYNADKAIY 302
QY 241 DSGTLLRLPKQVDAVEAVARASLIPEFSDGFWTGSQACMTNSETPMSYFPKISITYL 300
DB 303 DSGTLLRLPKQVDAVEAVARASLIPEFSDGFWTGSQACMTNSETPMSYFPKISITYL 362
QY 301 RDENSSRSFRITILPOLYIQPMGAGLNYECYRGISBSTNALVIQATWEGFYIIPDRA 360
DB 363 RDENSSRSFRITILPOLYIQPMGAGLNYECYRGISBSTNALVIQATWEGFYIIPDRA 422
QY 361 QKRVGFASPCAETAGAAVSEISGPFSTEDVASCVPQSLSEPII 406
DB 423 QKRVGFASPCAETAGAAVSEISGPFSTEDVASCVPQSLSEPII 468

```

```

RESULT 12
US-10-175-752-72
; Sequence 72, Application US/10175752
; Publication No. US20030022295A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Deenoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C60
; CURRENT APPLICATION NUMBER: US/10/175,752
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm

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NUMBER OF SEQ ID NOS: 612
 SEQ ID NO 72
 LENGTH: 518
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-175-752-72

Query Match 100.0%; Score 406; DB 9; Length 518;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALEPLASPAAGANFLAMVDNLQDSSGRGYLLEMLIGTPPOKQIIVDTGSSNFAVAGTP 60
 DB 63 ALEPLASPAAGANFLAMVDNLQDSSGRGYLLEMLIGTPPOKQIIVDTGSSNFAVAGTP 122
 QY 61 HSYIDYFDTERRSSTYRSKGFVDVTVKKTQGSWTGFWGEDLVITPKGNTSFLVNIAITFE 120
 DB 123 HSYIDYFDTERRSSTYRSKGFVDVTVKKTQGSWTGFWGEDLVITPKGNTSFLVNIAITFE 182
 QY 121 SENFPLPGIKKNGILGLAVATLAKPSSSLETFPDSLVTOANIPNVFSMOMCGAGLPVAGS 180
 DB 183 SENFPLPGIKKNGILGLAVATLAKPSSSLETFPDSLVTOANIPNVFSMOMCGAGLPVAGS 242
 QY 181 GTNGSLVLGGIEBPLKYKGDIMWTPPIKEWYQIEILKLEIGGOSLMDCEYNADKAIV 240
 DB 243 GTNGSLVLGGIEBPLKYKGDIMWTPPIKEWYQIEILKLEIGGOSLMDCEYNADKAIV 302
 QY 241 DSGTTLRLPKQVDAVEAVARASLIPEPSDGFMTGSOLACWNTSETPMSYFPKISITL 300
 DB 303 DSGTTLRLPKQVDAVEAVARASLIPEPSDGFMTGSOLACWNTSETPMSYFPKISITL 362
 QY 301 RDENSSRSFRITILPOLYIOPMAGLNECYRFGISPTNALVIGATVMEGFYVIFDRA 360
 DB 363 RDENSSRSFRITILPOLYIOPMAGLNECYRFGISPTNALVIGATVMEGFYVIFDRA 422
 QY 361 QKRVGFAASPCAEIAGAASEISGPFSTEDVANSNCVPAQSISEPTL 406
 DB 423 QKRVGFAASPCAEIAGAASEISGPFSTEDVANSNCVPAQSISEPTL 468

RESULT 13

US-10-176-482-72
 Sequence 72, Application US/10176482
 Publication No. US20030022296A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Chen, Jian
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Matanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P3430R1C70
 CURRENT APPLICATION NUMBER: US/10/176,482
 PRIOR APPLICATION REMOVED - See File Wrapper or Palm
 NUMBER OF SEQ ID NOS: 612
 SEQ ID NO 72
 LENGTH: 518
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-176-482-72

Query Match 100.0%; Score 406; DB 9; Length 518;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALEPLASPAAGANFLAMVDNLQDSSGRGYLLEMLIGTPPOKQIIVDTGSSNFAVAGTP 60
 DB 63 ALEPLASPAAGANFLAMVDNLQDSSGRGYLLEMLIGTPPOKQIIVDTGSSNFAVAGTP 122
 QY 61 HSYIDYFDTERRSSTYRSKGFVDVTVKKTQGSWTGFWGEDLVITPKGNTSFLVNIAITFE 120
 DB 123 HSYIDYFDTERRSSTYRSKGFVDVTVKKTQGSWTGFWGEDLVITPKGNTSFLVNIAITFE 182
 QY 121 SENFPLPGIKKNGILGLAVATLAKPSSSLETFPDSLVTOANIPNVFSMOMCGAGLPVAGS 180
 DB 183 SENFPLPGIKKNGILGLAVATLAKPSSSLETFPDSLVTOANIPNVFSMOMCGAGLPVAGS 242
 QY 181 GTNGSLVLGGIEBPLKYKGDIMWTPPIKEWYQIEILKLEIGGOSLMDCEYNADKAIV 240
 DB 243 GTNGSLVLGGIEBPLKYKGDIMWTPPIKEWYQIEILKLEIGGOSLMDCEYNADKAIV 302
 QY 241 DSGTTLRLPKQVDAVEAVARASLIPEPSDGFMTGSOLACWNTSETPMSYFPKISITL 300
 DB 303 DSGTTLRLPKQVDAVEAVARASLIPEPSDGFMTGSOLACWNTSETPMSYFPKISITL 362
 QY 301 RDENSSRSFRITILPOLYIOPMAGLNECYRFGISPTNALVIGATVMEGFYVIFDRA 360
 DB 363 RDENSSRSFRITILPOLYIOPMAGLNECYRFGISPTNALVIGATVMEGFYVIFDRA 422
 QY 361 QKRVGFAASPCAEIAGAASEISGPFSTEDVANSNCVPAQSISEPTL 406
 DB 423 QKRVGFAASPCAEIAGAASEISGPFSTEDVANSNCVPAQSISEPTL 468

RESULT 14

US-10-176-757-72
 Sequence 72, Application US/10176757
 Publication No. US20030022297A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Chen, Jian
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Matanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P3430R1C86
 CURRENT APPLICATION NUMBER: US/10/176,757
 PRIOR APPLICATION REMOVED - See File Wrapper or Palm
 NUMBER OF SEQ ID NOS: 612
 SEQ ID NO 72
 LENGTH: 518
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-176-757-72

Query Match 100.0%; Score 406; DB 9; Length 518;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALEPLASPAAGANFLAMVDNLQDSSGRGYLLEMLIGTPPOKQIIVDTGSSNFAVAGTP 60
 DB 63 ALEPLASPAAGANFLAMVDNLQDSSGRGYLLEMLIGTPPOKQIIVDTGSSNFAVAGTP 122
 QY 61 HSYIDYFDTERRSSTYRSKGFVDVTVKKTQGSWTGFWGEDLVITPKGNTSFLVNIAITFE 120
 DB 123 HSYIDYFDTERRSSTYRSKGFVDVTVKKTQGSWTGFWGEDLVITPKGNTSFLVNIAITFE 182
 QY 121 SENFPLPGIKKNGILGLAVATLAKPSSSLETFPDSLVTOANIPNVFSMOMCGAGLPVAGS 180
 DB 183 SENFPLPGIKKNGILGLAVATLAKPSSSLETFPDSLVTOANIPNVFSMOMCGAGLPVAGS 242

QY 181 GTNGSLVIGGIEPSLYKGDIMWTPIKEEMYYQIEILKLEIGGOSLNDCREYNADKAIV 240
DB 243 GTNGSLVIGGIEPSLYKGDIMWTPIKEEMYYQIEILKLEIGGOSLNDCREYNADKAIV 302
QY 241 DSGTTLRLPKVFDVAVAVARASLIPEFSDGFWTGSQACWTNSETPMWYFPKISIVL 300
DB 303 DSGTTLRLPKVFDVAVAVARASLIPEFSDGFWTGSQACWTNSETPMWYFPKISIVL 362
QY 301 RDNSSRSFRITTLIPOLYIQPMMGAGLNYECYRFGISPTNALVIGATWEGFYVIFDRA 360
DB 363 RDNSSRSFRITTLIPOLYIQPMMGAGLNYECYRFGISPTNALVIGATWEGFYVIFDRA 422
QY 361 QKRVGFAPSPCAETAGAAVSEISGPFSTEDVANSNCVPAQSISEPIL 406
DB 423 QKRVGFAPSPCAETAGAAVSEISGPFSTEDVANSNCVPAQSISEPIL 468

RESULT 15

US-10-176-913-72
; Sequence 72, Application US/10176913
; Publication No. US20030022298A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Guirney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C6
; CURRENT APPLICATION NUMBER: US/10/176,913
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-913-72

Query Match 100.0%; Score 406; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALEPPLASPAAGANFLAMVDNLQDSGRGYIEMLIGTPPKQLIIVDTGSSNFAVAGTP 60
DB 63 ALEPPLASPAAGANFLAMVDNLQDSGRGYIEMLIGTPPKQLIIVDTGSSNFAVAGTP 122
QY 61 HSYITVYFPTERSSTYRSKGFVDVTVKYTGSWTGFVGEDLVITIPKGFNTSFLVNIATIFE 120
DB 123 HSYITVYFPTERSSTYRSKGFVDVTVKYTGSWTGFVGEDLVITIPKGFNTSFLVNIATIFE 182
QY 121 SENFPLPGIKWNGILGLAVATLAKPSSLIETFFDSLVITQANIPNVFSMOMGAGLPAVAGS 180
DB 183 SENFPLPGIKWNGILGLAVATLAKPSSLIETFFDSLVITQANIPNVFSMOMGAGLPAVAGS 242
QY 181 GTNGSLVIGGIEPSLYKGDIMWTPIKEEMYYQIEILKLEIGGOSLNDCREYNADKAIV 240
DB 243 GTNGSLVIGGIEPSLYKGDIMWTPIKEEMYYQIEILKLEIGGOSLNDCREYNADKAIV 302
QY 241 DSGTTLRLPKVFDVAVAVARASLIPEFSDGFWTGSQACWTNSETPMWYFPKISIVL 300
DB 303 DSGTTLRLPKVFDVAVAVARASLIPEFSDGFWTGSQACWTNSETPMWYFPKISIVL 362
QY 301 RDNSSRSFRITTLIPOLYIQPMMGAGLNYECYRFGISPTNALVIGATWEGFYVIFDRA 360

DB 363 RDNSSRSFRITTLIPOLYIQPMMGAGLNYECYRFGISPTNALVIGATWEGFYVIFDRA 422
QY 361 QKRVGFAPSPCAETAGAAVSEISGPFSTEDVANSNCVPAQSISEPIL 406
DB 423 QKRVGFAPSPCAETAGAAVSEISGPFSTEDVANSNCVPAQSISEPIL 468

Search completed: April 1, 2003, 12:01:46
Job time : 50 secs

GenCore version 5.1.4_P5_4578
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OM protein - protein search, using sw model

Run on: April 1, 2003, 11:50:25 ; Search time 21 Seconds
(without alignments)
1858.599 Million cell updates/sec

Title: US-09-668-314C-2_COPY_63_468
Perfect score: 406
Sequence: 1 ALEPALASPAGANFLAMVD.....STEDVASNCVPAQSLSEPII 406

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

PIR_73:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	3.0	501	2	AS9090
2	8	2.0	166	2	H64131
3	8	2.0	237	2	U00729
4	8	2.0	287	2	G96659
5	8	2.0	303	2	H75528
6	8	2.0	319	2	AG0742
7	8	2.0	323	1	PRLJHD
8	8	2.0	327	2	T42999
9	8	2.0	340	1	PEIKL
10	8	2.0	352	1	C72748
11	8	2.0	365	2	T17720
12	8	2.0	449	2	E96676
13	8	2.0	472	2	JC7626
14	8	2.0	548	1	B65173
15	8	2.0	548	2	H81208
16	8	2.0	548	2	B86055
17	8	2.0	548	2	AF0957
18	8	2.0	637	2	T01961
19	8	2.0	904	2	C83030
20	8	2.0	1622	2	JE0378
21	7	1.7	88	2	PN0135
22	7	1.7	115	2	TS1324
23	7	1.7	128	1	UQDOR
24	7	1.7	131	2	B90553
25	7	1.7	141	2	D83834
26	7	1.7	180	2	G70912
27	7	1.7	206	2	B97594
28	7	1.7	206	2	AG2815
29	7	1.7	235	2	F86598

30	7	1.7	235	2	H72025
31	7	1.7	235	2	G81515
32	7	1.7	241	2	F71478
33	7	1.7	241	2	B81741
34	7	1.7	244	2	AD3266
35	7	1.7	245	2	E87719
36	7	1.7	254	2	B87630
37	7	1.7	257	2	T44278
38	7	1.7	267	2	T00114
39	7	1.7	267	2	H64044
40	7	1.7	267	2	B83109
41	7	1.7	268	1	NCECDL
42	7	1.7	268	2	G90935
43	7	1.7	268	2	C85784
44	7	1.7	270	2	H70690
45	7	1.7	276	2	G01564
46	7	1.7	276	2	C44324
47	7	1.7	291	2	D82491
48	7	1.7	296	2	JC6050
49	7	1.7	302	2	S61836
50	7	1.7	302	2	C64311
51	7	1.7	306	1	CCECDL
52	7	1.7	306	2	H90640
53	7	1.7	306	2	H85491
54	7	1.7	306	2	AG0518
55	7	1.7	319	2	AH3527
56	7	1.7	320	2	C81972
57	7	1.7	320	2	C81029
58	7	1.7	320	2	A40660
59	7	1.7	325	2	H96032
60	7	1.7	326	2	UQ0855
61	7	1.7	327	2	F95889
62	7	1.7	331	2	A83534
63	7	1.7	333	2	AH0268
64	7	1.7	334	2	JC4870
65	7	1.7	336	2	T49112
66	7	1.7	337	2	F70071
67	7	1.7	345	2	AG3186
68	7	1.7	345	2	A10926
69	7	1.7	345	2	B75274
70	7	1.7	346	2	E86715
71	7	1.7	347	2	AG1817
72	7	1.7	354	2	C71368
73	7	1.7	354	2	S60967
74	7	1.7	365	2	T49733
75	7	1.7	368	2	B97623
76	7	1.7	368	2	AB2846
77	7	1.7	373	2	T45747
78	7	1.7	379	2	B71331
79	7	1.7	380	2	S03433
80	7	1.7	381	2	JC7247
81	7	1.7	382	1	PECH
82	7	1.7	383	2	JC7573
83	7	1.7	384	2	AG3914
84	7	1.7	386	1	PEPG
85	7	1.7	387	2	D38302
86	7	1.7	387	2	C38302
87	7	1.7	387	2	B38302
88	7	1.7	387	2	E38302
89	7	1.7	387	2	I46617
90	7	1.7	387	2	JC7245
91	7	1.7	388	1	PEH
92	7	1.7	388	1	PEMOAR
93	7	1.7	388	1	PEMOAT
94	7	1.7	388	1	S19684
95	7	1.7	388	1	S19682
96	7	1.7	388	2	A30142
97	7	1.7	388	2	B30142
98	7	1.7	398	2	I51185
99	7	1.7	398	2	B75475
100	7	1.7	416	2	AG0125
101	7	1.7	428	2	S47096
102	7	1.7	428	2	B90636

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hypothetical prote
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D-alanine-D-alanin
D-alanine-D-alanin
D-alanine-D-alanin
D-xylase-binding P
probable 3-oxoacyl
3-oxoacyl-(acyl-ca
outer membrane pro
probable thiamine
hypothetical 36.8K
probable dehydroge
probable C4-dicarb
anthranilate phosp
pepsin A (EC 3.4.2
aspartic proteinase
hypothetical prote
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probable capsid po
conserved hypochet
transcription regu
rod shape-determin
probable UDP-N-ace
VGPI protein precu
probable homoserin
cpa protein (A700
Ca2+/H+ antiporter
GDP-D-mannose-4,6-
conserved hypochet
candidapepsin (EC
prochymosin - comm
pepsin A (EC 3.4.2
pepsinogen C - Afr
gastric (EC 3.4.2
pepsin A (EC 3.4.2
pepsin (EC 3.4.23.
pepsin (EC 3.4.23.
pepsin (EC 3.4.23.
pepsin (EC 3.4.23.
pregnancy-associat
pepsinogen A - com
pepsin A (EC 3.4.2
pepsin A (EC 3.4.2
pepsin A (EC 3.4.2
pepsin A (EC 3.4.2
pepsin A (EC 3.4.2
pepsin A (EC 3.4.2
pepsin A (EC 3.4.2
cathepsin D (EC 3.
glucose-fructose o
N-acetylmutamoyl-L
cynarase (EC 3.4.2
survival protein [

103	7	1.7	428	2	B85487	176	6	1.5	71	2	S22905	lysine protein S-
104	7	1.7	428	2	E64726	177	6	1.5	72	2	S01799	pepsin (EC 3.4.23.
105	7	1.7	433	2	E96649	178	6	1.5	73	1	F2NT0P	photosystem II pro
106	7	1.7	434	2	AD0061	179	6	1.5	73	2	S21754	gastricisin (EC 3.4
107	7	1.7	436	2	G96009	180	6	1.5	73	2	A87686	hypothetical prote
108	7	1.7	452	2	S41717	181	6	1.5	79	2	S03266	aspartic proteinas
109	7	1.7	460	2	T43224	182	6	1.5	79	2	D64596	hypothetical prote
110	7	1.7	462	2	G70544	183	6	1.5	81	2	H82515	hypothetical prote
111	7	1.7	474	2	T12049	184	6	1.5	87	2	Q01135	levilide precursor
112	7	1.7	491	2	C98275	185	6	1.5	88	2	A28056	hypothetical prote
113	7	1.7	491	2	AC33008	186	6	1.5	88	2	D64562	hypothetical prote
114	7	1.7	491	2	H84379	187	6	1.5	89	2	F84706	hypothetical prote
115	7	1.7	496	2	JS0732	188	6	1.5	91	1	S00060	phospholipid trans
116	7	1.7	506	2	T07915	189	6	1.5	91	2	T42907	hypothetical prote
117	7	1.7	506	2	S71591	190	6	1.5	92	2	S06034	hypothetical prote
118	7	1.7	506	2	F86253	191	6	1.5	92	2	S06033	hypothetical prote
119	7	1.7	508	2	D85056	192	6	1.5	94	2	S03380	major fecal allerg
120	7	1.7	509	2	UC7272	193	6	1.5	96	2	A87110	conserved hypotet
121	7	1.7	510	2	D89796	194	6	1.5	98	2	FQ0496	hypothetical prote
122	7	1.7	513	2	T09739	195	6	1.5	99	2	B95393	hypothetical prote
123	7	1.7	555	2	F86487	196	6	1.5	99	2	A11907	hypothetical prote
124	7	1.7	558	2	E70756	197	6	1.5	101	2	G72450	hypothetical prote
125	7	1.7	569	2	S64957	198	6	1.5	102	2	D90915	hypothetical prote
126	7	1.7	566	2	S57971	199	6	1.5	102	2	A85764	hypothetical prote
127	7	1.7	626	2	H82147	200	6	1.5	102	2	A12693	conserved hypotet
128	7	1.7	646	2	T38171	201	6	1.5	105	2	S62844	H+-transporting tw
129	7	1.7	682	2	AE0033	202	6	1.5	105	2	B69857	chaperonin homolog
130	7	1.7	690	2	B82409	203	6	1.5	105	2	T49332	hypothetical prote
131	7	1.7	707	2	F86925	204	6	1.5	105	2	AD3365	hypothetical prote
132	7	1.7	709	2	T29692	205	6	1.5	107	2	Q02035	hypothetical prote
133	7	1.7	722	2	T46560	206	6	1.5	107	2	T25670	hypothetical prote
134	7	1.7	754	2	S62512	207	6	1.5	110	1	PEBO	pepsin A (EC 3.4.2
135	7	1.7	773	1	JH0609	208	6	1.5	110	2	E69607	protein secretion
136	7	1.7	775	2	S55345	209	6	1.5	112	2	T48324	DNA protein-like
137	7	1.7	784	2	AC1091	210	6	1.5	112	2	AB0687	probable membrane
138	7	1.7	802	2	D85035	211	6	1.5	113	2	A70553	hypothetical prote
139	7	1.7	831	2	A48489	212	6	1.5	113	2	T42985	hypothetical prote
140	7	1.7	843	2	T16906	213	6	1.5	113	2	C83893	hypothetical prote
141	7	1.7	887	2	T20866	214	6	1.5	114	2	E72724	hypothetical prote
142	7	1.7	899	2	S62428	215	6	1.5	115	2	D64914	hypothetical prote
143	7	1.7	933	1	BV8CC	216	6	1.5	117	2	T09155	lipid transfer pro
144	7	1.7	933	2	C91017	217	6	1.5	119	2	S24294	chorion protein -
145	7	1.7	933	2	B85861	218	6	1.5	119	2	S24291	early chorion prot
146	7	1.7	939	2	AE2275	219	6	1.5	119	2	B45937	chorion class CA p
147	7	1.7	967	2	S58360	220	6	1.5	121	2	S24293	hypothetical 13k p
148	7	1.7	1015	2	I39697	221	6	1.5	122	2	J00150	hypothetical prote
149	7	1.7	1015	2	A42915	222	6	1.5	123	2	D84383	hypothetical prote
150	7	1.7	1039	2	G83748	223	6	1.5	124	1	NRCB	pancreatic ribonuc
151	7	1.7	1073	2	S56220	224	6	1.5	124	1	GCAP	glucagon 1 precurs
152	7	1.7	1131	2	AD2166	225	6	1.5	125	2	B97470	hypothetical prote
153	7	1.7	1142	2	C97080	226	6	1.5	125	2	AG2688	Na+/H+ antiporter
154	7	1.7	1236	2	T50904	227	6	1.5	126	2	H86347	hypothetical prote
155	7	1.7	1269	2	T14476	228	6	1.5	128	2	T30714	hypothetical prote
156	7	1.7	1379	2	T13718	229	6	1.5	129	2	E90535	hypothetical prote
157	7	1.7	1433	2	A46053	230	6	1.5	129	2	AB3459	hypothetical prote
158	7	1.7	1533	2	A46221	231	6	1.5	131	2	S24285	RNA-directed RNA p
159	7	1.7	1632	2	C70752	232	6	1.5	131	2	D90419	transcriptional re
160	7	1.7	2014	2	T21560	233	6	1.5	132	2	T35141	hypothetical prote
161	7	1.7	2025	2	D86201	234	6	1.5	132	2	AB1767	ATP synthase chain
162	7	1.7	2025	2	C64474	235	6	1.5	132	2	AH1391	ATP synthase chain
163	7	1.7	2894	2	PT0326	236	6	1.5	133	2	D87690	hypothetical prote
164	6	1.5	16	2	A44352	237	6	1.5	134	2	F72802	hypothetical prote
165	6	1.5	39	2	S35325	238	6	1.5	134	2	F97475	conserved hypotet
166	6	1.5	40	2	D96733	239	6	1.5	134	2	AC3323	hypothetical prote
167	6	1.5	48	2	D96733	240	6	1.5	135	2	D71228	photosystem II pro
168	6	1.5	49	2	SV0019	241	6	1.5	137	2	S53025	hypothetical prote
169	6	1.5	52	1	S07502	242	6	1.5	138	2	G65096	hypothetical prote
170	6	1.5	52	1	S42315	243	6	1.5	138	2	D91124	hypothetical prote
171	6	1.5	52	2	A34657	244	6	1.5	138	2	S20087	hypothetical prote
172	6	1.5	59	2	B87614	245	6	1.5	138	2	C85969	homeotic protein b
173	6	1.5	64	2	E96056	246	6	1.5	138	2	D72539	hypothetical prote
174	6	1.5	65	2	F81607	247	6	1.5	139	2	G69543	conserved hypotet
175	6	1.5	67	2	AB1771	248	6	1.5	141	2	A91249	probable transcrip

249	6	1.5	141	2	A90130	hypothetical prote	322	6	1.5	178	2	S03629	neurogenic gene co
250	6	1.5	141	2	AC3590	3-oxoadipate CoA-t	323	6	1.5	178	2	T08444	hypothetical prote
251	6	1.5	142	2	T40837	DNA-directed RNA p	324	6	1.5	178	2	E88637	protein M09G12.6 l
252	6	1.5	142	2	AC3345	lsu ribosomal prot	325	6	1.5	179	2	C75469	hypothetical prote
253	6	1.5	143	2	T13214	minor capsid prote	326	6	1.5	180	2	T16445	hypothetical prote
254	6	1.5	143	2	T41630	very hypothetical	327	6	1.5	182	2	S70689	adenine phosphorib
255	6	1.5	145	2	D83424	hypothetical prote	328	6	1.5	183	2	A72657	VP529-like phospho
256	6	1.5	146	2	A72115	conserved hypochet	329	6	1.5	185	2	B70072	conserved hypochet
257	6	1.5	146	2	D86508	hypothetical prote	330	6	1.5	186	2	AB2408	hypothetical prote
258	6	1.5	146	2	G90337	hypothetical prote	331	6	1.5	186	2	AF2556	hypothetical prote
259	6	1.5	147	2	A26687	ectinoidin - sea u	332	6	1.5	187	2	S69315	hypothetical prote
260	6	1.5	147	2	S05320	transhyretin prec	333	6	1.5	188	2	F83855	GTP cyclhydrolase
261	6	1.5	148	2	C72422	hypothetical prote	334	6	1.5	188	2	T02781	probable conjugal
262	6	1.5	148	2	D95849	hypothetical prote	335	6	1.5	188	2	B84719	hypothetical prote
263	6	1.5	149	2	D98196	hypothetical prote	336	6	1.5	189	2	A71569	hypothetical prote
264	6	1.5	149	2	AF3090	conserved hypochet	337	6	1.5	189	2	JC7262	receptor activity
265	6	1.5	151	2	A86705	transcriptional re	338	6	1.5	189	2	T18480	hypothetical prote
266	6	1.5	151	2	G84165	hypothetical prote	339	6	1.5	190	2	T10740	carbonate dehydrat
267	6	1.5	151	2	T18478	hypothetical prote	340	6	1.5	191	2	I45716	GTP-binding protei
268	6	1.5	152	2	B75042	aspartate carbamoy	341	6	1.5	191	2	E75132	molycopterin-guan
269	6	1.5	152	2	B72754	hypothetical prote	342	6	1.5	192	2	G71089	hypothetical prote
270	6	1.5	153	2	S12206	hypothetical prote	343	6	1.5	195	2	G70211	hypothetical prote
271	6	1.5	153	2	D83012	hypothetical prote	344	6	1.5	195	2	A96998	CDP-diacyceride sy
272	6	1.5	155	2	AB3512	modulation protein	345	6	1.5	196	2	F88382	protein M06B11.2 l
273	6	1.5	155	2	E72661	hypothetical prote	346	6	1.5	196	2	D81696	hypothetical prote
274	6	1.5	157	2	H83082	probable transcrip	347	6	1.5	197	2	S25106	capsid protein - b
275	6	1.5	157	2	C82121	phosphobistidine p	348	6	1.5	198	2	T29135	hypothetical prote
276	6	1.5	157	2	H72673	hypothetical prote	349	6	1.5	199	2	E95211	N-(5'-phosphoribos
277	6	1.5	159	2	G70841	hypothetical prote	350	6	1.5	199	2	S41316	coat protein - cuc
278	6	1.5	159	2	H86997	conserved hypochet	351	6	1.5	199	2	F86832	hypothetical prote
279	6	1.5	159	2	T35623	probable protein p	352	6	1.5	200	2	T18479	hypothetical prote
280	6	1.5	159	2	B71423	hypothetical prote	353	6	1.5	201	1	VCVQGB	coat protein - bee
281	6	1.5	160	2	B70718	hypothetical prote	354	6	1.5	201	2	D70519	probable lpnc prot
282	6	1.5	161	1	WCTWSH	coat protein - cuc	355	6	1.5	202	1	VCVQPL	coat protein - bee
283	6	1.5	161	2	S54434	phosphoribosylamin	356	6	1.5	202	2	C72701	probable heme expo
284	6	1.5	161	2	S27127	tropomyosin homolo	357	6	1.5	202	2	AC2875	hypothetical prote
285	6	1.5	163	2	H72759	probable dctp deam	358	6	1.5	205	2	C86862	guanylate kinase (
286	6	1.5	164	1	RGECLR	leucine-responsive	359	6	1.5	205	2	P00272	D-alanine-D-alanin
287	6	1.5	164	2	G64132	phosphoribosylamin	360	6	1.5	205	2	G64989	heme exporter prot
288	6	1.5	164	2	S59991	transcription regu	361	6	1.5	205	2	B91015	ATP binding protei
289	6	1.5	164	2	S59993	transcription regu	362	6	1.5	205	2	D85859	ATP binding protei
290	6	1.5	164	2	S59992	transcription regu	363	6	1.5	205	2	AC0960	heme exporter prot
291	6	1.5	164	2	B82142	leucine-responsive	364	6	1.5	205	2	AD0788	heme exporter prot
292	6	1.5	164	2	A10167	leucine-responsive	365	6	1.5	206	2	JC4268	fibroblast growth
293	6	1.5	164	2	F90750	leucine-responsive	366	6	1.5	206	2	AE0891	probable membrane
294	6	1.5	164	2	D85614	leucine-responsive	367	6	1.5	206	2	T48149	hypothetical prote
295	6	1.5	164	2	AE0611	leucine-responsive	368	6	1.5	206	2	H89628	conserved hypochet
296	6	1.5	165	2	A12904	hypothetical prote	369	6	1.5	207	2	B86498	superoxide dismuta
297	6	1.5	165	2	S61602	probable membrane	370	6	1.5	207	2	B72124	hypothetical prote
298	6	1.5	166	2	D69695	ribosomal protein	371	6	1.5	207	2	B84151	probable transcrip
299	6	1.5	168	2	D75259	hypothetical prote	372	6	1.5	207	2	T36937	hypothetical prote
300	6	1.5	169	2	A89912	hypothetical prote	373	6	1.5	208	2	T09901	hypothetical prote
301	6	1.5	169	2	D90857	hypothetical prote	374	6	1.5	209	1	S53657	hydrogenase matu
302	6	1.5	169	2	B75490	hypothetical prote	375	6	1.5	209	2	G98075	phosphoribosylanth
303	6	1.5	169	2	F85762	hypothetical prote	376	6	1.5	209	2	G72528	hypothetical prote
304	6	1.5	170	2	B90214	NADH dehydrogenase	377	6	1.5	210	2	F69510	fibryllarin (fbb)
305	6	1.5	171	2	C87418	hypothetical prote	378	6	1.5	211	2	D69888	micrococcal nuclea
306	6	1.5	171	2	G84421	probable auxin-ind	379	6	1.5	211	2	A69619	deoxyribose-phosph
307	6	1.5	171	2	A84561	probable bzif tran	380	6	1.5	211	2	A81700	conserved hypochet
308	6	1.5	172	2	A91070	hypothetical prote	381	6	1.5	212	1	R5HSLH	ribosomal protein
309	6	1.5	172	2	D85914	hypothetical prote	382	6	1.5	212	2	H84266	50S ribosomal prot
310	6	1.5	172	2	T02229	protein BYU15 - co	383	6	1.5	212	2	T05721	germin-like protei
311	6	1.5	172	2	B86439	protein T19E23.11	384	6	1.5	212	2	T44970	gas-vesicle operon
312	6	1.5	173	2	AF3293	crossover junction	385	6	1.5	213	2	B87694	cytidylate kinase
313	6	1.5	173	2	F45392	orf6 protein - por	386	6	1.5	213	2	T27841	hypothetical prote
314	6	1.5	173	2	A44281	envelope protein -	387	6	1.5	214	2	B87424	outer membrane pro
315	6	1.5	173	2	D83464	conserved hypochet	388	6	1.5	215	2	B35534	hypothetical 23k p
316	6	1.5	174	2	A47113	glucuronosyltransf	389	6	1.5	215	2	F97825	50S ribosomal prot
317	6	1.5	174	2	E65046	hypothetical prote	390	6	1.5	215	2	C72635	triase-phosphate i
318	6	1.5	174	2	B72712	hypothetical prote	391	6	1.5	215	2	AH3389	transporter BME111
319	6	1.5	174	2	S73052	hypothetical prote	392	6	1.5	216	2	A71672	ribosomal protein
320	6	1.5	176	2	I48752	gene RXRbeta1 prot	393	6	1.5	216	2	S09509	outer membrane pro
321	6	1.5	178	2	I40124	outer surface prot	394	6	1.5	216	2	S40720	hypothetical prote

395	1.5	217	2	D82407	outer membrane pro	468	1.5	243	1	WMVZP2	F2 protein - fowlp
396	1.5	217	2	F83502	hypothetical prote	469	1.5	244	2	C83953	ribosomal protein
397	1.5	218	2	T50070	superoxide dismuta	470	1.5	244	2	A39365	cyanamide hydratase
398	1.5	218	2	S75100	ABC transport prot	471	1.5	244	2	B83630	hypothetical prote
399	1.5	218	2	S73675	hypothetical prote	472	1.5	245	2	T47501	dofe zinc finger p
400	1.5	218	2	C72747	probable endonucle	473	1.5	245	2	AG2203	glucose inhibited
401	1.5	219	1	A35617	HDL receptor ERD2	474	1.5	246	2	E75481	RNA methyltransfer
402	1.5	219	2	S75541	hypothetical prote	475	1.5	247	2	C98340	2-deoxy-D-gluconat
403	1.5	219	2	B71511	probable sugar nuc	476	1.5	247	2	AG2942	2-deoxy-D-gluconat
404	1.5	219	2	T20732	hypothetical prote	477	1.5	247	2	H70432	ABC transporter -
405	1.5	219	2	C70855	hypothetical prote	478	1.5	247	2	B64147	hypothetical prote
406	1.5	219	2	A99194	iron (III) ABC tra	479	1.5	247	2	D69453	hypothetical prote
407	1.5	219	2	G87708	hypothetical prote	480	1.5	248	2	H70511	probable prca prot
408	1.5	219	2	H81824	hypothetical perip	481	1.5	249	1	B70693	probable echa16 pr
409	1.5	221	1	H1MSA1	H-2 class II histo	482	1.5	249	2	E75181	ribonuclease ph (r
410	1.5	223	2	AG3263	propanediol dehydr	483	1.5	249	2	E71032	hypothetical prote
411	1.5	223	2	A86057	hypothetical prote	484	1.5	249	2	S32609	phycoerythrin-asso
412	1.5	223	2	F91210	hypothetical prote	485	1.5	249	2	T10441	conserved hypochet
413	1.5	224	2	T32655	hypothetical prote	486	1.5	250	2	T43153	probable aldehyde
414	1.5	225	1	WZVZG2	G2R protein - Amsa	487	1.5	250	2	A82125	heme exporter prot
415	1.5	225	2	AC0587	KOP operon transcr	488	1.5	250	2	D69180	ABC transporter -
416	1.5	225	2	T29632	hypothetical prote	489	1.5	250	2	S28474	rfbi protein - Vib
417	1.5	225	2	F72642	probable shikimate	490	1.5	250	2	H72704	probable iron (III)
418	1.5	226	1	TVMVSS	POGF-related trans	491	1.5	250	2	A95261	response regulator
419	1.5	226	2	AC0388	probable short-cha	492	1.5	250	2	F98126	indole-3-glycerol
420	1.5	226	2	S75665	ABC-type transport	493	1.5	251	1	C36044	early EIA 27K prot
421	1.5	226	2	G75342	hypothetical prote	494	1.5	251	1	WMADP4	probable hydroxyc
422	1.5	226	2	H84213	hypothetical prote	495	1.5	251	2	F84958	hypothetical prote
423	1.5	227	2	B84696	probable glutathio	496	1.5	251	2	D71950	hypothetical prote
424	1.5	227	2	AG1314	hypothetical prote	497	1.5	252	2	A82146	3-deoxy-manno-ctu
425	1.5	227	2	AG1686	hypothetical prote	498	1.5	252	2	H90476	hypothetical prote
426	1.5	227	2	T45388	hypothetical prote	499	1.5	252	2	H75083	hypothetical prote
427	1.5	229	2	S33182	probable transport	500	1.5	253	2	T47757	hypothetical prote
428	1.5	229	2	T34277	hypothetical prote	501	1.5	253	2	T27279	hypothetical prote
429	1.5	229	2	F75482	transcription regu	502	1.5	253	2	AI0613	probable lipoprote
430	1.5	230	2	F71122	hypothetical prote	503	1.5	254	2	S11649	class II histocomp
431	1.5	230	2	H72244	conserved hypochet	504	1.5	254	2	S75814	hypothetical prote
432	1.5	230	2	E87578	hypothetical prote	505	1.5	255	2	S74930	hypothetical prote
433	1.5	231	2	G69403	conserved hypochet	506	1.5	255	2	C84071	hypothetical prote
434	1.5	231	2	S48966	hypothetical prote	507	1.5	255	2	T19747	hypothetical prote
435	1.5	232	2	T12740	hypothetical prote	508	1.5	256	1	H1MSA2	H-2 class II histo
436	1.5	232	2	G87629	hypothetical prote	509	1.5	256	2	H97649	probable gluconate
437	1.5	232	2	AG1452	hypothetical prote	510	1.5	256	2	AG2873	dehydrogenase Atu2
438	1.5	232	2	A87504	6-phospho-glucono-	511	1.5	256	2	T03371	glycine-rich prote
439	1.5	232	2	G84382	cobalt transport A	512	1.5	256	2	G83232	probable permease
440	1.5	232	2	D70537	hypothetical prote	513	1.5	256	2	C72261	spermidine/putresc
441	1.5	233	2	I79358	IA-alpha polyprote	514	1.5	256	2	B71264	hypothetical prote
442	1.5	233	2	I79357	IA-alpha polyprote	515	1.5	257	2	B83169	probable methyltra
443	1.5	233	2	AF0110	probable hemolysin	516	1.5	258	2	JC2567	UDP-N-acetylmuram
444	1.5	234	1	QOBE43	membrane antigen g	517	1.5	258	2	T19755	hypothetical prote
445	1.5	234	2	AC0431	conserved hypochet	518	1.5	259	2	A83750	transcription regu
446	1.5	234	2	E64331	hypothetical prote	519	1.5	259	2	S76205	hypothetical prote
447	1.5	235	2	C98204	probable permease	520	1.5	259	2	AB0565	probable membrane
448	1.5	235	2	AE3082	hypothetical prote	521	1.5	259	2	E84886	probable beta-expa
449	1.5	235	2	F97391	probable transcrip	522	1.5	259	2	D64362	hypochetical prote
450	1.5	235	2	AG2609	transcription regu	523	1.5	259	2	B64697	UDP-N-acetylenolpy
451	1.5	236	2	D72729	hypothetical prote	524	1.5	259	2	B71823	udp-n-acetylenolpy
452	1.5	237	2	E83674	3'-phosphoadenosin	525	1.5	260	2	E71045	probable ABC trans
453	1.5	237	2	A36149	spiralin - Spiropl	526	1.5	261	2	I48645	cell adhesion mole
454	1.5	237	2	D70463	hypothetical prote	527	1.5	263	2	G70583	probable dehydroge
455	1.5	237	2	G87286	conserved hypochet	528	1.5	263	2	S76548	hypochetical prote
456	1.5	237	2	AG3573	6-phosphogluconola	529	1.5	264	2	C84028	septum site-determ
457	1.5	238	2	T10771	NADPH-ferrithemop	530	1.5	265	2	T46733	citr protein [lampo
458	1.5	238	2	S67594	RAM59 protein - ye	531	1.5	265	2	T07800	inositol-1(or 4)-m
459	1.5	238	2	H87578	transcription regu	532	1.5	265	2	C70332	hypochetical prote
460	1.5	238	2	B97634	transcribable transcrip	533	1.5	265	2	E87074	protaosome [alpha]
461	1.5	238	2	AD2857	transcription regu	534	1.5	265	2	S72865	hypochetical prote
462	1.5	239	1	S34193	phosphoadenylyl-su	535	1.5	266	2	A90436	enoyl CoA hydratase
463	1.5	239	2	AP0261	fatty acid metabol	536	1.5	266	2	AB1630	cell division inhi
464	1.5	240	1	UJ0143	antigen BGM1 precu	537	1.5	266	2	AH1267	cell division inhi
465	1.5	241	1	D71233	probable 3-isoprop	538	1.5	266	2	F70595	hypochetical prote
466	1.5	241	1	A75200	hypochetical prote	539	1.5	266	2	G97483	hypochetical prote
467	1.5	242	2	S30888	PRB38 protein - ye	540	1.5	266	2	AF2701	aldolase Atu1014 [

541	6	1.5	266	2	B72108	conserved hypotnet	614	6	1.5	294	2	G01606	hypothetical prote
542	6	1.5	266	2	C86514	methyase [impor	615	6	1.5	295	2	A64514	hypothetical prote
543	6	1.5	266	2	T31217	transcription regu	616	6	1.5	295	2	G71707	hypothetical prote
544	6	1.5	267	2	B87578	hypothetical prote	617	6	1.5	295	2	AF2610	conserved hypotnet
545	6	1.5	267	2	B82068	ABC transporter, A	618	6	1.5	295	2	D97392	hypothetical prote
546	6	1.5	268	1	G45239	cell division inh	619	6	1.5	295	2	AD0306	probable membrane
547	6	1.5	268	2	AC0710	exodeoxyribonuclea	620	6	1.5	296	2	E83049	conserved hypotnet
548	6	1.5	268	2	G25311	chitinase (EC 3.2.	621	6	1.5	296	2	G97799	hypothetical prote
549	6	1.5	268	2	AE2363	inositol monophosp	622	6	1.5	297	2	H82500	conserved hypotnet
550	6	1.5	268	2	A64361	hypothetical prote	623	6	1.5	297	2	G70185	mevalonate kinase
551	6	1.5	268	2	B83020	lipopolysaccharide	624	6	1.5	297	2	H69391	hypothetical prote
552	6	1.5	269	2	G75558	hypothetical prote	625	6	1.5	297	2	AC2380	hypothetical prote
553	6	1.5	269	2	D83090	probable ATP-bind	626	6	1.5	298	2	S76437	hypothetical prote
554	6	1.5	269	2	B65110	hypothetical prote	627	6	1.5	299	2	T35844	hypothetical prote
555	6	1.5	269	2	B91138	hypothetical prote	628	6	1.5	300	2	S69052	cytochrome-c oxida
556	6	1.5	270	2	E85983	hypothetical prote	629	6	1.5	300	2	AF1286	CDP-bequose synth
557	6	1.5	270	2	FE4057	energy transducer	630	6	1.5	300	2	AG2055	hypothetical prote
558	6	1.5	270	2	T35721	hypothetical prote	631	6	1.5	302	1	PAFPIA	phosphoprotein pho
559	6	1.5	270	2	AH0904	probable ABC-trans	632	6	1.5	302	2	S29396	phosphoprotein pho
560	6	1.5	270	2	D69127	hypothetical prote	633	6	1.5	302	2	H95075	hypothetical prote
561	6	1.5	270	2	D72334	sugar kinase, pfkB	634	6	1.5	302	2	T50784	hypothetical prote
562	6	1.5	271	2	A11102	dlhydroperoxate sy	635	6	1.5	303	2	E70848	probable oxidoredu
563	6	1.5	271	2	A11464	dhhydroperoxate sy	636	6	1.5	303	2	B70875	hypothetical prote
564	6	1.5	271	2	A25669	PDGF-related trans	637	6	1.5	303	2	T11206	spao protein - Sal
565	6	1.5	271	2	G72380	conserved hypotnet	638	6	1.5	303	2	S37307	spao protein - Sal
566	6	1.5	271	2	F82346	lipopolysaccharide	639	6	1.5	303	2	AG0851	surface presentati
567	6	1.5	271	2	D70591	hypothetical prote	640	6	1.5	305	2	H95359	probable ABC trans
568	6	1.5	272	2	A44324	proteasome endope	641	6	1.5	306	2	T08504	rbg protein - Ent
569	6	1.5	272	2	AH0434	probable ABC trans	642	6	1.5	306	2	G83152	hypothetical prote
570	6	1.5	273	2	T11585	hypothetical prote	643	6	1.5	307	2	PC2050	legumain type A alp
571	6	1.5	273	2	B70550	probable c1cfc prot	644	6	1.5	307	2	T03502	conserved hypotnet
572	6	1.5	273	2	B37281	replication factor	645	6	1.5	308	2	H87095	conserved hypotnet
573	6	1.5	273	2	A99663	conserved hypotnet	646	6	1.5	309	2	E87559	peptidase M20/M25/
574	6	1.5	274	2	AG2312	5'-methylthiodeno	647	6	1.5	310	2	F82979	probable transcrip
575	6	1.5	274	2	T02797	thymidylate kinase	648	6	1.5	311	2	AB3322	transporter BME105
576	6	1.5	276	2	A41377	mxo protein precu	649	6	1.5	312	2	S71207	serine O-acetyltra
577	6	1.5	277	2	AF1312	ketopantoate hydro	650	6	1.5	312	2	C70901	probable fnt prote
578	6	1.5	278	2	B98296	sulfate ABC transp	651	6	1.5	312	2	G75514	hypothetical prote
579	6	1.5	278	2	T04504	hypothetical prote	652	6	1.5	312	2	T11951	hypothetical prote
580	6	1.5	278	2	S36101	CAMP response elem	653	6	1.5	312	2	D97552	lipid A biosynthes
581	6	1.5	279	2	F87577	serine acetyltrans	654	6	1.5	312	2	AF2772	lipid A biosynthes
582	6	1.5	279	2	AC2559	hypothetical prote	655	6	1.5	313	2	E96932	L-lactate dehydrog
583	6	1.5	279	2	E75573	transcription regu	656	6	1.5	314	2	A86879	carbamate kinase (
584	6	1.5	279	2	T52454	ATP-dependent C1p	657	6	1.5	314	2	A99446	ABC transporter, A
585	6	1.5	280	2	A98159	lactose transport	658	6	1.5	314	2	A87528	conserved hypotnet
586	6	1.5	280	2	AH3128	hypothetical prote	659	6	1.5	314	2	B86760	hypothetical prote
587	6	1.5	280	2	T22524	hypothetical prote	660	6	1.5	314	2	AB0402	probable transcrip
588	6	1.5	281	2	A50471	hypothetical prote	661	6	1.5	315	2	H82512	probable 3-hydroxy
589	6	1.5	281	2	T16813	hypothetical prote	662	6	1.5	315	2	H86836	carbamate kinase (
590	6	1.5	281	2	B86244	hypothetical prote	663	6	1.5	315	2	S27784	phenylethanolamine
591	6	1.5	281	2	S41854	phosphoprotein pho	664	6	1.5	316	2	F69978	sugar-phosphate de
592	6	1.5	282	2	D97280	fumate hydratase	665	6	1.5	317	2	AF0582	probable permease
593	6	1.5	282	2	A97214	uncinateacetylzed co	666	6	1.5	317	2	I59379	metaxin - mouse
594	6	1.5	283	2	F75195	agnatinnase (speb)	667	6	1.5	318	2	G72310	conserved hypotnet
595	6	1.5	283	2	AF2531	hypothetical prote	668	6	1.5	318	2	A11203	transketolase homo
596	6	1.5	284	2	AH0442	probable glutathio	669	6	1.5	319	2	S73159	hypothetical prote
597	6	1.5	285	2	G72415	sensor histidine k	670	6	1.5	320	2	B75457	polyprenyl synthas
598	6	1.5	285	2	S44561	hypothetical prote	671	6	1.5	320	2	T45034	hypothetical prote
599	6	1.5	287	2	AE2067	nicotinate-nucleot	672	6	1.5	321	2	T06845	hypothetical prote
600	6	1.5	287	2	C82965	hypothetical prote	673	6	1.5	322	1	A26370	hypothetical prote
601	6	1.5	287	2	T01758	hypothetical prote	674	6	1.5	322	1	T45567	flavonol synthase-
602	6	1.5	287	2	A12609	regulator protein	675	6	1.5	322	2	B87419	3-oxoacyl-(acyl-ca
603	6	1.5	287	2	H97391	probable regulator	676	6	1.5	322	2	D81962	probable inner mem
604	6	1.5	288	2	AE0056	probable right ori	677	6	1.5	322	2	AF0709	succinylglutamate
605	6	1.5	288	2	US0659	homeotic protein H	678	6	1.5	322	2	AC2023	hypothetical prote
606	6	1.5	289	2	AB3011	hypothetical prote	679	6	1.5	323	2	T04826	hypothetical prote
607	6	1.5	289	2	S48664	distal-less 3 prot	680	6	1.5	323	2	G84325	hypothetical prote
608	6	1.5	289	2	I53082	homeoprotein - rat	681	6	1.5	323	2	AC2479	hypothetical prote
609	6	1.5	290	2	T30215	monosaccharide tra	682	6	1.5	323	2	A89779	hypothetical prote
610	6	1.5	291	1	H97959	hypothetical prote	683	6	1.5	323	2	AF3630	nosk protein [imp
611	6	1.5	292	1	BE4226	hypothetical prote	684	6	1.5	324	2	T07832	probable steroid s
612	6	1.5	293	2	T38779	hypothetical RNA b	685	6	1.5	324	2	C72520	probable immunogen
613	6	1.5	294	2	A57478	serine O-acetyltra	686	6	1.5	324	2	F70531	hypothetical prote

687	6	1.5	324	2	T18818	hypothetical prote
688	6	1.5	325	2	S01698	alkanal monooxygen
689	6	1.5	326	2	C72483	probable formate d
690	6	1.5	326	2	AF0220	flagellar hook-ass
691	6	1.5	326	2	S76441	hypothetical prote
692	6	1.5	326	2	T52030	gamma-glutamyl hyd
693	6	1.5	327	2	F96815	hypothetical prote
694	6	1.5	327	2	AC2607	conserved hypotet
695	6	1.5	327	2	B97389	hypothetical prote
696	6	1.5	328	2	UN0882	gonadotropin-rela
697	6	1.5	328	2	T02046	prolamin box bindi
698	6	1.5	328	2	A13541	NADH2 dehydrogenas
699	6	1.5	329	2	E82644	sugar-phosphate de
700	6	1.5	329	2	F69849	probable heme A fa
701	6	1.5	329	2	C71091	hypothetical prote
702	6	1.5	330	2	T36194	probable acyl carr
703	6	1.5	330	2	AG1405	phosphotriesterase
704	6	1.5	330	2	AG1781	phosphotriesterase
705	6	1.5	331	2	AB1737	conserved hypotet
706	6	1.5	331	2	A11367	conserved hypotet
707	6	1.5	331	2	F86835	hypothetical prote
708	6	1.5	331	2	C89469	protein P0766.1 [i
709	6	1.5	332	2	S63660	NADH2 dehydrogenas
710	6	1.5	332	2	T34174	hypothetical prote
711	6	1.5	332	2	C72485	probable high-affi
712	6	1.5	332	2	H69360	ABC transporter AF
713	6	1.5	332	2	C84061	ferrichrome ABC tr
714	6	1.5	333	2	D95968	probable amino aci
715	6	1.5	333	2	H98282	hypothetical prote
716	6	1.5	334	1	D58EX2	urea11-DNA glycosy
717	6	1.5	334	2	T20728	hypothetical prote
718	6	1.5	334	2	G69028	conserved hypotet
719	6	1.5	334	2	D95942	probable deoxyribo
720	6	1.5	334	2	A89835	ferrichrome transp
721	6	1.5	335	2	C97053	mreB (imported) -
722	6	1.5	335	2	F86586	oxidoreductase (im
723	6	1.5	335	2	C72038	conserved hypotet
724	6	1.5	335	2	T39093	hypothetical prote
725	6	1.5	335	2	T32294	hypothetical prote
726	6	1.5	335	2	T52249	probable basic hel
727	6	1.5	335	2	B87328	transcription regu
728	6	1.5	336	2	F86923	probable oxidized
729	6	1.5	336	2	S22619	hypothetical prote
730	6	1.5	336	2	A95234	catabolite control
731	6	1.5	336	2	T37159	hypothetical prote
732	6	1.5	336	2	T36970	probable methyl est
733	6	1.5	337	2	AD1268	cell-shape determi
734	6	1.5	337	2	AF1630	cell-shape determi
735	6	1.5	337	2	A89047	protein G10G8.1 [i
736	6	1.5	337	2	S31131	hypothetical prote
737	6	1.5	338	2	A69278	branched-chain ami
738	6	1.5	338	2	AB3453	prolyl aminopeptid
739	6	1.5	338	2	T40495	homoserine kinase
740	6	1.5	338	2	B69439	signal-transducin
741	6	1.5	338	2	C75338	conserved hypotet
742	6	1.5	339	2	G87511	ketol-acid reducto
743	6	1.5	339	2	B69436	LSU ribosomal prot
744	6	1.5	339	2	S70218	slipd protein - sal
745	6	1.5	339	2	B86277	hypothetical prote
746	6	1.5	340	2	A99193	transcription repr
747	6	1.5	340	2	A13093	transcription repr
748	6	1.5	340	2	AC0850	pathogenicity isla
749	6	1.5	340	2	F88545	protein P5982.1 [i
750	6	1.5	340	2	B83177	probable aminotran
751	6	1.5	341	1	F85724	hypothetical prote
752	6	1.5	341	1	US0340	anthranilate phosp
753	6	1.5	341	2	AF1319	ferrichrome ABC tr
754	6	1.5	341	2	AF1691	ferrichrome ABC tr
755	6	1.5	341	2	B70373	rod shape determin
756	6	1.5	341	2	B86269	F21P23.4 protein -
757	6	1.5	341	2	A48422	ecdysone-inducible
758	6	1.5	341	2	S20827	cAMP response elem
759	6	1.5	341	2	S26686	cAMP response elem
760	6	1.5	342	2	S76463	hypothetical prote
761	6	1.5	342	2	S63404	hypothetical prote
762	6	1.5	342	2	E71101	probable geranylge
763	6	1.5	342	2	D86022	probable heme/hemo
764	6	1.5	342	2	C91176	probable heme/hemo
765	6	1.5	342	2	T16735	hypothetical prote
766	6	1.5	343	2	AH0328	probable 3',5'-cyc
767	6	1.5	343	2	S70549	sspd protein - Sal
768	6	1.5	343	2	D84390	sulfate transport
769	6	1.5	344	1	KHPGD	cathapsin D (EC 3.
770	6	1.5	344	2	AE2144	pyruvate dehydroge
771	6	1.5	344	2	C82835	anthranilate phosp
772	6	1.5	344	2	UC3601	CAMP response elem
773	6	1.5	344	2	UC5602	CAMP response elem
774	6	1.5	344	2	T46928	hypothetical prote
775	6	1.5	345	2	C90509	sorbitol dehydroge
776	6	1.5	345	2	AF0670	probable NADP-depe
777	6	1.5	345	2	AF0670	conserved hypotet
778	6	1.5	345	2	B83371	rod shape-determi
779	6	1.5	345	2	F83084	rod shape-determi
780	6	1.5	345	2	A97956	DNA polymerase III
781	6	1.5	345	2	S72833	periplasmic bindin
782	6	1.5	345	2	T38043	probable golgi per
783	6	1.5	346	2	F70666	probable alcohol d
784	6	1.5	346	2	C98098	catabolite control
785	6	1.5	346	2	D71637	rod shape-determi
786	6	1.5	346	2	G84028	cell-shape-determi
787	6	1.5	346	2	F97849	rod shape-determi
788	6	1.5	347	2	T09140	serine O-acetyltra
789	6	1.5	347	2	E71826	rod shape-determi
790	6	1.5	347	2	E64691	rod shape-determi
791	6	1.5	347	2	AC0446	rod shape-determi
792	6	1.5	347	2	AC0912	rod shape-determi
793	6	1.5	347	2	G72684	hypothetical prote
794	6	1.5	347	2	B87500	conserved hypotet
795	6	1.5	347	2	S53348	nuclear fusion pro
796	6	1.5	347	2	A95403	probable sulfate/c
797	6	1.5	348	2	A11037	probable capsid po
798	6	1.5	348	2	A12475	hypothetical prote
799	6	1.5	349	2	H72715	probable aspartate
800	6	1.5	349	2	T31934	hypothetical prote
801	6	1.5	349	2	G83605	probable ATP-bind
802	6	1.5	349	2	G98273	iron(III) diclitrac
803	6	1.5	349	2	AG3010	hypothetical prote
804	6	1.5	350	1	S52153	alcohol dehydrogen
805	6	1.5	350	2	G90199	acyl carrier prote
806	6	1.5	350	2	E90075	intercellular adhe
807	6	1.5	351	2	AE1923	c-type cytochrome
808	6	1.5	351	2	E97459	sulfate ABC transp
809	6	1.5	351	2	AG2677	hypothetical prote
810	6	1.5	351	2	G82232	anthranilate phosp
811	6	1.5	353	2	H83482	hypothetical prote
812	6	1.5	353	2	T25390	hypothetical prote
813	6	1.5	353	2	E81680	conserved hypotet
814	6	1.5	353	2	AF0676	hydrogenase-1 oper
815	6	1.5	355	1	H71363	conserved hypotet
816	6	1.5	355	1	G84651	biotin holocarboxy
817	6	1.5	356	2	G82938	hemim transport sy
818	6	1.5	356	2	T47313	hypothetical prote
819	6	1.5	356	2	AG3612	glycerol kinase (E
820	6	1.5	357	2	T17470	hydroxyphenyl pyru
821	6	1.5	357	2	AF1346	hypothetical prote
822	6	1.5	357	2	AF1716	hypothetical prote
823	6	1.5	358	2	C75375	branched-chain ami
824	6	1.5	358	2	E84467	hypothetical prote
825	6	1.5	359	2	F91219	hypothetical prote
826	6	1.5	359	2	A86804	prophage p13 prote
827	6	1.5	359	2	H86065	hypothetical prote
828	6	1.5	359	2	D97651	hypothetical prote
829	6	1.5	359	2	AF3470	transcription regu
830	6	1.5	360	2	T04535	hypothetical prote
831	6	1.5	361	2	C83350	probable transcrip
832	6	1.5	361	2	G83879	hypothetical prote

833	6	1.5	361	2	B83327	probable transcrip	906	6	1.5	388	2	B86193	hypothetical prote
834	6	1.5	362	2	D82644	sugar-phosphate de	907	6	1.5	388	2	F89773	hypothetical prote
835	6	1.5	362	2	T29053	branched-chain-ami	908	6	1.5	388	2	AF1907	hypothetical prote
836	6	1.5	363	2	A84032	3-isopropylmalate	909	6	1.5	389	2	JE0371	pepsin C (EC 3.4.2
837	6	1.5	363	2	F96992	polya polymerase r	910	6	1.5	389	2	A38302	pepsin (EC 3.4.23.
838	6	1.5	364	2	T04994	hypothetical prote	911	6	1.5	389	2	I46616	pregnancy-associat
839	6	1.5	364	2	T35353	hypothetical prote	912	6	1.5	389	2	T29410	hypothetical prote
840	6	1.5	365	2	S66466	cathepsin E (EC 3.	913	6	1.5	389	2	T28954	hypothetical prote
841	6	1.5	366	2	S03770	pectinesterase (EC	914	6	1.5	389	2	T32516	hypothetical prote
842	6	1.5	367	1	BVECEB	rod shape-determ	915	6	1.5	389	2	C96603	hypothetical prote
843	6	1.5	367	2	C91144	regulator of fesi	916	6	1.5	389	2	E95422	probable transmem
844	6	1.5	367	2	F85989	hypothetical prote	917	6	1.5	390	2	UT0334	acid proteinase (E
845	6	1.5	367	2	E90890	oxygen sensing pro	918	6	1.5	390	2	C65084	hypothetical prote
846	6	1.5	367	2	H85360	hypothetical prote	919	6	1.5	390	2	AG2549	hypothetical prote
847	6	1.5	367	2	E95930	probable sulfate u	920	6	1.5	390	2	D70834	hypothetical prote
848	6	1.5	367	2	D85727	oxygen sensing pro	921	6	1.5	390	2	C95954	hypothetical prote
849	6	1.5	367	2	H97686	hypothetical prote	922	6	1.5	391	2	D97201	aICR transformyla
850	6	1.5	367	2	AE2912	dehydrogenase Acu2	923	6	1.5	391	2	C70677	probable fadA5 pro
851	6	1.5	368	2	C70786	probable ilvE prot	924	6	1.5	391	2	A43356	cathepsin E (EC 3.
852	6	1.5	368	2	A53439	RP protein - human	925	6	1.5	391	2	AG3243	conjugal transfer
853	6	1.5	368	2	I80811	histone H2A.1 - ra	926	6	1.5	391	2	F96729	probable allinase
854	6	1.5	371	1	DEBSPA	pyruvate dehydroge	927	6	1.5	392	1	A24608	gastriccin (EC 3.4
855	6	1.5	371	1	MMBEYO	dUTP diphosphatase	928	6	1.5	392	2	H84679	hypothetical prote
856	6	1.5	371	2	S75555	hypothetical prote	929	6	1.5	393	2	A70958	probable pks18 pro
857	6	1.5	371	2	C87446	queuine tRNA ribos	930	6	1.5	393	2	T29412	hypothetical prote
858	6	1.5	371	2	F83487	hypothetical prote	931	6	1.5	393	2	S57671	hypothetical prote
859	6	1.5	371	2	T29605	hypothetical prote	932	6	1.5	393	2	F84381	hypothetical prote
860	6	1.5	373	1	MMBERT	uif6 protein - hum	933	6	1.5	394	2	T44867	hypothetical prote
861	6	1.5	374	2	T09111	probable magnesium	934	6	1.5	394	2	B43356	gastriccin (EC 3.4
862	6	1.5	376	2	D64897	probable NADPH2:qu	935	6	1.5	394	2	T32964	hypothetical prote
863	6	1.5	376	2	H85733	probable oxidoredu	936	6	1.5	394	2	G90387	hypothetical prote
864	6	1.5	376	2	E90885	aspartic proteinase	937	6	1.5	395	1	LIRTT	triacylglycerol 11
865	6	1.5	376	2	I45856	peptide ABC transp	938	6	1.5	395	2	T29411	hypothetical prote
866	6	1.5	377	1	A75381	gastriccin (EC 3.4	939	6	1.5	395	2	A47701	aspartic proteinase
867	6	1.5	377	1	PEMOCU	glibberellin 20-oxi	940	6	1.5	396	1	DCBYDM	adenosylmethionine
868	6	1.5	377	2	T10222	lps biosynthesis r	941	6	1.5	396	2	A44401	cathepsin E (EC 3.
869	6	1.5	379	1	G75095	gene P protein - p	942	6	1.5	396	2	T47207	aspartic proteinase
870.	6	1.5	379	1	ZBPBMU	hypothetical prote	943	6	1.5	396	2	T45033	hypothetical prote
871	6	1.5	379	2	C86821	hypothetical prote	944	6	1.5	396	2	T35254	conserved hypotet
872	6	1.5	379	2	A45443	tubulin-tyrosine 1	945	6	1.5	396	2	F84679	hypothetical prote
873	6	1.5	380	2	B41545	pregnancy-specific	946	6	1.5	397	2	H71116	hypothetical prote
874	6	1.5	380	2	I47176	chymosin (EC 3.4.2	947	6	1.5	397	2	H72668	hypothetical prote
875	6	1.5	380	2	D72641	probable chorismat	948	6	1.5	397	2	A96681	hypothetical prote
876	6	1.5	380	2	A12185	hypothetical prote	949	6	1.5	397	2	AH3170	conserved hypotet
877	6	1.5	381	2	S64089	probable membrane	950	6	1.5	398	2	S66465	cathepsin E (EC 3.
878	6	1.5	382	1	SYECCS	carbamoyl-phosphat	951	6	1.5	398	2	T33383	hypothetical prote
879	6	1.5	382	1	S01319	carbamoyl-phosphat	952	6	1.5	398	2	A45280	candidapepsin (EC
880	6	1.5	382	2	B85484	carbamoyl-phosphat	953	6	1.5	398	2	I59399	oncogene PTI-1 - h
881	6	1.5	382	2	C90633	carbamoyl-phosphat	954	6	1.5	398	2	A64982	hypothetical 43.3
882	6	1.5	382	2	AD0510	carbamoyl-phosphat	955	6	1.5	398	2	B85851	probable outer mem
883	6	1.5	382	2	S78285	conserved hypotet	956	6	1.5	398	2	S17428	interleukin-1 rece
884	6	1.5	382	2	G75294	probable transamin	957	6	1.5	399	2	D96717	hypothetical prote
885	6	1.5	382	2	T52391	hypothetical prote	958	6	1.5	400	1	S22539	transcription fact
886	6	1.5	383	2	A41545	pregnancy-specific	959	6	1.5	400	2	E96029	probable beta-keto
887	6	1.5	383	2	A41443	pepsin (EC 3.4.23.	960	6	1.5	400	2	I47099	renin (EC 3.4.23.1
888	6	1.5	383	2	I53870	Rdg-1 orphan recep	961	6	1.5	400	2	T51953	H-protein promoter
889	6	1.5	383	2	F86411	putorein FIK23.16	962	6	1.5	400	2	AH2303	hypothetical prote
890	6	1.5	384	2	JC7574	pepsinogen A - Afr	963	6	1.5	401	1	REMS8	renin (EC 3.4.23.1
891	6	1.5	384	2	B64515	hypothetical prote	964	6	1.5	401	2	H70658	probable arof prot
892	6	1.5	384	2	E70056	capsular polysacch	965	6	1.5	401	2	H75554	NiS-related prote
893	6	1.5	384	2	C64752	yaga protein - Bsc	966	6	1.5	401	2	D91082	probable transport
894	6	1.5	385	2	JC7575	pepsinogen A - bul	967	6	1.5	401	2	B85927	partial probable t
895	6	1.5	385	2	S48074	nuclear receptor T	968	6	1.5	402	1	REMSK	renin (EC 3.4.23.1
896	6	1.5	386	2	A89045	protein B0238.8 [i	969	6	1.5	402	2	B47701	aspartic proteinase
897	6	1.5	387	2	A82036	lactyl oxidation co	970	6	1.5	402	2	AE1354	transport system p
898	6	1.5	387	2	A45117	aspartic proteinase	971	6	1.5	402	2	AF1724	transport system p
899	6	1.5	387	2	D75594	sulfate adenylylitr	972	6	1.5	403	2	A70559	hypothetical prote
900	6	1.5	387	2	B98187	probable lacti-fami	973	6	1.5	403	2	D89786	hypothetical prote
901	6	1.5	387	2	JU0461	sarcosine oxidase	974	6	1.5	403	2	D86687	conserved hypotet
902	6	1.5	387	2	H65132	hypothetical 44.3	975	6	1.5	403	2	A82423	3-oxoacyl-(acyl-ca
903	6	1.5	388	2	A29937	gastriccin (EC 3.4	976	6	1.5	404	2	T34675	hypothetical prote
904	6	1.5	388	2	JC7246	pepsinogen C - com	977	6	1.5	404	2	B41317	O-antigen ligase C
905	6	1.5	388	2	B83228	probable MFS trans	978	6	1.5	404	2	AE0973	O-antigen ligase l

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979 6 1.5 404 2 AH3481 sulfate transport
980 6 1.5 405 2 A25379 saccharopepsin (EC
981 6 1.5 405 2 150608 bone morphogenetic
982 6 1.5 405 2 H71592 hypothetical prote
983 6 1.5 406 2 S33601 cell adhesion mole
984 6 1.5 405 2 RHHUK renin (EC 3.4.23.1
985 6 1.5 406 2 A67107 hypotetical prote
986 6 1.5 406 2 B96982 probable membrane
987 6 1.5 407 1 KHRTD cathepsin D (EC 3.
988 6 1.5 407 2 G71414 hydroxymandelonitr
989 6 1.5 407 2 D71862 probable zinc-met
990 6 1.5 407 2 F64567 zinc metalloprotei
991 6 1.5 408 1 BMH04 bone morphogenetic
992 6 1.5 408 2 JH0801 bone morphogenetic
993 6 1.5 408 2 S38343 bone morphogenetic
994 6 1.5 408 2 S58791 bone morphogenetic
995 6 1.5 409 1 F59814 fosmidmycin resist
996 6 1.5 409 2 A70932 probable ppe prote
997 6 1.5 409 2 A95944 probable periplasm
998 6 1.5 410 1 KHM5D cathepsin D (EC 3.
999 6 1.5 410 1 ZBRP4L cathepsin D - pha
1000 6 1.5 410 2 T04372 protein BEA1 - bar

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ALIGNMENTS

RESULT 1

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AS9090 aspartic proteinase (EC 3.4.23.-) BACE precursor - human
N:Alternate names: beta-secretase; beta-site APP cleaving enzyme
C:Species: Homo sapiens (man)
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 11-May-2000
C:Accession: AS9090
R:Vassar, R.; Bennett, B.D.; Babu-Khan, S.; Kahn, S.; Mendiaz, E.A.; Teplow,
M.A.; Biere, A.L.; Curran, E.; Burgess, T.; Louis, J.C.; Collins, F.; Treanor, J.; Rogers
Science 286, 735-741, 1999
A:Title: beta-secretase cleavage of Alzheimer's amyloid precursor protein by the transme
A:Reference number: AS9090; MUID:20002972; PMID:1051052
A:Note: submitted to Genbank, September 1999
A:Accession: AS9090
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-501 <VAS>
A:Cross-references: GB:AF190725; NID:G6118538; PIDN:AF04142.1; PID:G6118539
C:Genetics:
A:Gene: BACE
C:Superfamily: beta-secretase
C:Keywords: Alzheimer's disease; aspartic proteinase; brain; glycoprotein; hydrolase; pr
F:1-21/Domain: signal sequence #status predicted <SIG>
F:122-45/Domain: propeptide #status predicted <PRO>
F:146-501/Product: acid proteinase BACE #status predicted <MAT>
F:1461-477/Domain: transmembrane #status predicted <TRN>
F:193,289/Active site: Asp #status predicted
F:153,172,223,354/Binding site: carboxylate (Asn) (covalent) #status predicted
F:330-380/Disulfide bonds: #status predicted

```

Query Match 3.0%; Score 12; DB 2; Length 501;

Best Local Similarity 100.0%; Pred. No. 0.0009;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Oy 45 ILVDTGSSNFAV 56
    |||
Db 90 ILVDTGSSNFAV 101

```

RESULT 2

```

H64131 transcription regulator H1596, leucine-responsive - Haemophilus influenzae (strain Rd K
N:Alternate names: leucine-responsive regulatory protein
C:Species: Haemophilus influenzae
C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 26-Aug-1999
C:Accession: H64131

```

```

R:Feilschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage,
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.; Glodek, A.; Kelley, J.M.; Weidman,
; D.M.; Brandon, R.C.; Pine, L.D.; Fritchman, J.L.; Fuchs, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: H64131
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-166 <TIGR>
A:Cross-references: GB:U32833; GB:U42023; NID:G1574433; PIDN:AAC23241.1; PID:G1574433;
C:Function:
A:Description: activates a number of operons in response to the presence of exogenous l
C:Superfamily: regulatory protein asnc
C:Keywords: DNA binding; transcription regulation
F:34-60/Region: helix-turn-helix motif

```

Query Match 2.0%; Score 8; DB 2; Length 166;

Best Local Similarity 100.0%; Pred. No. 4.3;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Oy 243 GTTLRLRP 250
    |||
Db 136 GTTLRLRP 143

```

RESULT 3

```

J00729 60K inner-membrane protein - Proteus mirabilis (fragment)
C:Species: Proteus mirabilis
C>Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 08-Oct-1999
C:Accession: J00729
R:Skovgaard, O.
Gene 93, 27-34, 1990
A:Title: Nucleotide sequence of a Proteus mirabilis DNA fragment homologous to the 60K-
A:Reference number: J00729; MUID:91033012; PMID:2172087
A:Accession: J00729
A:Molecule type: DNA
A:Residues: 1-237 <SRO>
A:Cross-references: GB:M58352; GB:M31295; NID:G150873; PIDN:AA83954.1; PID:G150874
A:Experimental source: strain LM1509
C:Keywords: DNA replication; membrane protein

```

Query Match 2.0%; Score 8; DB 2; Length 237;

Best Local Similarity 100.0%; Pred. No. 6;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Oy 48 DTGSSNFA 55
    |||
Db 206 DTGSSNFA 213

```

RESULT 4

```

G96659 protein P2K1.24 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C:Accession: G96659
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
ansen, N.F.; Hughes, B.; Hutzar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C
A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Marzi, R.; Marziani
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: G96659
A:Status: preliminary
A:Molecule type: DNA

```

A;Residues: 1-287 <STO>
 A;Cross-references: GB:AE005173; NID:G6633844; PID:AAF19703.1; GSPDB:GN00141
 C;Genetics:
 A;Gene: F2K1.24
 A;Map position: 1
 C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 2.0%; Score 8; DB 2; Length 287;
 Best Local Similarity 100.0%; Pred. No. 7.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 239 IVDGTTL 246
 DB 269 IVDGTTL 276

RESULT 5
 H75528
 conserved hypothetical protein - Deinococcus radiodurans (strain R1)
 C;Species: Deinococcus radiodurans
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
 C;Accession: H75528
 R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 S.; Shen, M.; Vamathevan, J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A;Reference number: A75250; MUID:20036896; PMID:10567266
 A;Accession: H75528
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-303 <WHI>
 A;Cross-references: GB:AE001896; GB:AE000513; NID:G6458032; PID:AAF09938.1; PID:G645803
 A;Experimental source: strain R1
 C;Genetics:
 A;Gene: DR0358
 A;Map position: 1

Query Match 2.0%; Score 8; DB 2; Length 303;
 Best Local Similarity 100.0%; Pred. No. 7.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 184 GGSVLGG 191
 DB 137 GGSVLGG 144

RESULT 6
 AG0742
 high-affinity zinc uptake system periplasmic binding protein [imported] - Salmonella ent
 C;Species: Salmonella enterica subsp. enterica serovar Typhi
 A;Note: this species has also been called Salmonella typhi
 C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
 C;Accession: AG0742
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher,
 th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Moule, S.; O'Gaora, P.
 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
 A;Reference number: AB0502; PMID:11677608
 A;Accession: AG0742
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-319 <PAR>
 A;Cross-references: GB:AL513382; PID:CAD05642.1; PID:G16503138; GSPDB:GN00176
 C;Genetics:
 A;Gene: STR2099
 C;Superfamily: hypothetical protein HT0119

Query Match 2.0%; Score 8; DB 2; Length 319;
 Best Local Similarity 100.0%; Pred. No. 7.9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 256 AVEAVAR 263
 DB 271 AVEAVAR 278

RESULT 7
 PRLVHD
 proteinase (EC 3.4.23.-) - squirrel monkey retrovirus SMRV-H
 C;Species: squirrel monkey retrovirus SMRV-H
 C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 23-Feb-1997
 C;Accession: B31827
 R;Oda, T.; Ikeda, S.; Watanabe, S.; Hatsushika, M.; Akiyama, K.; Mitsunobu, F.
 A;Title: Molecular cloning, complete nucleotide sequence, and gene structure of the pro
 A;Reference number: A31827; MUID:89073750; PMID:3201749
 A;Accession: B31827
 A;Molecule type: DNA
 A;Residues: 1-323 <ODA>
 C;Genetics:
 A;Gene: prt
 C;Complex: homodimer
 C;Superfamily: retroviral proteinase
 C;Keywords: aspartic proteinase; homodimer; hydrolase
 F;193/Active site: Asp (shared with dimeric partner) #status predicted

Query Match 2.0%; Score 8; DB 1; Length 323;
 Best Local Similarity 100.0%; Pred. No. 8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 99 DLVTIPKG 106
 DB 126 DLVTIPKG 133

RESULT 8
 T42999
 ethanolamine-phosphate cytidyltransferase homolog - fission yeast (Schizosaccharomyce
 C;Species: Schizosaccharomyces pombe
 C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
 C;Accession: T42999
 R;Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
 A;Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
 A;Reference number: Z17323; MUID:98162722; PMID:9501991
 A;Accession: T42999
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-327 <YOS>
 A;Cross-references: EMBL:D89199; NID:G1749605; PID:BAI3860.1; PID:G1749606
 A;Experimental source: strain PR745

Query Match 2.0%; Score 8; DB 2; Length 327;
 Best Local Similarity 100.0%; Pred. No. 8.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 242 SGTTLRL 249
 DB 153 SGTTLRL 160

RESULT 9
 PEILHD
 polyprotein (EC 3.4.23.29) - Irtex lacteus
 C;Species: Irtex lacteus
 C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 31-Dec-1993
 C;Accession: JU0057
 R;Kobayashi, H.; Sekibara, S.; Shibuya, H.; Yoshida, S.; Kuwakabe, I.; Murakami, K.
 A;Title: Cloning and sequence analysis of cDNA for Irtex lacteus aspartic proteinase.
 A;Reference number: JU0057
 A;Accession: JU0057
 A;Molecule type: mRNA

A;Residues: 1-340 <KOB>
 A;Note: the amino-terminal 24 residues were sequenced on the isolated proteinase
 C;Superfamily: pepsin
 C;Keywords: aspartic proteinase; glycoprotein; hydrolase
 F;33,212/Active site: Asp #status predicted
 F;132,238/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 2.0%; Score 8; DB 1; Length 340;
 Best Local Similarity 100.0%; Pred. No. 8.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 46 LVDTGSSN 53
 |||||
 Db 30 LVDTGSSN 37

RESULT 10

C72748 probable sun protein APE0514 - Aeropyrum pernix (strain K1)

C;Species: Aeropyrum pernix

C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000

C;Accession: C72748

R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Hatawara, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K

DNA Res. 6, 83-101, 1999

A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr

A;Reference number: A72450; MUID:99310339; PMID:10382966

A;Accession: C72748

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-352 <KAN>

A;Cross-references: DDBJ:AP000059; NID:G5103911; PIDN:BAAY9479.1; PID:G5104163

A;Experimental source: strain K1

C;Genetics:

A;Gene: APE0514

C;Superfamily: hypothetical protein HI0624

Query Match 2.0%; Score 8; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 258 VEAVARAS 265
 |||||
 Db 11 VEAVARAS 18

RESULT 11

T37720 ethanolamine-phosphate cytidyltransferase (EC 2.7.7.14) - fission yeast (Schizosacchar

C;Species: Schizosaccharomyces pombe

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C;Accession: T37720

R;Murphy, L.; Harris, D.; Barrett, B.G.; Rajandram, M.A.; Lyne, M.H.

submitted to the EMBL Data Library, August 1999

A;Reference number: Z21739

A;Accession: T37720

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-365 <MPR>

A;Cross-references: EMBL:AL109770; PIDN:CBAS2424.1; GSPDB:GN00066; SPDB:SPAC15E1.05C

A;Experimental source: strain 972h-; cosmid c15E1

C;Genetics:

A;Gene: SPDB:SPAC15E1.05C

A;Map position: 1

C;Keywords: nucleotidyltransferase

Query Match 2.0%; Score 8; DB 2; Length 365;
 Best Local Similarity 100.0%; Pred. No. 8.9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 242 SGTTLRL 249
 |||||

Db 191 SGTTLRL 198

RESULT 12

E96676 hypothetical protein T23K8.15 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C;Accession: E96676

R;Theologidis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.,

ansen, N.F.; Hughes, B.; Huzar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, D.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maltl, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: E96676

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-449 <SPO>

A;Cross-references: GB:AE005173; NID:G4646203; PIDN:AAD26876.1; GSPDB:GN00141

C;Genetics:

A;Gene: T23K8.15

A;Map position: 1

Query Match 2.0%; Score 8; DB 2; Length 449;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 239 IVDSGTL 246
 |||||
 Db 301 IVDSGTL 308

RESULT 13

JC7626 amino acid transport system N transporter, SN2 - human

C;Species: Homo sapiens (man)

C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001

C;Accession: JC7626

R;Nakanishi, T.; Sugawara, M.; Huang, W.; Martindale, R.G.; Leibach, F.H.; Ganapathy, M

Biochem. Biophys. Res. Commun. 281, 1343-1348, 2001

A;Title: Structure, function, and tissue expression pattern of human SN2, a subtype of

A;Reference number: JC7626; MUID:21139776; PMID:11243884

A;Contents: Liver cell line HepG2

A;Accession: JC7626

A;Molecule type: mRNA

A;Residues: 1-472 <NAK>

A;Cross-references: GB:AF276889; GB:AF196972

C;Comment: This SN2, an amino acid transporter, mediates Na⁺-coupled transport of syste

line, and glycine. The transport function of SN2 is pH-dependent and Li⁺-tolerant.

C;Genetics:

A;Gene: sn2

A;Map position: X p11.23

C;Keywords: amino acid transport; transport system

Query Match 2.0%; Score 8; DB 2; Length 472;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 133 GILGLAYA 140
 |||||
 Db 65 GILGLAYA 72

RESULT 14

B65173 probable 60K inner membrane protein - Escherichia coli (strain K-12)

C;Species: Escherichia coli

C:/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Mar-2002
 C:/Accession: B65173
 R;/Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
 .A.; Rose, D.J.; Mau, B.; Shaoh, Y.
 Science 277, 1453-1462, 1997
 A;/Title: The complete genome sequence of *Escherichia coli* K-12.
 A;/Reference number: A64720; MUID:97426617; PMID:9278503
 A;/Accession: B65173
 A;/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;/Molecule type: DNA
 A;/Residues: 1-548 <BLAT>
 A;/Cross-references: GB:AE000447; GB:U00096; NID:q2367266; PIDN:AAC76728.1; PID:q1790140;
 A;/Experimental source: strain K-12, substrain MG1655
 C;/Genetics:
 A;/Gene: y1dC
 C;/Superfamily: probable 60K inner membrane protein; stage III sporulation protein homolo
 C;/Keywords: inner membrane; transmembrane protein
 F;335-531/Domain: stage III sporulation protein homology <SPOR>

Query Match 2.0%; Score 8; DB 1; Length 548;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 DTGSSNFA 55
 |||||||
 Db 207 DTGSSNFA 214

RESULT 15
 H91208
 60 KD inner-membrane protein [imported] - *Escherichia coli* (strain O157:H7, substrain R1
 C;/Species: *Escherichia coli*
 C;/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
 C;/Accession: H91208
 R;/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
 gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A;/Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and gene
 A;/Reference number: A99629; MUID:21156231; PMID:11258796
 A;/Accession: H91208
 A;/Status: preliminary
 A;/Molecule type: DNA
 A;/Residues: 1-548 <HA>
 A;/Cross-references: GB:BA000007; PIDN:BA838063.1; PID:q13364115; GSPDB:GN00154
 A;/Experimental source: strain O157:H7, substrain R1MD 0509952
 C;/Genetics:
 A;/Gene: EC94640
 C;/Superfamily: probable 60K inner membrane protein; stage III sporulation protein homolo

Query Match 2.0%; Score 8; DB 2; Length 548;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 DTGSSNFA 55
 |||||||
 Db 207 DTGSSNFA 214

Search completed: April 1, 2003, 11:53:51
 Job time : 36 secs

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 1, 2003, 11:47:10 ; Search time 14 Seconds
(without alignments)
1202.814 Million cell updates/sec

Title: US-09-668-314C-2_COPY_63_468
Perfect score: 406
Sequence: 1 ALBPALASPGAAANFLAMVD.....STEDVASNCVPAQSLSEPL 406

Scoring table:
OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	406	100.0	518	1	BAE2_HUMAN
2	12	3.0	501	1	BACE_HUMAN
3	12	3.0	501	1	BACE_MOUSE
4	12	3.0	501	1	BACE_RAT
5	8	2.0	166	1	LRP_HAEM
6	8	2.0	237	1	60IM_PROMI
7	8	2.0	323	1	VPRT_SMRVH
8	8	2.0	340	1	CARP_POUHU
9	8	2.0	365	1	ECT1_SCHPO
10	8	2.0	548	1	60IM_ECOLI
11	8	2.0	1620	1	DNM1_MOUSE
12	8	2.0	1622	1	DNM1_RAT
13	8	1.7	126	1	G8_HUMAN
14	7	1.7	267	1	EX3_HAEMIN
15	7	1.7	268	1	EX3_ECOLI
16	7	1.7	276	1	PSB8_HUMAN
17	7	1.7	296	1	KHSE_LACIC
18	7	1.7	302	1	Y091_METUA
19	7	1.7	305	1	DDLB_ECO57
20	7	1.7	305	1	DDLB_ECOLI
21	7	1.7	305	1	DDLB_SALTI
22	7	1.7	305	1	DDLB_SALTI
23	7	1.7	324	1	PEP1_GADMO
24	7	1.7	326	1	YR75_ECOLI
25	7	1.7	337	1	YXAG_BACSU
26	7	1.7	354	1	MURB_TREPA
27	7	1.7	354	1	YGP1_YEAST
28	7	1.7	367	1	PEPA_CHICK
29	7	1.7	379	1	MRAM_TREPA
30	7	1.7	381	1	CHYM_CALJA
31	7	1.7	386	1	PEPA_PIG
32	7	1.7	387	1	PEP1_RABIT
33	7	1.7	387	1	PEP2_RABIT

34	7	1.7	387	1	PEP3_RABIT
35	7	1.7	387	1	PEP4_RABIT
36	7	1.7	387	1	PEPA_CALJA
37	7	1.7	388	1	PEP1_MACFU
38	7	1.7	388	1	PEP2_MACFU
39	7	1.7	388	1	PEP4_MACFU
40	7	1.7	388	1	PEPA_HUMAN
41	7	1.7	388	1	PEPA_MACMU
42	7	1.7	398	1	CATD_CHICK
43	7	1.7	419	1	CARV_CANAL
44	7	1.7	420	1	PAG2_PIG
45	7	1.7	428	1	SURA_ECOLI
46	7	1.7	452	1	PLMT1_PLAFA
47	7	1.7	460	1	VATB_TREVO
48	7	1.7	462	1	GSA_MYCTU
49	7	1.7	473	1	CYPI_CYNCA
50	7	1.7	496	1	ASPR_ORYSA
51	7	1.7	513	1	ASPR_CUCPE
52	7	1.7	558	1	Y083_MYCTU
53	7	1.7	569	1	YAP3_YEAST
54	7	1.7	596	1	MKC7_YEAST
55	7	1.7	602	1	VE1_MNPV
56	7	1.7	646	1	KDBE_SCHPO
57	7	1.7	754	1	YAF6_SCHPO
58	7	1.7	775	1	PTNC_MOUSE
59	7	1.7	831	1	NAPA_ALCEU
60	7	1.7	841	1	RELA_STRAT
61	7	1.7	863	1	AD17_DROME
62	7	1.7	899	1	YA8D_SCHPO
63	7	1.7	949	1	RCSC_ECOLI
64	7	1.7	1009	1	WS14_CABEL
65	7	1.7	1015	1	BGAL_ARSP
66	7	1.7	1073	1	YED4_YEAST
67	7	1.7	1343	1	VGR2_RAT
68	7	1.7	1533	1	PUM_DROME
69	7	1.7	1625	1	CTPI_MYCTU
70	6	1.5	52	1	V59_BP13
71	6	1.5	52	1	V59_BP17
72	6	1.5	58	1	Y06H_BP14
73	6	1.5	71	1	VLVS_BP21
74	6	1.5	72	1	PEP2_THRTO
75	6	1.5	72	1	PSBH_TOBAC
76	6	1.5	73	1	PEPC_PIG
77	6	1.5	80	1	Y6A9_YEREN
78	6	1.5	80	1	Y6A9_YERPE
79	6	1.5	87	1	Y123_BURCE
80	6	1.5	88	1	LEVI_XENLA
81	6	1.5	96	1	YS98_MYCLE
82	6	1.5	100	1	P1NL_HUMAN
83	6	1.5	105	1	ATPL_MYCPN
84	6	1.5	105	1	YKXD_BACSU
85	6	1.5	108	1	RSBV_BACTI
86	6	1.5	110	1	CSAA_BACSU
87	6	1.5	110	1	PEPA_BOVIN
88	6	1.5	115	1	YNFD_ECOLI
89	6	1.5	117	1	NLTI_PRUDU
90	6	1.5	117	1	NLTP_PRIVAV
91	6	1.5	117	1	NLTP_SPTOL
92	6	1.5	119	1	CHCI_BOMMO
93	6	1.5	119	1	CHC2_BOMMO
94	6	1.5	119	1	CHCS_BOMMO
95	6	1.5	121	1	CHC4_BOMMO
96	6	1.5	124	1	GLUT_LOPAM
97	6	1.5	124	1	HIS3_ZYMO
98	6	1.5	124	1	RNP_CHIRB
99	6	1.5	128	1	CYB_CROUV
100	6	1.5	131	1	RRPB_CVPR8
101	6	1.5	134	1	CC42_ANOGA
102	6	1.5	134	1	VG24_BPM2
103	6	1.5	137	1	PSBW_SPTOL
104	6	1.5	138	1	YGUM_ECOLI
105	6	1.5	141	1	TNGI_HUMAN
106	6	1.5	142	1	RPB6_SCHPO

P27822	oryctolagus
P28713	oryctolagus
Q9n2d4	callithrix
P03954	macaca fusc
P27677	macaca fusc
P27678	macaca fusc
P00790	homo sapien
P14893	macaca mula
Q05744	gallus galli
P10977	candida alb
Q29079	sus scrofa
P21202	escherichia
P39898	plasmodium
Q07379	thermoplas
O06390	mycobacteri
P40783	cynara card
P42211	oryza sativ
O04057	cucubita p
Q10873	mycobacteri
P32329	saccharomyc
P33379	saccharomyc
O84356	maestomys na
Q10364	escherichia
Q09860	schizosacch
P35831	mus musculu
P39185	alcaligenes
O85709	streptomyces
Q09745	drosophila
Q09778	schizosacch
P14376	escherichia
P18464	caenorhabdi
Q59140	arthrobacte
P33564	saccharomyc
O06875	rattus norv
P25822	drosophila
Q10900	mycobacteri
P20405	bacterioph
P20406	bacterioph
P33315	bacterioph
P27360	bacterioph
P20140	thumus thy
P06415	nitcoliana t
P20879	sus scrofa
O85269	yersinia en
Q92958	yersinia pe
P45573	burskolderi
P13684	xenopus lae
O33054	mycobacteri
O15428	homo sapien
O95550	mycoplasma
P49857	bacillus su
O60220	bacillus li
P17384	bacillus su
P00792	bos taurus
P61012	escherichia
Q95588	prunus avu
P10976	spinacia ol
P13531	bombyx mori
Q17212	bombyx mori
Q17214	bombyx mori
P08829	bombyx mori
P12728	lophius ame
O93301	zymomonas m
P00675	chinchilla
Q95776	ctotatus vi
Q04158	porcine res
O17031	anopheles g
O64228	mycobacteri
Q41387	spinacia ol
P42594	escherichia
P56846	homo sapien
P36595	schizosacch

107	6	1.5	146	1	RBFA_RHIL0	Q98b17 rhizobium 1	180	6	1.5	231	1	YHS2_YEAST	P38829 saccharomyc
108	6	1.5	147	1	LECE_ANTCR	P06027 antihocidari	181	6	1.5	232	1	6PGL_CAVCR	Q9a611 caulobacter
109	6	1.5	147	1	THYX_SHERP	P12303 ovis aries	182	6	1.5	233	1	HA2P_MOUSE	P14453 mus musculus
110	6	1.5	152	1	PHR1_PYRAB	P77919 pyrococcus	183	6	1.5	233	1	HA2R_MOUSE	P14436 mus musculus
111	6	1.5	153	1	YHS3_PSEAB	Q9h910 pseudomonas	184	6	1.5	233	1	HA2S_MOUSE	P03224 mus musculus
112	6	1.5	160	1	COAT_CGNVS	P19521 cucumber gir	185	6	1.5	234	1	VGPR_EBY	Q9pdd2 epstein-bar
113	6	1.5	160	1	Y964_MYCTO	P71546 mycobacteri	186	6	1.5	237	1	CYSH_XYLFA	Q9pdd2 xylella fas
114	6	1.5	161	1	TPM_SCHPO	Q02088 schizosacch	187	6	1.5	237	1	YI94_AQUAE	Q9pdd2 aquifex aeo
115	6	1.5	163	1	LRP_ECOLI	P19494 escherichia	188	6	1.5	239	1	CYSH_THIRO	P52672 thiocapasa r
116	6	1.5	163	1	LRP_KLEBN	P37424 klebsiella	189	6	1.5	240	1	CD48_MOUSE	P18181 mus musculus
117	6	1.5	163	1	LRP_SALTY	P37403 salmonella	190	6	1.5	240	1	TPMT_MOUSE	Q50660 mus musculus
118	6	1.5	163	1	LRP_SBRMA	P37425 serratia ma	191	6	1.5	240	1	TPMT_MOUSE	Q9qxc2 mus spretus
119	6	1.5	164	1	PUR6_HAEIN	P43849 haemophilus	192	6	1.5	241	1	SPIR_SPIWE	P21625 spiroplasma
120	6	1.5	165	1	RL10_BACSU	P42923 bacillus su	193	6	1.5	242	1	PR38_YEAST	Q007734 saccharomyc
121	6	1.5	165	1	YGZD_YEAST	P55057 saccharomyc	194	6	1.5	243	1	YI28_YEAST	P15910 fowlpox vir
122	6	1.5	169	1	MSA1_STAM	Q9qdc7 straphylococ	195	6	1.5	244	1	CYAH_MRYVE	P22143 myrothecium
123	6	1.5	170	1	HPAC_KLEBN	Q44441 klebsiella	196	6	1.5	244	1	NGN1_MOUSE	P70660 mus musculus
124	6	1.5	173	1	RUVK_BRUME	Q8y1v7 bruceella me	197	6	1.5	244	1	NGN1_RAT	P70595 rattus norv
125	6	1.5	173	1	VENV_LELV	Q04565 lelystad vi	198	6	1.5	244	1	RS2_BACHD	Q9Kae3 bacillus ha
126	6	1.5	174	1	YGAP_ECOLI	P55734 escherichia	199	6	1.5	245	1	GIDB_ANASP	Q8yae7 anabaena sp
127	6	1.5	178	1	ESMS_DROME	P15096 drosophila	200	6	1.5	246	1	YOR4_ANATH	Q44408 anaerocellu
128	6	1.5	180	1	CFTR_CAVPO	Q00552 cavia porce	201	6	1.5	247	1	SITI_CABEL	Q9u3j5 caenorhabdi
129	6	1.5	182	1	APT_STRCO	P52561 streptomyc	202	6	1.5	247	1	YFBB_HAEIN	P44611 haemophilus
130	6	1.5	185	1	YXAK_BACSU	P42110 bacillus su	203	6	1.5	247	1	YGZ2_ARCFU	Q28664 archaeoglob
131	6	1.5	188	1	GCHI_RHICH	Q9Kc17 bacillus su	204	6	1.5	249	1	HMX1_CHICK	P28361 gallus gall
132	6	1.5	188	1	PUR2_CHRYT	P55417 rhizobium s	205	6	1.5	249	1	PYR2_FREDI	P18543 firemyella d
133	6	1.5	189	1	Y006_CHLTR	Q4482 chromatium s	206	6	1.5	251	1	E1A_ADE41	P10542 human adeno
134	6	1.5	189	1	CAH2_FLALI	Q84009 chlamydia t	207	6	1.5	251	1	GLOZ_BUCAI	P57336 buchiera ap
135	6	1.5	190	1	CC42_DROME	P46513 flaventia li	208	6	1.5	251	1	TRPC_HALVO	P18304 halobacteri
136	6	1.5	191	1	MOBA_PYRAB	P40793 drosophila	209	6	1.5	252	1	KDSB_VIBCH	Q9Kqg2 vibrio chol
137	6	1.5	191	1	MOBA_PYRAB	Q9v0d0 pyrococcus	210	6	1.5	254	1	HA2U_MOUSE	P23130 mus musculu
138	6	1.5	192	1	MOBA_PYRAB	Q58708 pyrococcus	211	6	1.5	254	1	ST19_MOUSE	P23130 mus musculu
139	6	1.5	198	1	RI19_CABEL	Q02639 caenorhabdi	212	6	1.5	256	1	HA2D_MOUSE	P44228 mus musculu
140	6	1.5	202	1	COAT_BMYVF	P09508 beet wester	213	6	1.5	256	1	MYF5_NOTVI	Q91154 notophthalm
141	6	1.5	202	1	COAT_BMYVG	P08509 beet wester	214	6	1.5	256	1	Y929_TREPA	Q81899 treponema p
142	6	1.5	205	1	DDL_AVACE	P35660 anaplasm	215	6	1.5	259	1	EXB4_ARATH	Q9shd1 arabidopsis
143	6	1.5	205	1	KGUA_LACLA	Q9ce63 lactococcus	216	6	1.5	259	1	MURB_HELPJ	Q9z2j4 helicobacte
144	6	1.5	205	1	YJ11_MYCTU	O07722 mycobacteri	217	6	1.5	259	1	Y500_METUA	Q57923 methanococ
145	6	1.5	206	1	FGF4_BOVIN	P48803 bos taurus	218	6	1.5	259	1	YG47_SYNY3	P44365 synechocyst
146	6	1.5	207	1	CCMA_ECOLI	P33931 escherichia	219	6	1.5	260	1	PSA1_CHICK	Q42265 gallus gall
147	6	1.5	207	1	SODW_CHLBN	Q929c4 chlamydia p	220	6	1.5	260	1	SUMT_SYNY3	Q55749 synechocyst
148	6	1.5	209	1	HUPM_AZOCH	Q43954 azotobacter	221	6	1.5	263	1	VAL1_WDV	P06847 wheat dwarf
149	6	1.5	210	1	FGFL_MOUSE	Q91j11 mus musculu	222	6	1.5	264	1	MYO2_LYCES	P44921 lycopersico
150	6	1.5	210	1	FLPA_ARCFU	O28192 archaeoglob	223	6	1.5	265	1	CRK_DROME	Q06209 brassica na
151	6	1.5	211	1	DBOC_BACSU	P33121 bacillus su	224	6	1.5	268	1	CHI4_BRANA	Q92612 salmoneila
152	6	1.5	211	1	RL1_HALCU	P05966 halobacteri	225	6	1.5	268	1	EX3_SALTY	O01464 bacillus su
153	6	1.5	211	1	RL1_HALNI	P13575 halobacteri	226	6	1.5	268	1	MIND_BACSU	Q57993 methanococ
154	6	1.5	213	1	PYRF_METUA	Q57700 methanococ	227	6	1.5	269	1	YRBF_ECOLI	P45393 escherichia
155	6	1.5	214	1	CYB_AKCO	P92845 agkistrodon	228	6	1.5	270	1	TONB_HAEIN	P42872 haemophilus
156	6	1.5	214	1	CYB_AKCO	P92852 agkistrodon	229	6	1.5	271	1	CRK_DROME	Q9xymd haemophilu
157	6	1.5	214	1	CYB_BOTAT	P92846 bothriops at	230	6	1.5	271	1	YV23_AQUAE	O05879 mycobacteri
158	6	1.5	214	1	CYB_BOTAT	P92847 bothriops at	231	6	1.5	271	1	YV23_AQUAE	O66414 aquifex aeo
159	6	1.5	214	1	CYB_BOTSC	P92849 bothriops at	232	6	1.5	273	1	YV23_AQUAE	P26754 saccharomyc
160	6	1.5	214	1	CYB_BOTSC	P87419 cerastes ce	233	6	1.5	273	1	YV23_AQUAE	Q40477 escherichia
161	6	1.5	214	1	CYB_CERCE	P92850 croctalus at	234	6	1.5	273	1	YV23_AQUAE	P19900 paracoccus
162	6	1.5	214	1	CYB_CROAT	P92853 lachesis mu	235	6	1.5	276	1	CEMA_CVACA	Q0tm6 cyanidium c
163	6	1.5	214	1	CYB_CROAT	P92853 lachesis mu	236	6	1.5	276	1	CEMA_CVACA	Q0tm6 cyanidium c
164	6	1.5	215	1	YFGS_TRIST	P35924 lactobacilli	237	6	1.5	281	1	RER2_YEAST	P35198 saccharomyc
165	6	1.5	216	1	RIJ3_RICPR	P48952 rickettsia	238	6	1.5	281	1	RER2_YEAST	P35198 saccharomyc
166	6	1.5	216	1	YHJ3_CABEL	P34357 caenorhabdi	239	6	1.5	286	1	SMN_BOVIN	O18870 bos taurus
167	6	1.5	217	1	OMPW_VIBCH	P17266 vibrio chol	240	6	1.5	287	1	SMN_BOVIN	O02771 canis famli
168	6	1.5	218	1	SGAH_MYCPN	P75293 mycoplasma	241	6	1.5	287	1	SMN_CANFA	P50223 gallus galli
169	6	1.5	218	1	SODM_SCHPO	Q9uxx0 schizosacch	242	6	1.5	288	1	HMXX_CHICK	P03224 mus musculus
170	6	1.5	219	1	ERD2_YEAST	P14414 saccharomyc	243	6	1.5	289	1	DLX5_MOUSE	P05076 mus musculu
171	6	1.5	219	1	ISPD_CHLTR	Q84468 chlamydia t	244	6	1.5	289	1	DLX5_MOUSE	P05076 mus musculu
172	6	1.5	220	1	TRBP_RHISN	P55403 rhizobium s	245	6	1.5	292	1	Y240_MYCBE	P47482 mycoplasma
173	6	1.5	221	1	HA2Q_MOUSE	P04227 mus musculu	246	6	1.5	293	1	CMFL_SCHPO	O14161 schizosacch
174	6	1.5	221	1	TPIS_AERPE	Q9ybr1 aeropyrum p	247	6	1.5	295	1	Y005_RICPR	Q02671 rickettsia
175	6	1.5	225	1	GIDB_THETH	Q91cy2 thermus the	248	6	1.5	295	1	Y234_METUA	O60256 methanococ
176	6	1.5	225	1	VGZR_AMERY	P28818 amacca moo	249	6	1.5	297	1	Y103_HUMAN	O15006 homo sapien
177	6	1.5	225	1	Y574_AERPE	Q9yek4 aeropyrum p	250	6	1.5	299	1	DAPA_STRCO	O68841 streptomyc
178	6	1.5	226	1	TSIS_SMSAV	P01128 simian sarc	251	6	1.5	300	1	COX2_YEAST	P19516 saccharomyc
179	6	1.5	229	1	YOBI_STRAT	Q53683 streptomyc	252	6	1.5	302	1	PP12_DROME	P12982 drosophila

253	6	1.5	302	1	PP13_DROME	Q05547	drosophila	326	6	1.5	370	1	ODPA_BACSU	P21881	bacillus su
254	6	1.5	303	1	SPAO_SALDU	Q53968	salmonella	327	6	1.5	371	1	CYB_BACO	P92848	boa constrict
255	6	1.5	303	1	SPAO_SALTI	Q56022	salmonella	328	6	1.5	371	1	CYB_CALKE	P92847	calliphora
256	6	1.5	303	1	SPAO_SALTY	P40699	salmonella	329	6	1.5	371	1	CYB_CALMC	O90146	calliphora
257	6	1.5	309	1	MTW3_HAEIN	P43871	haemophilus	330	6	1.5	371	1	CYB_CANAS	O48023	candida asp
258	6	1.5	312	1	FWT_MYCTU	P71674	mycobacteri	331	6	1.5	371	1	CYB_CANCA	O48025	candida car
259	6	1.5	312	1	YC39_CYACA	Q19883	cyanidium c	332	6	1.5	371	1	CYB_CASDU	O48027	casarea dus
260	6	1.5	313	1	LDH_CLOAB	Q97481	clostridium	333	6	1.5	371	1	CYB_COLCO	Q94052	coluber con
261	6	1.5	314	1	YC39_GUITH	O78472	guillardia	334	6	1.5	371	1	CYB_ERIMO	O48056	epicrates m
262	6	1.5	317	1	KDT2_SALTI	O848h3	salmonella	335	6	1.5	371	1	CYB_ERVYC	O48067	eryx colubr
263	6	1.5	317	1	KDT2_SALTY	O848g4	salmonella	336	6	1.5	371	1	CYB_ERYCL	O48067	eryx colubr
264	6	1.5	317	1	MTX1_HUMAN	Q13505	homo sapien	337	6	1.5	371	1	CYB_ERYEL	O48076	eryx elegan
265	6	1.5	317	1	MTX1_MOUSE	P47802	mus musculu	338	6	1.5	371	1	CYB_ERYXA	O48076	eryx jaculu
266	6	1.5	318	1	Y986_THEMEA	Q94081	thermoptoga	339	6	1.5	371	1	CYB_ERYMI	O48079	eryx miliar
267	6	1.5	319	1	YC39_PORPU	P51238	porphyra pu	340	6	1.5	371	1	CYB_ERYNI	O48080	eryx miliar
268	6	1.5	321	1	YC39_CYAPA	P48272	cyanophora	341	6	1.5	371	1	CYB_ERYTA	O48085	eryx tatar
269	6	1.5	322	1	ARG1_HUMAN	P05089	homo sapien	342	6	1.5	371	1	CYB_MICRU	O48085	eryx tatar
270	6	1.5	322	1	VANH_ENTFA	Q47748	enterococcu	343	6	1.5	371	1	CYB_TOXPR	O48085	eryx tatar
271	6	1.5	325	1	LXBI_PHOTOE	P09141	photobacter	344	6	1.5	371	1	DUT_HSV11	O48085	eryx tatar
272	6	1.5	326	1	GQH_ARATH	O65355	arabidopsis	345	6	1.5	371	1	H2AY_HUMAN	O48085	eryx tatar
273	6	1.5	327	1	XYNA_ASPAC	O59859	aspergillus	346	6	1.5	371	1	TGT_CAUCR	O48085	eryx tatar
274	6	1.5	328	1	GRHR_BOVIN	P32236	bos taurus	347	6	1.5	371	1	V816_SVNY3	O48085	eryx tatar
275	6	1.5	328	1	GRHR_SHEEP	P32237	ovis aries	348	6	1.5	372	1	CYB_ACRDU	O48085	eryx tatar
276	6	1.5	329	1	CTAO_BACSU	O31652	bacillus su	349	6	1.5	372	1	CYB_ACRMA	O48085	eryx tatar
277	6	1.5	332	1	TRPD_VIBPA	P22096	vibrio para	350	6	1.5	372	1	CYB_ASPSC	O48085	eryx tatar
278	6	1.5	333	1	HK32_HUMAN	P78367	homo sapien	351	6	1.5	372	1	CYB_ELABA	O48085	eryx tatar
279	6	1.5	333	1	MRPL_CAEEL	Q93459	caenorhabdi	352	6	1.5	372	1	CYB_ELAOB	O48085	eryx tatar
280	6	1.5	334	1	UNG_HSV11	O10186	herpes stimp	353	6	1.5	372	1	CYB_ELAVU	O48085	eryx tatar
281	6	1.5	334	1	YC11_MERTH	O27279	methanobact	354	6	1.5	372	1	CYB_HETSI	O48085	eryx tatar
282	6	1.5	335	1	YD59_SCHPO	Q10312	schizosacch	355	6	1.5	372	1	CYB_PARMU	O48085	eryx tatar
283	6	1.5	338	1	HRSE_SCHPO	O43056	schizosacch	356	6	1.5	372	1	CYB_SANNE	O48085	eryx tatar
284	6	1.5	339	1	ILVC_CAUCR	O946h4	caulobacter	357	6	1.5	372	1	CYB_WALAE	O48085	eryx tatar
285	6	1.5	339	1	RLAO_ARCEU	O28781	archaeoglob	358	6	1.5	373	1	UL16_HSV11	O48085	eryx tatar
286	6	1.5	340	1	YMAJ_CAEEL	P34486	caenorhabdi	359	6	1.5	376	1	PAG2_BOVIN	O48085	eryx tatar
287	6	1.5	341	1	CREM_MOUSE	P27699	mus musculu	360	6	1.5	377	1	PEPC_MACFU	O48085	eryx tatar
288	6	1.5	341	1	CREM_RAT	Q03061	rattus norv	361	6	1.5	377	1	TTL_BOVIN	O48085	eryx tatar
289	6	1.5	341	1	TRPD_LACCA	P17170	lactobacilli	362	6	1.5	379	1	VTP_BPMU	O48085	eryx tatar
290	6	1.5	342	1	Y99A_YEAST	P53757	saccharomyc	363	6	1.5	379	1	AROQ_ASERE	O48085	eryx tatar
291	6	1.5	344	1	CREM_CANPA	P79145	canis famli	364	6	1.5	380	1	PAG2_BOVIN	O48085	eryx tatar
292	6	1.5	345	1	CATD_PIG	P00795	sus scrofa	365	6	1.5	380	1	PAG1_BOVIN	O48085	eryx tatar
293	6	1.5	345	1	VAT2_SCHPO	Q10149	echinobacth	366	6	1.5	381	1	RM13_CHICK	O48085	eryx tatar
294	6	1.5	347	1	MRER_ECOLI	P13519	escherichia	367	6	1.5	381	1	YG12_YEAST	O48085	eryx tatar
295	6	1.5	348	1	ADH1_PICST	O00097	pichia stip	368	6	1.5	382	1	CARA_ECOLI	O48085	eryx tatar
296	6	1.5	350	1	ADH1_CANAL	P43067	candida alb	369	6	1.5	382	1	CARA_SALTI	O48085	eryx tatar
297	6	1.5	351	1	COLF_ARATH	O9fhn8	arabidopsis	370	6	1.5	382	1	CARA_SALTY	O48085	eryx tatar
298	6	1.5	351	1	KLFP2_RAT	O9et58	rattus norv	371	6	1.5	382	1	EDG1_MOUSE	O48085	eryx tatar
299	6	1.5	353	1	Y634_CHLMU	Q9pk39	chlamydia m	372	6	1.5	382	1	PAG1_SHEEP	O48085	eryx tatar
300	6	1.5	353	1	YNCB_ECOLI	P76113	escherichia	373	6	1.5	382	1	RS1H_BACCE	O48085	eryx tatar
301	6	1.5	354	1	KLFP2_MOUSE	O60843	mus musculu	374	6	1.5	382	1	VE2_HPV61	O48085	eryx tatar
302	6	1.5	355	1	KLFP2_HUMAN	O9Y5w3	homo sapien	375	6	1.5	382	1	YC44_ODOSI	O48085	eryx tatar
303	6	1.5	355	1	Y121_TREPA	O83158	treponema p	376	6	1.5	383	1	EDG1_RAT	O48085	eryx tatar
304	6	1.5	356	1	VCOM_ADRE40	P48753	human adeno	377	6	1.5	383	1	PEPE_CHICK	O48085	eryx tatar
305	6	1.5	358	1	Y4BE_RHLSN	P55428	rhizobium s	378	6	1.5	384	1	YAGA_ECOLI	O48085	eryx tatar
306	6	1.5	359	1	WECE_EC057	Q8x428	escherichia	379	6	1.5	384	1	YZ43_MERYA	O48085	eryx tatar
307	6	1.5	359	1	WECE_ECOLI	P56258	escherichia	380	6	1.5	385	1	NR21_CHICK	O48085	eryx tatar
308	6	1.5	362	1	ILVE_STRCO	O86505	streptomyce	381	6	1.5	386	1	CMG2_HUMAN	O48085	eryx tatar
309	6	1.5	365	1	CATD_SHEEP	O9mz88	ovis aries	382	6	1.5	387	1	ASPC_ADPAE	O48085	eryx tatar
310	6	1.5	366	1	PMEA_ERWCH	P07863	erwinia chr	383	6	1.5	387	1	GLGC_BACST	O48085	eryx tatar
311	6	1.5	366	1	YGH0_ECOLI	Q46840	escherichia	384	6	1.5	387	1	MSOX_BACSN	O48085	eryx tatar
312	6	1.5	368	1	ILVE_MYCTU	Q10339	mycobacteri	385	6	1.5	387	1	SAT_DEIRA	O48085	eryx tatar
313	6	1.5	368	1	ST19_HUMAN	P49842	homo sapien	386	6	1.5	387	1	YHFX_ECOLI	O48085	eryx tatar
314	6	1.5	370	1	CYB_COREN	O48039	corallus en	387	6	1.5	388	1	PEPC_CALJA	O48085	eryx tatar
315	6	1.5	370	1	CYB_EPIAN	O48043	epicrates a	388	6	1.5	388	1	PEPC_HUMAN	O48085	eryx tatar
316	6	1.5	370	1	CYB_EPICE	O48047	epicrates c	389	6	1.5	388	1	PEPC_RABIT	O48085	eryx tatar
317	6	1.5	370	1	CYB_EPIX	O48047	epicrates e	390	6	1.5	389	1	PAG1_PIG	O48085	eryx tatar
318	6	1.5	370	1	CYB_EPIPO	O48049	epicrates f	391	6	1.5	390	1	CARP_SACFI	O48085	eryx tatar
319	6	1.5	370	1	CYB_EPIBP	O48060	epicrates s	392	6	1.5	390	1	CATD_BOVIN	O48085	eryx tatar
320	6	1.5	370	1	CYB_EPIBM	O48065	epicrates s	393	6	1.5	391	1	CARI_CANAL	O48085	eryx tatar
321	6	1.5	370	1	CYB_EPISS	O48057	epicrates s	394	6	1.5	391	1	CATE_CAVPO	O48085	eryx tatar
322	6	1.5	370	1	CYB_EPIST	O48053	epicrates s	395	6	1.5	392	1	PEPC_RAT	O48085	eryx tatar
323	6	1.5	370	1	CYB_EPIBU	O48052	epicrates s	396	6	1.5	393	1	ILIS_CERAE	O48085	eryx tatar
324	6	1.5	370	1	CYB_EUNNO	O48055	eunectes no	397	6	1.5	394	1	PEPC_CAVPO	O48085	eryx tatar
325	6	1.5	370	1	H2AY_RAT	Q02874	rattus norv	398	6	1.5	394	1	SUC1_STRCO	O48085	eryx tatar

399	6	1.5	395	1	LIPG_RAT	P04634	rattus norv	472	6	1.5	433	1	RHO_CHEVI	P52152	chromatium
400	6	1.5	396	1	CARP_NEUCR	O01294	neurospora	473	6	1.5	435	1	FIXC_BRAVA	P10331	bradyrhizob
401	6	1.5	396	1	CATE_HUMAN	P14091	homo sapien	474	6	1.5	435	1	YOD7_CAEEL	O09267	caenorhabdi
402	6	1.5	396	1	DCAM_YEAST	P21182	saccharomyc	475	6	1.5	436	1	COAT_CHVP1	P30328	paramecium
403	6	1.5	397	1	CATE_MOUSE	P70269	mus muscucu	476	6	1.5	436	1	EPB2_RALSO	O45411	talatonia s
404	6	1.5	398	1	APLI_HUMAN	O14791	homo sapien	477	6	1.5	436	1	MNTH_DEIRA	O91p8	deinococcus
405	6	1.5	398	1	ASP3_CAEEL	P59566	caenorhabdi	478	6	1.5	437	1	GLA2_RHILO	O98881	rhizobium 1
406	6	1.5	398	1	CAR2_CANAL	P28871	candida alb	479	6	1.5	437	1	NEOR_STRCY	P14501	streptomyce
407	6	1.5	398	1	CATE_RAT	P16289	rattus norv	480	6	1.5	437	1	YOEZ_BACSV	P54495	bacillus su
408	6	1.5	398	1	ILIS_HUMAN	P27930	rattus norv	481	6	1.5	438	1	SVS_HELAN	O81983	heliandus
409	6	1.5	400	1	PRIZ_HUMAN	P22891	homo sapien	482	6	1.5	438	1	YI6F_MYCIO	O49573	mycoplasma
410	6	1.5	400	1	RENI_SHEEP	P52115	ovis aries	483	6	1.5	439	1	IDNT_ECOLI	P39344	escherichia
411	6	1.5	401	1	AROC_MYCTU	P95013	mycobacteri	484	6	1.5	440	1	BIR1_YEAST	P11709	saccharomyc
412	6	1.5	401	1	RENS_MOUSE	P00796	mus muscucu	485	6	1.5	440	1	HIPa_ECOLI	P23874	escherichia
413	6	1.5	402	1	CAR1_CANPA	P32951	candida par	486	6	1.5	441	1	FLID_AQUAE	O67805	aquifex aeo
414	6	1.5	402	1	RENI_MOUSE	P06281	mus muscucu	487	6	1.5	441	1	HISX_STRCO	P16245	streptomyce
415	6	1.5	404	1	RFAL_SALTY	P26471	salmonella	488	6	1.5	443	1	FTSA_AGRTS	O30991	agrobacteri
416	6	1.5	405	1	BMP4_CHICK	O90752	gallus gall	489	6	1.5	444	1	XK_HUMAN	P51811	homo sapien
417	6	1.5	405	1	CAR8_CANAL	O42778	candida alb	490	6	1.5	445	1	YGCS_ECOLI	O46909	escherichia
418	6	1.5	405	1	CARP_YEAST	P07267	saccharomyc	491	6	1.5	450	1	MOO_HELPJ	O924913	helicobacte
419	6	1.5	406	1	DXR_MYCIE	O9cbu3	mycobacteri	492	6	1.5	451	1	SYS_ARATH	O39230	arabidopsis
420	6	1.5	406	1	RENI_HUMAN	P00797	homo sapien	493	6	1.5	451	1	PLW2_PLAFA	P46925	plasmodium
421	6	1.5	407	1	CATD_RAT	P24268	rattus norv	494	6	1.5	453	1	VG_DROME	O26365	drosophila
422	6	1.5	408	1	BMP4_DAMDA	O29607	dama dama (495	6	1.5	453	1	MNTH_RHILO	O98139	rhizobium 1
423	6	1.5	408	1	BMP4_HUMAN	P12644	homo sapien	496	6	1.5	454	1	YGBN_ECOLI	O46892	escherichia
424	6	1.5	408	1	BMP4_MOUSE	P21275	mus muscucu	497	6	1.5	456	1	MNTH_BRUME	O8y176	bruceella me
425	6	1.5	409	1	BMP4_RAT	O06826	rattus norv	498	6	1.5	456	1	EXL1_PSEAE	O9yx18	pseudomonas
426	6	1.5	409	1	BMP4_RABIT	O46576	oryctolagus	499	6	1.5	459	1	EXL1_ORVIA	O9y100	oryzias lat
427	6	1.5	410	1	CATD_MOUSE	P18242	mus muscucu	500	6	1.5	461	1	EF10_XENLA	P13549	xenopus lae
428	6	1.5	410	1	BFTU_COPFR	P50372	codium frag	501	6	1.5	462	1	EF11_CRIGR	P20001	cricetus
429	6	1.5	410	1	VE47_LAMBD	P03752	bacteriophag	502	6	1.5	462	1	EF11_HUMAN	P047701	homo sapien
430	6	1.5	411	1	AATC_CHICK	P00504	gallus gall	503	6	1.5	462	1	EF11_MOUSE	P101026	mus muscucu
431	6	1.5	411	1	BCAT_RAT	P54690	rattus norv	504	6	1.5	462	1	EF1A_BRARE	O92005	brachydanio
432	6	1.5	412	1	CAR2_CANPA	P32950	candida par	505	6	1.5	462	1	OCT8_MOUSE	O00196	mus muscucu
433	6	1.5	412	1	CATD_HUMAN	P07339	homo sapien	506	6	1.5	462	1	OCT8_MOUSE	O00196	mus muscucu
434	6	1.5	412	1	PUR2_LACTA	O92144	lactococcus	507	6	1.5	463	1	COAT_FRG3V	O67473	ftog virus
435	6	1.5	413	1	DXR_MYCTU	P39817	bacillus su	508	6	1.5	463	1	COAT_FRG3V	O67473	ftog virus
436	6	1.5	414	1	GLTP_BACSV	P23306	escherichia	509	6	1.5	463	1	MURD_RHIME	O52953	rhizobium m
437	6	1.5	414	1	MTR_ECOLI	O09173	escherichia	510	6	1.5	464	1	DLDH_ZYMOX	P50970	zymonas m
438	6	1.5	414	1	P2C3_SCIPO	O9yhu9	pseudomonas	511	6	1.5	464	1	DLDH_ZYMOX	P50970	zymonas m
439	6	1.5	416	1	DAD2_PSEAE	P16617	rattus norv	512	6	1.5	467	1	EUTA_SALTY	O924f2	salmonella
440	6	1.5	416	1	PGK_RAT	P50310	cricetus	513	6	1.5	468	1	SYFA_SULSO	P95361	sulfolobus
441	6	1.5	416	1	PGK_HORSE	P00559	equus cabal	514	6	1.5	471	1	YEGB_ECOLI	P36554	escherichia
442	6	1.5	416	1	PGK_CRIGR	P43094	candida alb	515	6	1.5	474	1	CREC_ECOLI	P08401	escherichia
443	6	1.5	417	1	CAR4_CANAL	P43094	candida alb	516	6	1.5	474	1	DLDH_ALCEU	P52992	alcaligenes
444	6	1.5	418	1	CAR6_CANAL	P43094	candida alb	517	6	1.5	475	1	MOTD_RHIME	O52964	rhizobium m
445	6	1.5	418	1	CAR6_CANAL	P43094	candida alb	518	6	1.5	477	1	BAIG_EUBSP	P32359	eubacterium
446	6	1.5	418	1	LEU2_THETN	O8rdx2	thermoanaer	519	6	1.5	477	1	FIBB_PETWA	P02678	petriomyzon
447	6	1.5	418	1	RHDA_BACDH	O9kc19	bacillus ha	520	6	1.5	477	1	FIBB_PETWA	P02678	petriomyzon
448	6	1.5	419	1	GSC_DROME	P54366	drosophila	521	6	1.5	477	1	NOM1_PSEAE	P25553	escherichia
449	6	1.5	419	1	KDAP_MOUSE	O09043	mus muscucu	522	6	1.5	478	1	ALDA_ECOLI	O00911	rattus norv
450	6	1.5	419	1	NOBF_RHISN	P55472	rhizobium s	523	6	1.5	478	1	OCT2_HUMAN	P09086	homo sapien
451	6	1.5	419	1	RHO_BUCAL	P57652	buchnera ap	524	6	1.5	478	1	PUO_MICRU	P40974	micrococcus
452	6	1.5	420	1	NAP1_HUMAN	O96009	homo sapien	525	6	1.5	478	1	YOHG_ECOLI	P33369	escherichia
453	6	1.5	420	1	PGK_TETIN	P50313	tetrahymena	526	6	1.5	479	1	6PGD_TRYBB	P11072	trypanosoma
454	6	1.5	420	1	RHO_HAETN	P44619	haemophilus	527	6	1.5	482	1	MANC_ECO57	O85342	escherichia
455	6	1.5	420	1	VTT3_DROME	P06607	drosophila	528	6	1.5	484	1	HEMZ_HORVU	P42045	hordum vul
456	6	1.5	421	1	TRAB_AGRTS	O44351	agrobacteri	529	6	1.5	487	1	SVX2_THEMEA	O67241	thermotoga
457	6	1.5	421	1	MNTH_MYCIE	O50103	mycobacteri	530	6	1.5	487	1	FLIE_AQUAE	O67241	aquifex aeo
458	6	1.5	426	1	SEAA_HUMAN	P53796	homo sapien	531	6	1.5	489	1	MURE_THEMEA	O67241	aquifex aeo
459	6	1.5	426	1	VA20_VACCC	P20995	vacinia vi	532	6	1.5	490	1	TIG_RHILO	O98168	rhizobium 1
460	6	1.5	426	1	VA20_VARY	P33843	variolia vir	533	6	1.5	492	1	NUSA_ECOLI	P30303	escherichia
461	6	1.5	427	1	DSL1_CHICK	P33842	gallus gall	534	6	1.5	495	1	NUSA_ECOLI	P57459	buchnera ap
462	6	1.5	427	1	RHO_BACSV	O09222	bacillus su	535	6	1.5	496	1	NUSA_BUCAL	O60551	homo sapien
463	6	1.5	428	1	GLYA_AQUAE	O66776	aquifex aeo	536	6	1.5	498	1	NMT2_HUMAN	O55279	homo sapien
464	6	1.5	428	1	ZP26_MOUSE	P10076	mus muscucu	537	6	1.5	499	1	CIW5_HUMAN	P37440	salmonella
465	6	1.5	429	1	PUR2_ECOLI	P15640	escherichia	538	6	1.5	500	1	NUSA_SALTY	P28532	mus muscucu
466	6	1.5	429	1	PUR2_SALTI	O82334	salmonella	539	6	1.5	503	1	HSFI_MOUSE	O01653	vibrio prot
467	6	1.5	429	1	PUR2_SALTY	P26977	salmonella	540	6	1.5	504	1	AMPX_VIBPR	P27705	saccharomyc
468	6	1.5	430	1	GLGC_ECOLI	P00584	escherichia	541	6	1.5	504	1	PALI_PHAVU	P07218	phaeoselin v
469	6	1.5	431	1	NOOE_THERH	O86229	thermus the	542	6	1.5	506	1	CPJ5_BOVIN	P79102	bos taurus
470	6	1.5	432	1	YAIL_RHISN	P55495	rhizobium s	543	6	1.5	507	1	FUMH_MOUSE	P97807	mus muscucu
471	6	1.5	433	1	ENO_CAEEL	O27527	caenorhabdi	544	6	1.5	507	1	FUMH_MOUSE	P97807	mus muscucu

545	6	1.5	508	1	ASPR_HORVU	P42210 hordeum vul	618	6	1.5	602	1	2A5D_HUMAN	Q1478 h serine/th
546	6	1.5	508	1	YL12_YEAST	Q12303 saccharomyc	619	6	1.5	602	1	PEHX_ERWCH	P15922 erwinia chr
547	6	1.5	509	1	APRI_ORYSA	Q42456 oryza sativ	620	6	1.5	602	1	TX15_MOUSE	O70306 mus musculu
548	6	1.5	509	1	NUOM_ECOLI	P11978 escherichia	621	6	1.5	604	1	HEMA_CDVA	P24306 canine dist
549	6	1.5	512	1	HUTH_STRCO	O96w1 streptomyces	622	6	1.5	607	1	DNAX_STRPN	P58829 streptococc
550	6	1.5	512	1	K2C5_XENLA	P16878 xenopus lae	623	6	1.5	607	1	DNAX_STRPY	P55831 streptococc
551	6	1.5	513	1	EX7L_BROME	Q8yck1 bruceella me	624	6	1.5	607	1	HEMA_CDVA6	O66001 canine dist
552	6	1.5	513	1	SAD1_SCHPO	Q09828 eschiosacch	625	6	1.5	607	1	HEMA_CDVA4	O66000 canine dist
553	6	1.5	515	1	RHO_BORBU	P31645 borrelia bu	626	6	1.5	608	1	HEMA_PHODV	P28882 phocine dis
554	6	1.5	515	1	SIR2_CANAL	O59923 candida alb	627	6	1.5	608	1	DEXT_PENMI	P48845 penicillium
555	6	1.5	520	1	T2D5_YEAST	P51040 saccharomyc	628	6	1.5	608	1	YDEC_SCHPO	Q10324 schiosacch
556	6	1.5	520	1	SCOT_PIG	Q29551 sus scrofa	629	6	1.5	609	1	DNAX_STRAG	P55633 streptococc
557	6	1.5	520	1	YEAE_SCHPO	O14079 schiosacch	630	6	1.5	609	1	GLPO_LACTA	Q9c655 lactococcus
558	6	1.5	521	1	EX7L_RHILIO	Q987v3 rhizobium 1	631	6	1.5	609	1	PRXC_CURIN	P49053 curvularia
559	6	1.5	521	1	FD33_MYCTU	Q11015 mycobacteri	632	6	1.5	611	1	CALG_MOUSE	P52134 mus musculu
560	6	1.5	522	1	PHLB_MYCTU	P95246 mycobacteri	633	6	1.5	614	1	CYSN_MYCTU	Q10600 m cyan/cytc
561	6	1.5	522	1	NIFK_AZOVI	P07329 azotobacter	634	6	1.5	614	1	TU11_SCHPO	O09275 schiosacch
562	6	1.5	522	1	NU62_HUMAN	P37198 homo sapien	635	6	1.5	616	1	MUT1_STRCP	Q05064 streptomyc
563	6	1.5	522	1	UAP1_HUMAN	Q16222 h udp-n-ace	636	6	1.5	617	1	VG31_BPMD2	O64225 mycobacteri
564	6	1.5	523	1	TRXB_CABEL	Q17745 caenorhabdi	637	6	1.5	626	1	GPBA_HUMAN	P07359 homo sapien
565	6	1.5	523	1	UL21_PRYN3	O00703 pseudorabie	638	6	1.5	626	1	NR43_HUMAN	Q92570 homo sapien
566	6	1.5	525	1	SEBA_MERTH	O27051 methanobact	639	6	1.5	628	1	ASM_HUMAN	P51179 rattus norv
567	6	1.5	525	1	VMU1_HUMAN	P54219 homo sapien	640	6	1.5	629	1	ASM_HUMAN	P17405 homo sapien
568	6	1.5	526	1	VSM4_TRYBB	P02866 trypanosoma	641	6	1.5	629	1	MUTL_HAEIN	P44494 haemophilus
569	6	1.5	528	1	BGI_ARATH	Q9se50 arabidopsis	642	6	1.5	630	1	MIA3_HUMAN	Q9n134 homo sapien
570	6	1.5	529	1	PEPB_MOUSE	P24823 mus musculu	643	6	1.5	630	1	PARE_ECOLI	P20083 escherichia
571	6	1.5	530	1	TRPG_ECOLI	P00904 escherichia	644	6	1.5	631	1	PTBA_ERWCH	P26207 erwinia chr
572	6	1.5	530	1	TRPG_SALTU	P00905 salmonella	645	6	1.5	632	1	AFUB_HAEIN	O57343 haemophilus
573	6	1.5	531	1	KPKY_EIMTE	O44006 elmeria ten	646	6	1.5	632	1	RCAC_FREDI	Q01473 fremyella d
574	6	1.5	533	1	PPBI_BOVIN	P19111 bos taurus	647	6	1.5	634	1	GHR_BOVIN	P79108 bos taurus
575	6	1.5	533	1	RRPB_CVPPS	P18457 porcine tira	648	6	1.5	635	1	S6AB_BOVIN	O18875 bos taurus
576	6	1.5	535	1	YD19_MYCTU	Q10633 mycobacteri	649	6	1.5	635	1	S6AB_HUMAN	O48029 homo sapien
577	6	1.5	536	1	SR54_YARLI	O99150 variola li	650	6	1.5	635	1	S6AB_RABIT	P16651 cryocollagus
578	6	1.5	536	1	ZF94_RAT	Q942k3 rattus norv	651	6	1.5	635	1	S6AB_RAT	P28570 rattus norv
579	6	1.5	537	1	YIV9_YEAST	P40583 saccharomyc	652	6	1.5	641	1	LIP_STRAY	P04625 staphylococ
580	6	1.5	538	1	YA94_HUMAN	Q9up88 homo sapien	653	6	1.5	641	1	TEIS_LISTMO	Q48791 listeria mo
581	6	1.5	541	1	CGT_HUMAN	Q16880 homo sapien	654	6	1.5	643	1	VEI_HPV27	P61673 human papil
582	6	1.5	541	1	CGT_MOUSE	O64676 mus musculu	655	6	1.5	645	1	HRC2_XANCV	P80180 xanthomomas
583	6	1.5	541	1	CGT_RAT	O09426 rattus norv	656	6	1.5	646	1	TETS_LACTIA	O48712 lactococcus
584	6	1.5	542	1	CBP7_CANAL	P30574 candida alb	657	6	1.5	654	1	RAB1_RAT	P37727 rattus norv
585	6	1.5	544	1	DSK1_SCHPO	P36616 schiosacch	658	6	1.5	654	1	SPH2_HUMAN	Q9n180 homo sapien
586	6	1.5	544	1	EX7L_ZYMMO	Q91d14 zymomonas m	659	6	1.5	658	1	GSPD_PSEAE	P35818 pseudomonas
587	6	1.5	548	1	VG31_BPMU5	O05240 mycobacteri	660	6	1.5	659	1	POL_CERY	P05400 carnation e
588	6	1.5	550	1	SRG8_HUMAN	Q14247 homo sapien	661	6	1.5	668	1	PBS2_YEAST	P80818 saccharomyc
589	6	1.5	551	1	CH62_SYNY3	P22034 synchocyst	662	6	1.5	672	1	SL52_HUMAN	P16169 homo sapien
590	6	1.5	553	1	GPT1_CANAL	O74248 candida alb	663	6	1.5	672	1	SL52_RABIT	P26430 cryocollagus
591	6	1.5	555	1	TNSC_ECOLI	P05846 escherichia	664	6	1.5	673	1	COAT_PAVBO	P07237 bovine parv
592	6	1.5	558	1	ILVD_SULSO	Q97ub2 sulfolobus	665	6	1.5	678	1	GSPD_AERHY	P31780 aeromonas h
593	6	1.5	558	1	ZDS_ARATH	Q38893 arabidopsis	666	6	1.5	678	1	GSPD_AERHY	P31780 aeromonas h
594	6	1.5	559	1	POTA_MYCCE	P42581 mycoplasma	667	6	1.5	684	1	RPSD_AGR75	P33452 agrobacteri
595	6	1.5	561	1	HEMA_IACKG	P12581 influenza a	668	6	1.5	690	1	HRCV_PALISO	P35656 ralestonia s
596	6	1.5	565	1	HEMA_IAMIN	P12439 influenza a	669	6	1.5	692	1	ERG_STAM	P81683 staphylococ
597	6	1.5	565	1	ESR3_MITUN	P57783 micropogoni	670	6	1.5	692	1	FLHA_ECOLI	P76288 escherichia
598	6	1.5	565	1	VNUC_INCCA	P08028 influenza c	671	6	1.5	692	1	FLHA_SALTU	P40729 salmonella
599	6	1.5	572	1	LAC3_THACU	Q02079 thanatophor	672	6	1.5	694	1	LCF3_YEAST	P39002 saccharomyc
600	6	1.5	573	1	DPOL_MOUSE	Q9c429 mus musculu	673	6	1.5	694	1	LCF3_YEAST	P37912 saccharomyc
601	6	1.5	575	1	DPOL_HUMAN	Q9ug55 homo sapien	674	6	1.5	696	1	FLHA_PROMI	O51910 proteus mir
602	6	1.5	576	1	ACEA_BRANA	P25248 brassica na	675	6	1.5	697	1	CEAD_ECOLI	P17998 escherichia
603	6	1.5	578	1	PSP2_YEAST	P50108 saccharomyc	676	6	1.5	700	1	BIB_DROME	P23645 drosophila
604	6	1.5	579	1	YD49_MYCTU	Q11019 mycobacteri	677	6	1.5	702	1	UMOB_PROMI	O86988 proteus mir
605	6	1.5	581	1	FKBX_MOUSE	O61576 mus musculu	678	6	1.5	707	1	FLHA_TREPA	O56328 treponema p
606	6	1.5	581	1	HEMI_STRCO	Q9xli5 streptomyc	679	6	1.5	707	1	RHO_STRLI	P52157 streptomyc
607	6	1.5	584	1	DNLI_PYRAE	O93723 pyroaculum	680	6	1.5	708	1	ABBI_MOUSE	Q9gk13 mus musculu
608	6	1.5	584	1	ITRI_YEAST	P310605 saccharomyc	681	6	1.5	708	1	HPS4_HUMAN	O9ngq7 homo sapien
609	6	1.5	585	1	PUR9_SCHPO	O74928 s bifunctio	682	6	1.5	710	1	ABBI_HUMAN	O00213 homo sapien
610	6	1.5	591	1	PUR1_YEAST	P54113 s bifunctio	683	6	1.5	710	1	PAL3_PPAVU	P19143 phaseolus v
611	6	1.5	591	1	PUR9_HUMAN	P31939 homo sapien	684	6	1.5	713	1	PMIP_RAT	O01992 rattus norv
612	6	1.5	592	1	PUR2_YEAST	O9cwi9 s bifunctio	685	6	1.5	713	1	PAL1_SOYBN	P27991 glycine max
613	6	1.5	593	1	PUR9_MOUSE	Q9cwi9 mus musculu	686	6	1.5	714	1	CDG1_PAFMA	O99797 homo sapien
614	6	1.5	593	1	ARSD_HUMAN	P51689 homo sapien	687	6	1.5	714	1	NARB_STRY3	P04830 paenibacill
615	6	1.5	593	1	PRIM_HAEIN	Q08346 haemophilus	688	6	1.5	714	1	NARB_STRY3	P73448 synchocyst
616	6	1.5	593	1	PUR9_CHICK	P31335 gallus gall	689	6	1.5	714	1	NCPR_CATRO	O05001 catharanthu
617	6	1.5	600	1	DNAX_ERVRH	O05647 erysipeloth	690	6	1.5	716	1	KIF2_MOUSE	P28740 mus musculu

691	1.5	716	1	PEP DROME	P41073 drosophila	764	6	1.5	960	1	CSE1_YEAST	P3307 saccharomyc
692	1.5	722	6	AD21_HUMAN	G9uk18 homo sapien	765	6	1.5	967	1	AT51_RAT	G9wu1 rattus norv
693	1.5	726	1	BPL1_HUMAN	P50747 h biotin-p	766	6	1.5	968	1	SLA2_YEAST	P3338 saccharomyc
694	1.5	731	1	NGP1_HUMAN	Q13823 homo sapien	767	6	1.5	969	1	YEAC_SCHPO	O14077 schizosacch
695	1.5	733	1	ADDA_MOUSE	Q9gyco mus musculu	768	6	1.5	993	1	YIS2_YEAST	P40562 saccharomyc
696	1.5	735	1	ADDA_MOUSE	Q63028 rattus norv	769	6	1.5	994	1	MERK_RAT	P57077 rattus norv
697	1.5	737	1	YDD7_SCHPO	Q10432 schizosacch	770	6	1.5	997	1	AT57_HUMAN	G9ukx4 homo sapien
698	1.5	737	1	ADDA_HUMAN	P35611 homo sapien	771	6	1.5	999	1	RLKS_ARATH	P47735 arabidopsis
699	1.5	738	1	ARI0_HUMAN	Q9nrk6 homo sapien	772	6	1.5	1000	1	S155_YEAST	P33612 saccharomyc
700	1.5	739	1	CMTA_MYCSM	O59557 mycobacteri	773	6	1.5	1002	1	VGMN_CPEMV	P16300 compoa seve
701	1.5	743	1	CUL2_CAEBL	Q17390 caenorhabdi	774	6	1.5	1014	1	ACA2_ARATH	O81108 arabidopsis
702	1.5	757	1	CIKF_HUMAN	Q14003 homo sapien	775	6	1.5	1015	1	ACA7_ARATH	O64806 arabidopsis
703	1.5	762	1	SLAP_ACERI	P22258 acetogenium	776	6	1.5	1015	1	HIRA_MOUSE	O61666 mus musculu
704	1.5	764	1	TGMH_TACTR	Q05187 tachypleus	777	6	1.5	1017	1	TRL3_HUMAN	Q9hck6 homo sapien
705	1.5	770	1	NASB_BACSU	P42433 bacillus su	778	6	1.5	1030	1	STK9_HUMAN	O76039 homo sapien
706	1.5	771	1	CRPG_MYCTU	O10866 mycobacteri	779	6	1.5	1041	1	DD16_HUMAN	O60201 homo sapien
707	1.5	771	1	NTRY_AZOCA	Q04850 azorhizobiu	780	6	1.5	1047	1	RIR1_CHIMU	O9p193 chlamydia m
708	1.5	775	1	SM3E_HUMAN	O15041 homo sapien	781	6	1.5	1047	1	RIR1_CHITR	O84834 chlamydia t
709	1.5	775	1	SM3E_MOUSE	P70275 mus musculu	782	6	1.5	1054	1	IF2_STIAU	P55875 stigmatella
710	1.5	779	1	LEU2_YEAST	P07264 saccharomyc	783	6	1.5	1056	1	AMPI_PLAFQ	O96935 plasmodium
711	1.5	783	1	GCR_MOUSE	O06537 mus musculu	784	6	1.5	1070	1	Y355_HUMAN	O15063 homo sapien
712	1.5	790	1	RELX_MYCTU	O50638 mycobacteri	785	6	1.5	1081	1	MSH3_ARATH	O65607 arabidopsis
713	1.5	791	1	POLG_DENIC	P27913 dengue viru	786	6	1.5	1082	1	A3B2_HUMAN	O13367 homo sapien
714	1.5	792	1	GCR_RAT	P27912 dengue viru	787	6	1.5	1082	1	RGR1_YEAST	P19263 saccharomyc
715	1.5	795	1	YDDU_ECOLI	P06536 rattus norv	788	6	1.5	1083	1	T2D3_HUMAN	O00268 homo sapien
716	1.5	799	1	RR3_CHLEU	P76129 escherichia	789	6	1.5	1087	1	POM1_SCHPO	O09690 schizosacch
717	1.5	800	1	RR3_CHLEU	P46307 chlamydomon	790	6	1.5	1090	1	PUL1_KLEPN	P07260 klebsiella
718	1.5	810	1	HTR4_HAANI	O9np84 halobacteri	791	6	1.5	1091	1	ATN1_YEAST	P13587 saccharomyc
719	1.5	810	1	HTR4_HAUSA	Q46317 halobacteri	792	6	1.5	1091	1	ATN2_YEAST	O01896 saccharomyc
720	1.5	815	1	ACH_HAEIN	P44505 haemophilus	793	6	1.5	1091	1	ATN3_YEAST	Q12631 saccharomyc
721	1.5	816	1	ACH_BUCAL	P57290 buchnera ap	794	6	1.5	1093	1	TMF1_HUMAN	P82094 homo sapien
722	1.5	819	1	AHMI_ARATH	O9m3h5 arabidopsis	795	6	1.5	1097	1	DPOL_MCVVS	P27112 murine cyto
723	1.5	819	1	AKIH_SERMA	P27725 serratia ma	796	6	1.5	1097	1	TOLL_DROME	P08953 drosophila
724	1.5	820	1	AKIH_ECOLI	P00561 escherichia	797	6	1.5	1103	1	PMAL_DUNAC	P54210 dunaliella
725	1.5	823	1	YNS2_CAEBL	P3586 caenorhabdi	798	6	1.5	1116	1	RPOB_HERCA	P36440 heterosigma
726	1.5	831	1	NAH3_RAT	P26433 rattus norv	799	6	1.5	1125	1	CYGS_STRPU	P16065 stronyloce
727	1.5	832	1	NAH3_RABIT	P26433 oryctolagus	800	6	1.5	1131	1	PMAL_DUNBI	P54211 dunaliella
728	1.5	834	1	NAH3_HUMAN	P48761 homo sapien	801	6	1.5	1132	1	NUT1_YEAST	P53139 saccharomyc
729	1.5	836	1	GLK1_MOUSE	O60934 mus musculu	802	6	1.5	1137	1	MSB1_YEAST	P21339 saccharomyc
730	1.5	840	1	MUTS_LACLA	O9cd46 lactococcus	803	6	1.5	1146	1	YHC3_YEAST	P38742 saccharomyc
731	1.5	843	1	SECA_STANU	O06446 staphylococ	804	6	1.5	1150	1	APMU_PIG	P12021 sus scrofa
732	1.5	844	1	SECA_STACA	P47994 staphylococ	805	6	1.5	1156	1	C9AA_BACTG	Q99031 bacillus th
733	1.5	849	1	AKA4_MOUSE	Q06062 mus musculu	806	6	1.5	1186	1	DNBI_HSVB2	P12639 bovine heip
734	1.5	856	1	POLG_PVVO	P22602 potaco viru	807	6	1.5	1187	1	M10L_MOUSE	Q09m65 mus musculu
735	1.5	863	1	Y597_CAEBL	O09966 caenorhabdi	808	6	1.5	1191	1	NKCI_SQUAC	P55013 equalus aca
736	1.5	865	1	LAC9_KLUJA	P08657 kluyveromyc	809	6	1.5	1197	1	Y4CA_RHSN	P55383 rhizobium s
737	1.5	877	1	DPO1_STRPN	P12552 streptococ	810	6	1.5	1220	1	SLN1_YEAST	P39928 saccharomyc
738	1.5	881	1	GND_VIBCH	O9kpv0 vibrio chol	811	6	1.5	1225	1	KP4A_CHICK	Q90640 gallus gall
739	1.5	883	1	CHB_VIBHA	P13670 vibrio harv	812	6	1.5	1237	1	YG2L_YEAST	P53254 saccharomyc
740	1.5	885	1	UE3A_MOUSE	O08759 mus musculu	813	6	1.5	1238	1	BVGS_BORPE	P16575 bordetella
741	1.5	886	1	SYA_BARBA	P70865 bartonella	814	6	1.5	1253	1	SC25_YEAST	P14771 saccharomyc
742	1.5	887	1	GND_KLEPN	P43393 klebsiella	815	6	1.5	1254	1	POLS_EEYV8	P05674 venezuelan
743	1.5	887	1	MCM2_DROME	P49735 drosophila	816	6	1.5	1254	1	POLS_EEYV6	P36330 venezuelan
744	1.5	889	1	CIKF_RAT	Q01956 rattus norv	817	6	1.5	1254	1	POLS_EEYV4	P26331 venezuelan
745	1.5	896	1	NAH5_HUMAN	O91940 homo sapien	818	6	1.5	1254	1	POLS_EEYV7	P09592 venezuelan
746	1.5	897	1	RB88_HUMAN	O99708 homo sapien	819	6	1.5	1255	1	POLS_EEYV3	P36329 venezuelan
747	1.5	901	1	VP3_BTVIA	P20608 bluetongue	820	6	1.5	1255	1	POLS_EEYV9	P36332 venezuelan
748	1.5	903	1	AD12_MOUSE	Q61824 mus musculu	821	6	1.5	1255	1	METH_HUMAN	O99707 homo sapien
749	1.5	908	1	PSD2_HUMAN	Q11200 homo sapien	822	6	1.5	1271	1	TRPS_XENLA	O90266 xenopus lae
750	1.5	910	1	GLK1_HUMAN	P39086 homo sapien	823	6	1.5	1273	1	WEB1_YEAST	P39926 saccharomyc
751	1.5	920	1	CO4_BOVIN	P01030 bos taurus	824	6	1.5	1275	1	COBN_PSEDE	P29929 pseudomonas
752	1.5	921	1	DPO1_RICHE	O91b6 rickettsia	825	6	1.5	1284	1	NRX4_DROME	Q44887 drosophila
753	1.5	922	1	DPO1_RICPE	O9raa9 rickettsia	826	6	1.5	1289	1	MCE_REOVD	P11079 reovirus (t
754	1.5	923	1	HEPA_HAELN	P44781 haemophilus	827	6	1.5	1290	1	PIGI_HUMAN	P19174 homo sapien
755	1.5	928	1	PM11_CHLPN	O86164 chlamydia p	828	6	1.5	1291	1	RDPO_BOVIN	P08487 bos taurus
756	1.5	929	1	ART1_HUMAN	O9n208 h adipocyte	829	6	1.5	1333	1	RDPO_SCHPO	Q05654 echizosacch
757	1.5	929	1	DPOM_MAIZE	P10582 zea mays (m	830	6	1.5	1356	1	VGR2_HUMAN	P35968 homo sapien
758	1.5	933	1	ODO1_ECOLI	P07015 escherichia	831	6	1.5	1367	1	VGR2_MOUSE	P35968 mus musculu
759	1.5	935	1	IT38_MEPRV	O9whm1 medicago tr	832	6	1.5	1375	1	RPOB_VIBCH	Q9kva3 drosophila
760	1.5	943	1	ODO1_AZOVI	P20707 azotobacter	833	6	1.5	1411	1	Y197_DROME	O15360 homo sapien
761	1.5	946	1	RIG4_HUMAN	P98171 homo sapien	834	6	1.5	1455	1	FACA_HUMAN	P19015 cricetus
762	1.5	948	1	CDAA_HUMAN	O9512 homo sapien	835	6	1.5	1476	1	AT7A_CRIGR	P33202 saccharomyc
763	1.5	949	1	GLK1_RAT	P22756 rattus norv	836	6	1.5	1483	1	UFDA_YEAST	

837	6	1.5	1538	1	PRSB_MYCTU	Q10978 mycobacteri	910	5	1.2	57	1	RBL_CMSI	P31181 camelilia si
838	6	1.5	1574	1	STY1_RAT	Q62910 rattus norv	911	5	1.2	58	1	PEPT_THUTO	P20119 thunnus thy
839	6	1.5	1609	1	FIG2_YEAST	P25653 saccharomyc	912	5	1.2	58	1	RBL_EUOB	P31185 euonymus bu
840	6	1.5	1675	1	POL_RTBVP	P27502 rice tungro	913	5	1.2	58	1	RBL_EUOMA	P31186 euonymus ma
841	6	1.5	1738	1	CO4_MOUSE	P01029 mus musculu	914	5	1.2	58	1	RBL_EUPCH	P31187 euphorbia c
842	6	1.5	1886	1	GP21_RAT	P11654 rattus norv	915	5	1.2	58	1	RBL_WEISY	P31203 weinmannia
843	6	1.5	1980	1	MY9B_RAT	Q61358 rattus norv	916	5	1.2	58	1	Y354_METUA	Q57800 methanococc
844	6	1.5	2026	1	CYAA_YEAST	P08678 saccharomyc	917	5	1.2	59	1	AT18_YEAST	P81450 saccharomyc
845	6	1.5	2033	1	EVPL_HUMAN	Q92812 homo sapien	918	5	1.2	60	1	RCSB_KLEAE	P05339 klebsiella
846	6	1.5	2035	1	EVPL_MOUSE	Q95952 mus musculu	919	5	1.2	61	1	ASSY_LACTIC	P05339 lactococcus
847	6	1.5	2038	1	FSH_DROME	P13709 drosophila	920	5	1.2	61	1	DNBI_BFPV	P13893 budgerigar
848	6	1.5	2114	1	MY9B_MOUSE	Q99706 mus musculu	921	5	1.2	61	1	RS14_BACST	P54788 bacillus st
849	6	1.5	2183	1	RRLP_MEASA	P25975 measles vir	922	5	1.2	61	1	SECE_PIRAB	Q97481 pyrococcus
850	6	1.5	2183	1	RRLP_MEASE	P12576 measles vir	923	5	1.2	61	1	TEMG_RANTE	P19875 rana tempor
851	6	1.5	2324	1	COAC_CHICK	P11029 gallus galli	924	5	1.2	62	1	RL19_MAIZE	Q08066 zea mays (m
852	6	1.5	2345	1	COAL_RAT	P14973 rattus norv	925	5	1.2	62	1	YCF9_PINTH	P14642 pinus thunb
853	6	1.5	2346	1	COAL_BOVIN	Q91437 bos taurus	926	5	1.2	63	1	GBAK_CRTGR	Q60397 cinctulus
854	6	1.5	2346	1	COAL_HUMAN	Q13085 homo sapien	927	5	1.2	65	1	YCF9_CVAPA	P17159 cyanophora
855	6	1.5	2346	1	COAL_SHEEP	Q28559 ovis aries	928	5	1.2	66	1	Y2A8_PSEAE	Q51384 pseudomonas
856	6	1.5	2481	1	UN52_CABEL	Q06561 caenorhabdi	929	5	1.2	67	1	YORR_TTV1	P19302 thermoprote
857	6	1.5	2483	1	COA2_HUMAN	O00763 homo sapien	930	5	1.2	68	1	LCNB_LACTIC	P35518 lactococcus
858	6	1.5	2493	1	YBA4_YEAST	P35194 saccharomyc	931	5	1.2	70	1	RS21_HAEIN	P44386 haemophilus
859	6	1.5	3010	1	POLG_HCVTA	P26663 h genome po	932	5	1.2	71	1	BRIE_PANES	P32412 rana esculu
860	6	1.5	3010	1	POLG_HCVBK	P26662 h genome po	933	5	1.2	72	1	RL40_TOBAC	P19379 nicotiana t
861	6	1.5	3010	1	POLG_HCVTW	P29846 h genome po	934	5	1.2	72	1	VSMO_TRYBB	P07209 trypanosoma
862	6	1.5	3110	1	HD_RAT	P51111 rattus norv	935	5	1.2	73	1	H171_HUMAN	Q43727 homo sapien
863	6	1.5	3381	1	PGCV_BOVIN	P81282 bos taurus	936	5	1.2	73	1	PUPF_RHOSU	Q9488 rhodovulum
864	6	1.5	3390	1	POLG_DEN3	P27915 d genome po	937	5	1.2	73	1	RS27_METKA	Q81987 methanopyru
865	6	1.5	3396	1	PGCV_HUMAN	P33611 homo sapien	938	5	1.2	73	1	YUEG_BACSU	Q32054 bacillus su
866	6	1.5	3396	1	POLG_DENIS	P23478 d genome po	939	5	1.2	74	1	ATP9_MAIZE	P00840 zea mays (m
867	6	1.5	3707	1	PGEM_MOUSE	Q05793 mus musculu	940	5	1.2	74	1	ATP9_MARPO	P26855 marichantia
868	6	1.5	4196	1	DYHC_SCHPO	O13290 schizosacch	941	5	1.2	74	1	ATP9_PEA	P05717 pisum sativ
869	6	1.5	4451	1	GRSB_BACBR	P14688 b gramicidi	942	5	1.2	74	1	ATP9_WHEAT	P13547 triticum ae
870	6	1.5	5376	1	ZAN_MOUSE	O88799 mus musculu	943	5	1.2	74	1	DEP2_CAPAN	Q65740 capsitum an
871	5	1.2	12	1	FREI_LITIN	P82021 litorea inf	944	5	1.2	74	1	RS3_COXBU	O85368 coxiella bu
872	5	1.2	17	1	BOLS_MERGE	P07456 megadomus	945	5	1.2	75	1	LAFR_LACCU	P24022 lactobacill
873	5	1.2	20	1	SODM_HORVU	P28524 hordeum vul	946	5	1.2	77	1	YLDR_ALCEU	P40289 alcaligenes
874	5	1.2	24	1	GAB6_RANRU	P80400 rana rugosa	947	5	1.2	78	1	MT2_MUSAC	O22317 musa acumin
875	5	1.2	25	1	ATPD_MICLU	P80285 micrococcus	948	5	1.2	79	1	DEF_TACTR	P80957 taylorpleus
876	5	1.2	26	1	THIL_PIG	P14610 sus scrofa	949	5	1.2	79	1	RS16_BUCAI	P57474 buchnera ap
877	5	1.2	31	1	PSAM_EUGER	P31479 euglena gra	950	5	1.2	79	1	SNSP_HUMAN	P80657 homo sapien
878	5	1.2	32	1	IAPF_BOVIN	Q28207 bos taurus	951	5	1.2	79	1	YTXI_BORPE	Q45369 bordetella
879	5	1.2	32	1	IAPF_SHEEP	Q28605 ovis aries	952	5	1.2	79	1	YZ_SHEEP	P08105 ovis aries
880	5	1.2	33	1	ALOX_PICPA	P04842 pichia past	953	5	1.2	80	1	PERX_WHEAT	P15994 triticum ae
881	5	1.2	42	1	RL32_MAIZE	P51471 zea mays (m	954	5	1.2	80	1	PRGI_SALTY	P41784 salmonella
882	5	1.2	44	1	THHR_HORVU	P33044 hordeum vul	955	5	1.2	80	1	PSAC_SKECO	O96894 skeletonema
883	5	1.2	46	1	DIUX_ACHDO	P23834 acheta dome	956	5	1.2	81	1	DINT_ECOLI	Q47113 escherichia
884	5	1.2	49	1	TPX2_STRPN	P42365 streptococc	957	5	1.2	81	1	PSAC_ODOSI	P49477 odontella s
885	5	1.2	49	1	Y185_MERUA	Q57644 methanococc	958	5	1.2	81	1	RS18_CHLMU	P24286 chlamydia m
886	5	1.2	51	1	ZNPF_LYCVF	P19326 lymphocytic	959	5	1.2	81	1	RS18_CHLTR	O84808 chlamydia t
887	5	1.2	52	1	RL40_ACACA	P49633 acanthamoeb	960	5	1.2	81	1	YE47_ARCFU	O28825 archaeoglob
888	5	1.2	52	1	RL40_ARATH	P19232 arabidopsis	961	5	1.2	81	1	YFEM_ECOLI	P76544 escherichia
889	5	1.2	52	1	RL40_BRARA	PS1423 brassica ra	962	5	1.2	81	1	YQGY_BACSU	P54502 bacillus su
890	5	1.2	52	1	RL40_CABEL	P49632 caenorhabdi	963	5	1.2	82	1	FER_CHRVI	P00208 chromatium
891	5	1.2	52	1	RL40_CHIRE	P14695 chlamydomon	964	5	1.2	82	1	NUMM_MOUSE	P52503 mus musculu
892	5	1.2	52	1	RL40_DICDI	P14765 dictyosteli	965	5	1.2	82	1	RS18_CHLUP	Q92644 chlamydia p
893	5	1.2	52	1	RL40_DROME	P18101 drosophila	966	5	1.2	82	1	V082_ASEB7	P18557 african swi
894	5	1.2	52	1	RL40_HUMAN	P14793 homo sapien	967	5	1.2	82	1	Y233_ARCFU	Q30066 archaeoglob
895	5	1.2	52	1	RL40_NICSY	P49636 nicotiana s	968	5	1.2	83	1	CYCS_AZOVI	P11732 azotobacter
896	5	1.2	52	1	RL40_YEAST	P14796 saccharomyc	969	5	1.2	83	1	Y098_RICPR	Q92496 rickettsia
897	5	1.2	52	1	Y039_TREPA	O83081 treponema p	970	5	1.2	84	1	DHSD_CHOCR	P54333 chondrus cr
898	5	1.2	53	1	RHGG_FUGRU	O57414 fugru rubrip	971	5	1.2	84	1	IAC2_HUMAN	P20155 homo sapien
899	5	1.2	53	1	RL40_CRYNE	O49099 cryptococcu	972	5	1.2	84	1	RL34_PYRAE	O82172 pyrobaculum
900	5	1.2	53	1	RL40_EIMBO	P46575 elmeria bov	973	5	1.2	84	1	RNS_GIRCA	Q29555 giraffa cam
901	5	1.2	53	1	RL40_ORISA	P25296 oryza sativ	974	5	1.2	84	1	RS18_MYCLE	O53125 mycobacteri
902	5	1.2	54	1	ATPE_CABEL	P43539 caenorhabdi	975	5	1.2	84	1	TOLE_ACTPL	Q44156 actinobacil
903	5	1.2	54	1	CHYM_FELCA	P09873 felis silve	976	5	1.2	84	1	YB72_METUA	Q5872 methanococc
904	5	1.2	54	1	YP14_VIBAL	P26064 vibrio algi	977	5	1.2	84	1	YBFI_ECOLI	P46146 escherichia
905	5	1.2	55	1	YP18_CLOPE	P18018 clostridium	978	5	1.2	85	1	RPOL_METHH	O27372 methanobact
906	5	1.2	56	1	SCP2_MESMA	O9107 mesobutinus	979	5	1.2	85	1	VG35_HAEIN	P44228 haemophilus
907	5	1.2	56	1	SCP3_MESMA	Q9861 mesobutinus	980	5	1.2	85	1	YCPR_ECOLI	P75993 escherichia
908	5	1.2	56	1	VGK_BPPXK	P03653 bacterioph	981	5	1.2	85	1	Y173_BUCPE	P29473 burkholderi
909	5	1.2	57	1	RBL_BUXSE	P31180 buxus sempe	982	5	1.2	85	1	Y1DD_BUCAP	P29432 buchnera ap

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983 5 1.2 86 1 PAK1_SUNY3 P27212 synecocyst
984 5 1.2 86 1 REV_HV123 P05867 human immun
985 5 1.2 86 1 RL3E_ARCPU 028389 archaeoglob
986 5 1.2 86 1 RX86_CIOAB 097100 clostridium
987 5 1.2 87 1 FRY4_RAT 061113 ractus norv
988 5 1.2 87 1 VAPL_BP186 P21681 bacterioph
989 5 1.2 87 1 VG07_BPMU 038417 bacterioph
990 5 1.2 87 1 Y476_MYCLE 09c643 mycobacteri
991 5 1.2 88 1 MS25_MOUSE 092224 mus musculu
992 5 1.2 88 1 RS15_HAEN P44369 haemophilu
993 5 1.2 88 1 RS15_YEREN 034274 yersinia en
994 5 1.2 88 1 S108_MOUSE P27005 mus musculu
995 5 1.2 88 1 YDFK_ECOLI P76154 escherichia
996 5 1.2 88 1 YNAE_ECOLI P67073 escherichia
997 5 1.2 89 1 DRPH_ROMMI 009929 romalea mic
998 5 1.2 89 1 RPOK_TAREE 09y419 aeropyrum p
999 5 1.2 89 1 RS15_TREBA 088857 treponema p
1000 5 1.2 89 1 YS22_BORBU P70844 borrelia bu

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ALIGNMENTS

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RESULT 1
BAE2_HUMAN STANDARD; PRT; 518 AA.

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ID BAE2_HUMAN STANDARD; PRT; 518 AA.
AC 09Y520; 09UT6;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Beta secretase 2 precursor (EC 3.4.23.-) (Beta-site APP-cleaving
DE enzyme 2) (Aspartyl protease 1) (Asp 1) (Membrane-associated
DE aspartic protease 1) (Memapsin-1).
GN BACE2 OR ASP21.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20057170; PubMed=10591213;
RA Yan R., Bienkowski M.J., Snuck M.B., Miao H., Tory M.C., Pauley A.M.,
RA Brashler J.G., Strattan L.C., Mathews W.R., Buhl A.E., Carter D.B.,
RA Tomasselli A.R., Parodi L.A., Heinrichson R.L., Gurney M.E.;
RT "Membrane-anchored aspartyl protease with Alzheimer's disease
RT beta-secretase activity.";
RL Nature 402:533-537(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Xin H., Stephens J.C., Duan X., Harrowe G., Kim E., Grieshammer U.,
RA Giese K.;
RT "Identification of a novel aspartic-like protease differentially
RT expressed in human breast cancer cell lines.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Accarino M.P., Fumagalli P., Ottolenghi S., Taramelli R.;
RT "Cloning of a gene from chromosome 21 Down region encoding a potential
RT transmembrane aspartyl protease.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Solans A., Estivill X., de la Luna S.;
RT "Cloning of a novel mammalian aspartyl protease.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=20120043; PubMed=10656250;
RA Hussain I., Powell D.J., Howlett D.R., Tew D.G., Meek T.D.,
RA Chapman C., Glover I.S., Murphy K.E., Southan C.D., Ryan D.M.,
RA Smith T.S., Simons D.L., Walsh F.S., Dingwall C., Christie G.;
RT "Identification of a novel aspartic proteinase (Asp 2) as

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RT beta-secretase.";
RL Mol. Cell. Neurosci. 14:419-427(1999).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=20144060; PubMed=10677483;
RA Lin X., Koelsch G., Wu S., Downs D., Dashti A., Tang J.;
RT "Human aspartic protease memapsin 2 cleaves the beta-secretase site of
RT beta-amyloid precursor protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:1456-1460(2000).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=20289799; PubMed=10830953;
RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA Park H.-S., Toyoda A., Ishii K., Tocchi Y., Choi D.-K., Soeda E.,
RA Onki M., Takagi T., Sakai Y., Taudien S., Blechschmidt K., Polley A.,
RA Menzel U., Delabar A., Kumpf K., Lehmann R., Patterson D.,
RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
RA Rosenthal A., Kidon U., Shibuya K., Kawasaki K., Asakawa S.,
RA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
RA Minoshima S., Shimizu N., Nordstiek G., Hornischer K., Brandt P.,
RA Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloeker H.,
RA Ramser J., Beck A., Klages S., Hennig S., Riessmann L., Dagand E.,
RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
RA Leinrach H., Reinhardt R., Yaspo M.-L.;
RT "The DNA sequence of human chromosome 21.";
RL Nature 405:311-319(2000).
RN [8]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strauberg R.;
RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RL -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
CC -----
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CC -----
DR EMBL; AF200342; AAFL17048.1; -
DR EMBL; AF117892; AAD45240.1; -
DR EMBL; AF050171; AAD45963.1; -
DR EMBL; AF178532; AAF29494.1; -
DR EMBL; AF204944; AAF263368.1; -
DR EMBL; AF200192; AAF13714.1; -
DR EMBL; AL163284; CAB90458.1; -
DR EMBL; AL163285; CAB90554.1; -
DR EMBL; BC014453; AAH14453.1; -
DR HSSP; P00797; 2REN.
DR MEROPS; A01.041; -
DR Genew; HGNC:934; BACE2.
DR MIM; 605668; -
DR InterPro; IPR001461; AsproteaseA1.
DR InterPro; IPR001969; Asprotease_site.
DR Pfam; PF00026; asp.1.
DR PRINTS; PR00792; PERSIN.
DR PROSITE; PS00141; ASP_PROTEASE; 2.
KW Hydroxylase; Aspartyl protease; Glycoprotein; Zymogen; Transmembrane;
KW Signal.
FT SIGNAL. 1 20
FT PROPEP 21 ?
FT CHAIN 21 518
FT DOMAIN 21 473
FT TRANSMEM 474 494
FT DOMAIN 495 518
FT ACT_SITE 110 110
FT ACT_SITE 303 303
FT CARBOHYD 170 170
FT CARBOHYD 366 366
FT CONFLICT 36 36
FT A -> T (IN REF. 6).

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SQ SEQUENCE 518 AA; 56180 MM; 2E90315082376003 CRC64;
 Query Match 100.0%; Score 406; DB 1; Length 518;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPALASPAGANFLAMVNDLQDSGRGYLLEMLIGTPPKQLIVDTGSSNFAVACTP 60
 DB 63 ALPALASPAGANFLAMVNDLQDSGRGYLLEMLIGTPPKQLIVDTGSSNFAVACTP 122
 QY 61 HSYIDYFDPERSSSTYSKGFVTVKTKQSGMTGFGVGDVLTIPKGFNTSLVNIATFE 120
 DB 123 HSYIDYFDPERSSSTYSKGFVTVKTKQSGMTGFGVGDVLTIPKGFNTSLVNIATFE 182
 QY 121 SENFELPKIKNGKILGLAVATLAKPSSSLFETFPDPLVTQANIPIVFSMQMGAGLPVAGS 180
 DB 183 SENFELPKIKNGKILGLAVATLAKPSSSLFETFPDPLVTQANIPIVFSMQMGAGLPVAGS 242
 QY 181 GTNGGSLVGGIPEPSLYKGDIVTPYPIKEWYVQIEILKLEIGGSLINDCEYNADKAI 240
 DB 243 GTNGGSLVGGIPEPSLYKGDIVTPYPIKEWYVQIEILKLEIGGSLINDCEYNADKAI 302
 QY 241 DSGTTLRLPKXFDVAWEAARASLIPEFSDGFWTSGQLACWNTSETPMSYFPKISLYL 300
 DB 303 DSGTTLRLPKXFDVAWEAARASLIPEFSDGFWTSGQLACWNTSETPMSYFPKISLYL 362
 QY 301 RDENSSRSFRITLIPOLYIOPMAGALNCEYRCFISPTNALYIGATVMEGFYIPDRA 360
 DB 363 RDENSSRSFRITLIPOLYIOPMAGALNCEYRCFISPTNALYIGATVMEGFYIPDRA 422
 QY 361 QKRVGPAAPCAETAGAAVSEISGPFSTEDVANSNCVPAQSISEPI 406
 DB 423 QKRVGPAAPCAETAGAAVSEISGPFSTEDVANSNCVPAQSISEPI 468

RESULT 2
 BACE_HUMAN
 ID BACE_HUMAN STANDARD; PRT; 501 AA.
 AC P56817; Q9JUT5; Q9BYC1; Q9BYC0; Q9BYB9;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Beta-secretase precursor (EC 3.4.23.-) (Beta-site APP cleaving enzyme)
 DE (Beta-site amyloid precursor protein cleaving enzyme) (Aspartyl
 protease 2) (Asp 2) (ASP2) (Membrane-associated aspartic protease 2)
 DE (Memapsin-2).
 GN BACE OR BACE1.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM A).
 RC TISSUE=Brain;
 RX MEDLINE=20057111; PubMed=10531052;
 RA Vassar R., Bennett B.D., Babu-Khan S., Kahn S., Mendiaz E.A.,
 RA Denis P., Teplow D.B., Ross S., Amarante P., Loebner R., Luo Y.,
 RA Fisher S., Fuller J., Edenson S., Lile J., Jacosini M.A.,
 RA Biere A.L., Curran E., Burgess T., Louis J.-C., Collins F.,
 RA Trearor J., Rogers R., Citron M.,
 RA "Beta-secretase cleavage of Alzheimer's amyloid precursor protein by
 RT the transmembrane aspartic protease BACE".
 RL Science 286:735-741(1999).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM A), SEQUENCE OF 46-66, AND
 RP CHARACTERIZATION.
 RC TISSUE=Brain;
 RX MEDLINE=20057111; PubMed=10531214;
 RA Sinha S., Anderson J.P., Barbour R., Basl G.S., Caccavello R.,
 RA Davis D., Dean M., Doye H.F., Fridon N., Hong J., Jacobson-Croak K.,
 RA Jewett N., Keim P., Koeps J., Lieberburg I., Power M., Tan H.,
 RA Tatsuno G., Tung J., Schenk D., Seubert P., Sommersaari S.M., Wang S.,
 Walker D., Zhao J., McConlogue L., Varghese J.;

RT "Purification and cloning of amyloid precursor protein beta-secretase
 RT from human brain.";
 RL Nature 402:537-540(1999).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM A).
 RX MEDLINE=20057170; PubMed=10591213;
 RA Yan R., Bienkowski M.J., Shuck M.E., Miao H., Tory M.C., Pauley A.M.,
 RA Brashler J.R., Strattan N.C., Mathews W.R., Buhl A.E., Carter D.B.,
 RA Tomasselli A.G., Parodi L.A., Heinrikson R.L., Gurney M.E.;
 RT "Membrane-anchored aspartyl protease with Alzheimer's disease beta-
 RT secretase activity".
 RL Nature 402:533-537(1999).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM A).
 RX MEDLINE=20120043; PubMed=10656250;
 RA Hsueh S.I., Powell D.J., Howlett D.R., Tew D.G., Meek T.D.,
 RA Chapman C., Glögl I.S., Murphy K.E., Southern C.D., Ryan D.M.,
 RA Smith T.S., Simmons D.L., Walsh F.S., Dingwall C., Christie G.;
 RT "Identification of a novel aspartic protease (Asp 2) as beta-
 RT secretase.";
 RL Mol. Cell. Neurosci. 14:419-427(1999).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM B).
 RC TISSUE=Brain, and Pancreas;
 RA Michel B., De Pietri Tonelli D., Zaccchetti D., Keller P.;
 RT "New beta-site APP cleaving enzyme isoform (BACE-1B) obtained from
 RT human brain and pancreas.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM C).
 RC TISSUE=Pancreas;
 RA Zaccchetti D., De Pietri Tonelli D., Schurbus R.;
 RT "New beta-site APP cleaving enzyme isoform (BACE-1C) obtained from
 RT human pancreas.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORMS B; C AND D).
 RC TISSUE=Brain;
 RX MEDLINE=21408467; PubMed=11516562;
 RA Tanahashi H., Tabira T.;
 RT "Three novel alternatively spliced isoforms of the human beta-site
 RT amyloid precursor protein cleaving enzyme (BACE) and their effect on
 RT amyloid beta-peptide production.";
 RL Neurosci. Lett. 307:9-12(2001).
 RN [8]
 RP SEQUENCE OF 14-501 FROM N.A. (ISOFORM A), AND CHARACTERIZATION.
 RX MEDLINE=20144060; PubMed=10677483;
 RA Lin X., Koelsch G., Wu S., Downs D., Dashti A., Tang J.;
 RT "Human aspartic protease memapsin 2 cleaves the beta-secretase site of
 RT beta-amyloid precursor protein.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1456-1460(2000).
 RN [9]
 RP DISULFIDE BONDS.
 RX MEDLINE=21950860; PubMed=11953458;
 RA Fischer F., Molinari M., Bodendorf U., Paganetti P.;
 RT "The disulphide bonds in the catalytic domain of BACE are critical but
 RT not essential for amyloid precursor protein processing activity.";
 RL J. Neurochem. 80:1079-1088(2002).
 CC -1- FUNCTION: RESPONSIBLE FOR THE PROTEOLYTIC PROCESSING OF THE
 CC AMYLOID PRECURSOR PROTEIN (APP). CLEAVES AT THE AMINO TERMINUS OF
 CC THE A-BETA PEPTIDE SEQUENCE, BETWEEN RESIDUES 671 AND 672 OF APP,
 CC LEADS TO THE GENERATION AND EXTRACELLULAR RELEASE OF BETA-CLEAVED
 CC SOLUBLE APP, AND A CORRESPONDING CELL-ASSOCIATED CARBOXY-TERMINAL
 CC FRAGMENT WHICH IS LATER RELEASED BY GAMMA-SECRETASE.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 4 isoforms; A/BACE-1A/BAC-501 (shown here),
 CC B/BACE-1B/BACE-1-476; C/BACE-1C/BACE-1-457 and D/BACE-1D/BACE-1-
 CC 432; are produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: BRAIN.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
 CC -----
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DR EMBL/AF190725; AAF04142.1; -
 DR EMBL/AF201468; AAF18982.1; -
 DR EMBL/AF200343; AAF17079.1; -
 DR EMBL/AF204943; AAF26367.1; -
 DR EMBL/AF338816; AAK38374.1; -
 DR EMBL/AF338817; AAK38375.1; -
 DR EMBL/AB050436; BAB40931.1; -
 DR EMBL/AB050437; BAB40932.1; -
 DR EMBL/AB050438; BAB40933.1; -
 DR EMBL/AF200193; AAF13715.1; -
 DR HSSP; P32329; 1YPS.
 DR MEROPS; A01.004; -
 DR Genew; HGNC:933; BACE.
 DR MIM; 604252; -
 DR InterPro; IPR001461; Aspproteaseal.
 DR InterPro; IPR001969; Aspprotease_site.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPsin.
 DR PROSITE; PS00141; ASP PROTEASE; 1.
 KM Hydrolyase; Aspartyl protease; Glycoprotein; Zymogen; Transmembrane;
 KM Signal; Alternative splicing.
 FT SIGNAL 1 21
 FT PROPEP 22 45
 FT CHAIN 46 501
 FT DOMAIN 22 457
 FT TRANSMEM 458 478
 FT DOMAIN 479 501
 FT ACT_SITE 93 93
 FT ACT_SITE 289 289
 FT DISULFID 216 420
 FT DISULFID 278 443
 FT DISULFID 330 380
 FT CARBOHYD 153 153
 FT CARBOHYD 172 172
 FT CARBOHYD 223 223
 FT CARBOHYD 354 354
 FT VARSPLIC 146 189
 FT VARSPLIC 190 214
 SQ SEQUENCE 501 AA; 55763 MW; 377CEAC824ACBF05 CRC64;
 Query Match 3.0%; Score 12; DB 1; Length 501;
 Best Local Similarity 100.0%; Pred. No. 0.00037;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 45 ILVDTGSSNFAY 56
 DB 90 ILVDTGSSNFAY 101
 RESULT 3
 BACE_MOUSE STANDARD; PRT; 501 AA.
 AC P56818;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Beta-secretase precursor (BC 3.4.23.-) (Beta-site APP cleaving enzyme)
 DE (Beta-site amyloid precursor protein cleaving enzyme) (Aspartyl
 DE protease 2) (ASP 2) (ASP2) (Membrane-associated aspartic protease 2)
 DE (Memapsin-2).
 DE BACE.
 GN Mus musculus (Mouse).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclirognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=20002972; PubMed=10531052;
 RA Vassar R., Bennett B.D., Babu-Khan S., Kahn S., Mendiaz E.A.,
 RA Desair P., Teplow D.B., Ross S., Amarante P., Loeffler R., Luo Y.,
 RA Fisher S., Fuller J., Edenson S., Lile J., Jarosinski M.A.,
 RA Bhat A.L., Curran E., Burgess T., Louis J.-C., Collins F.,
 RA Treanor J., Rogers G., Citron M.,
 RT "Beta-secretase cleavage of Alzheimer's amyloid precursor protein by
 RT the transmembrane aspartic protease BACE";
 RL Science 286:735-741(1999).
 RN [2]
 RP REVISIONS TO 6 AND 81-87.
 RA Bennett B.D., Vassar R., Citron M.,
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20051170; PubMed=10591213;
 RA Yan R., Bienkowski M.J., Shuck M.E., Miao H., Tory M.C., Pauley A.M.,
 RA Brashler J.R., Strattan N.C., Mathews W.R., Buhl A.E., Carter D.B.,
 RA Tomasselli A.G., Parodi L.A., Heinrichson R.L., Garney M.E.;
 RT "Membrane-anchored aspartyl protease with Alzheimer's disease
 RT beta-secretase activity";
 RL Nature 402:533-537(1999).
 CC -1- FUNCTION: RESPONSIBLE FOR THE PROTEOLYTIC PROCESSING OF THE
 CC AMYLOID PRECURSOR PROTEIN (APP). CLEAVES AT THE AMINO TERMINUS OF
 CC THE A-BETA PEPTIDE SEQUENCE, BETWEEN RESIDUES 671 AND 672 OF APP,
 CC LEADS TO THE GENERATION AND EXTRACELLULAR RELEASE OF BETA-CLEAVED
 CC SOLUBLE APP, AND A CORRESPONDING CELL-ASSOCIATED CARBOXY-TERMINAL
 CC FRAGMENT WHICH IS LATER RELEASED BY GAMMA-SECRETASE (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: BRAIN.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
 CC -----
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DR EMBL/AF190726; AAF04143.2; -
 DR EMBL/AF200346; AAF17082.1; -
 DR HSSP; P56272; 1AMS.
 DR MEROPS; A01.004; -
 DR MGD; MGI:1346542; Bace.
 DR InterPro; IPR001461; Aspproteaseal.
 DR InterPro; IPR001969; Aspprotease_site.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPsin.
 DR PROSITE; PS00141; ASP PROTEASE; 1.
 KM Hydrolyase; Aspartyl protease; Glycoprotein; Zymogen; Transmembrane;
 KM Signal.
 FT SIGNAL 1 21
 FT PROPEP 22 45
 FT CHAIN 46 501
 FT DOMAIN 22 457
 FT TRANSMEM 458 478
 FT DOMAIN 479 501
 FT ACT_SITE 93 93
 FT ACT_SITE 289 289
 FT DISULFID 216 420
 FT DISULFID 278 443
 FT DISULFID 330 380
 FT CARBOHYD 153 153
 FT CARBOHYD 172 172
 FT CARBOHYD 223 223
 FT CARBOHYD 354 354
 SQ SEQUENCE 501 AA; 55747 MW; C085A0131458474E CRC64;
 Query Match 3.0%; Score 12; DB 1; Length 501;
 Best Local Similarity 100.0%; Pred. No. 0.00037;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 ILVDTGSSNFAY 56
 DB 90 ILVDTGSSNFAY 101

RESULT 4

BACE_RAT ID BACE_RAT STANDARD; PRT; 501 AA.

AC P56819;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Beta-secretase precursor (EC 3.4.23.-) (Beta-site APP cleaving enzyme)
 DE Beta-site amyloid precursor protein cleaving enzyme (Aspartyl
 protease 2) (ASP2) (Membrane-associated aspartic protease 2)
 DE (Memapsin-2).
 GN BACE.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]

SEQUENCE FROM N.A.

RA MEDLINE=20002972; PubMed=10531052;
 RA Vaasas R., Bennett B.D., Babu-Khan S., Kahn S., Mendiaz E.A.,
 RA Denis P., Teplow D.B., Ross S., Amarante P., Loeloff R., Luo Y.,
 RA Fisher S., Fuller J., Edenson S., Lile J., Jarosinski M.A.,
 RA Biere A.L., Curran E., Burgess T., Louis J.-C., Collins F.,
 RA Treanor J., Rogers G., Citron M.,
 RA "Beta-secretase cleavage of Alzheimer's amyloid precursor protein by
 the transmembrane aspartic protease BACE.";
 RL Science 286:735-741(1999).

-1- FUNCTION: RESPONSIBLE FOR THE PROTEOLYTIC PROCESSING OF THE

CC AMYLOID PRECURSOR PROTEIN (APP). CLEAVES AT THE AMINO TERMINUS OF
 CC THE A-BETA PEPTIDE SEQUENCE, BETWEEN RESIDUES 671 AND 672 OF APP,
 CC LEADS TO THE GENERATION AND EXTRACELLULAR RELEASE OF BETA-CLEAVED
 CC SOLUBLE APP, AND A CORRESPONDING CELL-ASSOCIATED CARBOXY-TERMINAL
 CC FRAGMENT WHICH IS LATER RELEASED BY GAMMA-SECRETASE (BY
 CC SIMILARITY).

-1- SUBCELLULAR LOCATION: Type I membrane protein.

-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.

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DR EMBL: AF190727; AAF04144.1; -
 DR HSP: P33329; IYPS.

DR MEROPS: A01.004; -

DR InterPro: IPR001461; AspproteaseA1.
 DR InterPro: IPR001669; Aspprotease_site.

DR Pfam: PF00026; asp.1.

DR PRINTS: PR00792; PEPSPIN.

DR PROSITE: PS00141; ASP_PROTEASE; 1.

KW Hydroxylase; Aspartyl protease; Glycoprotein; Zymogen; Transmembrane;
 KW Signal.

FT SIGNAL 1 21 POTENTIAL.
 FT PROPEP 22 45 POTENTIAL.
 FT CHAIN 46 501 BETA-SECRETASE.
 FT DOMAIN 22 457 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 458 478 POTENTIAL.
 FT DOMAIN 479 501 CYTOPLASMIC (POTENTIAL).
 FT ACT_SITE 93 93 BY SIMILARITY.
 FT ACT_SITE 289 289 BY SIMILARITY.
 FT DISULFID 216 420 BY SIMILARITY.
 FT DISULFID 278 443 BY SIMILARITY.
 FT CARBOHYD 153 153 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 172 172 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 223 223 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 354 354 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 501 AA; 55806 MW; 24B445BC8B87DE3 CRC64;

Query Match 3.0%; Score 12; DB 1; Length 501;

Best Local Similarity 100.0%; Pred. No. 0.00037;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 ILVDTGSSNFAY 56
 DB 90 ILVDTGSSNFAY 101

RESULT 5

LRP_HAEIN ID LRP_HAEIN STANDARD; PRT; 166 AA.

AC P45265;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Leucine-responsive regulatory protein.
 DE LRP OR H11596.
 GN LRP OR H11596.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellales;
 OC Haemophilus.
 OX NCBI_TaxId=727;
 RN [1]

SEQUENCE FROM N.A.

RA STRAIN=Rd / KW20 / ATCC 51907;
 RA MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Wetback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RA "Whole-genome random sequencing and assembly of Haemophilus influenzae
 RA Rd.";
 RL Science 269:496-512(1995).

-1- FUNCTION: MEDIATES A GLOBAL RESPONSE TO LEUCINE. EXOGENOUS LEUCINE

CC AFFECTS THE EXPRESSION OF A NUMBER OF DIFFERENT OPERONS. LRP
 CC MEDIATES THIS EFFECT FOR AT LEAST SOME OF THESE OPERONS
 CC (BY SIMILARITY).

-1- SUBUNIT: HOMODIMER (BY SIMILARITY).

-1- SIMILARITY: BELONGS TO THE ASNC FAMILY OF TRANSCRIPTIONAL

REGULATORS.

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DR EMBL: U32833; AAC23241.1; -

DR TIGR: H11596; -

DR InterPro: IPR000485; ASNC trans. reg.

DR Pfam: PF01037; ASNC trans_reg.1.

DR PRINTS: PR00033; HTHASNC.

DR SMART: SM00344; HTH ASNC; 1.

DR PROSITE: PS00519; HTH ASNC FAMILY; 1.

KW DNA-binding; Transcription regulation; Activator; Complete proteome.

FT DNA_BIND 35 54 H-T-H MOTIF (POTENTIAL).
 FT SEQUENCE 166 AA; 18910 MW; 22C0F1B78B110CEB CRC64;

Query Match

Best Local Similarity 100.0%; Score 8; DB 1; Length 166;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 243 GTTLRLRP 250
Db 136 GTTLRLRP 143

RESULT 6
601M PROMI STANDARD; PRT; 237 AA.
AC P22833;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 60 kDa inner-membrane protein homolog (Fragment).
OS Proteus mirabilis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Proteus.
OX NCBI_TaxID=584;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LM1509;
RX MEDLINE=91033012; PubMed=2172087;
RA Shovgaard O.;
RT "Nucleotide sequence of a Proteus mirabilis DNA fragment homologous
RT to the 60K-rmpA-rmpH-dnaA-dnaN-recF-gyrB region of Escherichia
RT coli."
RL Gene 93:27-34(1990).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Probable).
CC -1- SIMILARITY: BELONGS TO THE OXA1 / 60 KDA IMP FAMILY.
CC -----
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CC -----
DR EMBL; M58352; AAA83954.1; -
DR PIR; J00729; J00729.
KW Transmembrane; Inner membrane.
FT TRANSMEM 7 23 POTENTIAL.
FT NON TER 237 237
SQ SEQUENCE 237 AA; 26664 MW; 07FCC405B9DB3F36 CRC64;

Query Match 2.0%; Score 8; DB 1; Length 237;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 48 DTGSSNFA 55
Db 206 DTGSSNFA 213

RESULT 7
VPRT SMRVH STANDARD; PRT; 323 AA.
AC P21407;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protease (EC 3.4.23.-).
OS Squirrel monkey retrovirus (SMRV-H) (SMRV-HLB).
OC Viruses; Retroviridae; Retroviridae; Betaretrovirus.
OX NCBI_TaxID=11856;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89073750; PubMed=3201749;
RA Oda T., Ikeda S., Watanabe S., Hatsushika M., Akiyama K.,
RA Mitsuoka F.;
RT "Molecular cloning, complete nucleotide sequence, and gene structure

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RT of the provirus genome of a retrovirus produced in a human
RT lymphoblastoid cell line."
RL Virology 167:468-476(1988).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A2.
CC -1- SIMILARITY: CONTAINS 1 G-PATCH DOMAIN.
CC -----
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CC -----
DR EMBL; M23385; AAA66452.1; ALT_INIT.
DR PIR; B31827; PRLJHD.
DR HSSP; P06568; LEUW.
DR MEROPS; A02_UPW; -
DR InterPro; IPR001995; Asparticase_rtrv.
DR InterPro; IPR001969; Asparticase_site.
DR InterPro; IPR001428; DeoxyUTPase.
DR InterPro; IPR000467; G_patch.
DR Pfam; PF00077; rvp; 1.
DR Pfam; PF00692; dUTPase; 1.
DR Pfam; PF01585; G_patch; 1.
DR ProDom; PD000946; DeoxyUTPase; 1.
DR SMART; SM00443; G_patch; 1.
DR PROSITE; PS00141; ASP_PROTEASE; 1.
DR PROSITE; PS50175; ASP_PROT_RETROV; 1.
DR PROSITE; PS50174; G_PATCH; 1.
KW Hydrolyase; Aspartyl protease.
FT DOMAIN 275 321 G-PATCH.
FT ACT SITE 193 193 BY SIMILARITY.
SQ SEQUENCE 323 AA; 35126 MW; 5D6CEA38BA932786 CRC64;

Query Match 2.0%; Score 8; DB 1; Length 323;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 99 DLVTIPKG 106
Db 126 DLVTIPKG 133

RESULT 8
CARP POLTU STANDARD; PRT; 340 AA.
AC P17576;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Polyporopepsin (EC 3.4.23.29) (Aspartic proteinase).
OS Polyporus tulipiferae (Irpex lacteus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricomycotina; Polyporaceae; Polyporus.
OX NCBI_TaxID=29885;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-24.
RA Kobayashi H., Sekibata S., Shibuya H., Yoshida S., Kusakabe I.,
RA Murakami K.;
RT "Cloning and sequence analysis of cDNA for Irpex lacteus aspartic
RT proteinase."
RL Agric. Biol. Chem. 53:1927-1933(1989).
CC -1- CATALYTIC ACTIVITY: Milk clotting activity, broad specificity, but
CC fails to cleave 15-Leu-Tyr-16 or 16-Tyr-Leu-17 of insulin B
CC chain.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
CC -----
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CC EMBL; D00589; BAA00467.1; -.

DR PIR; J00057; PEIKL.

DR HSSP; P33329; 1YPS.

DR MEROPS; A01.019; -.

DR InterPro; IPR001461; AsproteaseA1.

DR InterPro; IPR001969; Asprotease_site.

DR Pfam; PF00026; asp; 1.

DR PRINTS; PR00792; PEPSTN.

DR PROSITE; PS00141; ASP_PROTEASE; 2.

KM HydroLase; Aspartyl protease; Glycoprotein.

FT ACT_SITE 32 32

FT ACT_SITE 212 212

FT CARBOHYD 192 192

FT CARBOHYD 238 238

SO SEQUENCE 340 AA; 35050 MW; 9BAF837264D42FEF CRC64;

Query Match

Best Local Similarity 100.0%; Score 8; DB 1; Length 340;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 LVDTGSSN 53

Db 30 LVDTGSSN 37

RESULT 9

EC1_SCHPO STANDARD; PRT; 365 AA.

ID EC1_SCHPO

AC Q9UT16;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Probable ethanolamine-phosphate cytidyltransferase (EC 2.7.7.14)

DE (Phosphorylethanolamine transferase) (CTP:phosphoethanolamine

DE cytidyltransferase).

GN SPAC15E1.05C.

OS Schizosaccharomyces pombe (Fission Yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomyces.

OX NCBI_TaxID=4896;

XP [1]

RP SEQUENCE FROM N.A.

RC STRAIN=972;

RX MEDLINE=21848401; PubMed=11859360;

RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

RA Brooke K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,

RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

RA Holroyd S., Hornsby T., Howarth S., Huckle E.D., Hunt S., Jagels K.,

RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeh C.,

RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,

RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

RA Shelton J., Simmonds M., Squares R., Squares S., Stevens K.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Woodward J., Voicikert G., Aert R., Robben J., Grymopiez B.,

RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

RA Gabel C., Fuchs M., Fritz C., Holzer E., Moesli D., Hilbert H.,

RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,

RA Eger P., Zimmermann W., Weiler H., Wambutt R., Purnelle B.,

RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaue V., Motier S.,

RA Galibert F., Aves S.J., Xiang Z., Hunt K., Moore K., Hurst S.M.,

RA Lucas M., Rocher M., Galliard C., Tallada V.A., Garzon A., Rhode G.,

RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Fossburg S.L.,

RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,

RA Spakovski G.V., Ussery D., Barrett B.G., Nurse P.;

RT "The genome sequence of Schizosaccharomyces pombe.";

RL Nature 415:871-880(2002).

CC -1- CATALYTIC ACTIVITY: CTP + ethanolamine phosphate = diphosphate +

CC CDP-ethanolamine.

CC -1- PATHWAY: PHOSPHOLIPID BIOSYNTHESIS; CDP-ETHANOLAMINE SYNTHESIS;

CC SECOND STEP.

CC -1- SIMILARITY: BELONGS TO THE CYTIDYLTRANSFERASE FAMILY.

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CC EMBL; AL109770; CAB52424.1; -.

DR InterPro; IPR004821; Cyt tran rel.

DR InterPro; IPR004820; Cytidyltransferase.

DR Pfam; PF01467; Cytidyltransferase; 1.

DR TIGRfams; TIGR00125; Cyt tran_rel; 2.

KM Transferase; Nucleotidyltransferase; Phospholipid biosynthesis.

FT DOMAIN 1 182

SO SEQUENCE 365 AA; 41556 MW; ACDB6A974ABB4734 CRC64;

Query Match

Best Local Similarity 100.0%; Score 8; DB 1; Length 365;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 SGTLLRL 249

Db 191 SGTLLRL 198

RESULT 10

60IM_ECOLI STANDARD; PRT; 548 AA.

ID 60IM_ECOLI

AC P25714;

DT 01-MAY-1992 (Rel. 22, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE 60 kDa inner-membrane protein.

GN YIDC OR B3705.

OS Escherichia coli.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Escherichia.

OX NCBI_TaxID=562;

XP [1]

RP SEQUENCE FROM N.A.

RC STRAIN=K12 / MG1655;

RX MEDLINE=93315143; PubMed=7686882;

RA Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.;

RT "DNA sequence and analysis of 136 kilobases of the Escherichia coli

RT genome: organizational symmetry around the origin of replication.";

RL Genomics 16:551-561(1993).

RM [2]

RP SEQUENCE OF 1-2 FROM N.A.

RX MEDLINE=86056995; PubMed=2415431;

RA Hansen F.G., Hansen E.B., Atlung T.;

RT "Physical mapping and nucleotide sequence of the rnpA gene that

RT encodes the protein component of ribonuclease P in Escherichia

RT coli.";

RL Gene 38:85-93(1985).

RM [3]

RP TOPOLOGY.

RX MEDLINE=99023968; PubMed=9804807;

RA Saeel A., Monne M., de Gier J.W., von Heijne G.;

RT "Membrane topology of the 60-kDa Oxa1p homologue from Escherichia

RT coli.";

RL J. Biol. Chem. 273:30415-30418(1998).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane

CC (Probable).

CC -1- SIMILARITY: BELONGS TO THE OXA1 / 60 KDA IMP FAMILY.

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DR EMBL; AA0328; AAA62056.1; -
 DR EMBL; AL000447; AAC76728.1; -
 DR EMBL; M1056; -; NOT ANNOTATED_CDS.
 DR EcoGene; EG1197; y1dC.
 DR InterPro; IPR01708; 60kDa innermem.
 DR Pfam; PF02096; 60KD IMP; 1.
 DR PRINTS; PR00701; 60KDINNERMP.
 KW Transmembrane; Inner membrane; Complete proteome.
 FT DOMAIN 1
 FT TRANSMEM 6
 FT DOMAIN 23
 FT TRANSMEM 342
 FT DOMAIN 343
 FT TRANSMEM 370
 FT DOMAIN 371
 FT TRANSMEM 416
 FT DOMAIN 417
 FT TRANSMEM 446
 FT DOMAIN 447
 FT TRANSMEM 463
 FT DOMAIN 464
 FT TRANSMEM 481
 FT TRANSMEM 482
 FT TRANSMEM 493
 FT DOMAIN 494
 FT TRANSMEM 510
 FT TRANSMEM 512
 FT TRANSMEM 513
 FT TRANSMEM 535
 FT DOMAIN 536
 FT TRANSMEM 548
 FT TRANSMEM 61526 MM; 95EBCSDAB4F2FCFB CRC64;
 SQ SEQUENCE

Query Match 2.0%; Score 8; DB 1; Length 548;
 Best Local Similarity 100.0%; Prod. No. 5.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 DTGSSNFA 55
 |||||
 Db 207 DTGSSNFA 214

RESULT 11
 DNMT_MOUSE STANDARD; PRT; 1620 AA.
 ID DNMT_MOUSE
 AC P13864; P97413; O90X6; O9CS6;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE DNA (cytosine-5-methyltransferase 1 (EC 2.1.1.37) (Dnmt1) (DNA
 DE methyltransferase Mnu1) (DNA MTase Mnu1) (MCM1) (Met-1).
 GN DNMT1 OR DNMT OR UIM OR MET1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=89094873; PubMed=3210246;
 RA Bestor T.H., Laudano A., Mattaliano R., Ingram V.,
 RT "Cloning and sequencing of a cDNA encoding DNA methyltransferase of
 RT mouse cells. The carboxyl-terminal domain of the mammalian enzymes is
 RT related to bacterial restriction methyltransferases.";
 RL J. Mol. Biol. 203:971-983 (1988).
 RN [2]
 RP REVISIONS TO N-TERMINUS.
 RC TISSUE=Embryo;
 RX MEDLINE=97094871; PubMed=8940105;
 RA Yoder J.A., Yen R.-W.C., Vartino P.M., Bestor T.H., Baylín S.B.;
 RT "New 5' regions of the murine and human genes for DNA (cytosine-5)-
 RT methyltransferase.";
 RL J. Biol. Chem. 271:31092-31097 (1996).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX STRAIN=C57BL/6; TISSUE=Skeletal muscle;

RX MEDLINE=20515133; PubMed=11063128;
 RA Aguirre-Arteaga A.M., Grunewald I., Cardoso M.C., Leonhardt H.;
 RT "Expression of an alternative Dnmt1 isoform during muscle
 RT differentiation.";
 RL Cell Growth Differ. 11:551-559 (2000).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN=C57BL/6;
 RX MEDLINE=20181859; PubMed=10715201;
 RA Margot J.B., Aguirre-Arteaga A.M., Di Giacomo B.V., Pradhan S.,
 RA Roberts R.J., Cardoso M.C., Leonhardt H.;
 RT "Structure and function of the mouse DNA methyltransferase gene: Dnmt1
 RT shows a tripartite structure.";
 RL J. Mol. Biol. 297:293-300 (2000).
 RN [5]
 RP SEQUENCE OF 1-127 AND 119-1619 FROM N.A. (ISOFORMS 1 AND 2).
 RX MEDLINE=98119729; PubMed=9449671;
 RA Mertine C., Yoder J.A., Taketo T., Laird D.W., Trasler J.M.,
 RA Bestor T.H.;
 RT "Sex-specific exons control DNA methyltransferase in mammalian germ
 RT cells.";
 RL Development 125:889-897 (1998).
 RN [6]
 RP SEQUENCE OF 1-144 FROM N.A. (ISOFORMS 1 AND 2), AND SEQUENCE OF 3-6.
 RC STRAIN=129/Sv, and BALB/c; TISSUE=Embryonic stem cells;
 RX MEDLINE=99047652; PubMed=9830015;
 RA Gaudet F., Talbot D., Leonhardt H., Jaenisch R.;
 RT "A short DNA methyltransferase isoform restores methylation in vivo.";
 RL J. Biol. Chem. 273:32725-32729 (1998).
 RN [7]
 RP SEQUENCE OF 1-119 FROM N.A. (ISOFORM 1).
 RC STRAIN=129/Sv; TISSUE=Embryonic stem cells, and Kidney;
 RX MEDLINE=97075093; PubMed=8917520;
 RA Tucker K.L., Talbot D., Lee M.A., Leonhardt H., Jaenisch R.;
 RT "Complementation of methylation deficiency in embryonic stem cells by
 RT a DNA methyltransferase minigene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:12920-12925 (1996).
 RN [8]
 RP SEQUENCE OF 1-272 FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schiraldi L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Boffelli D., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bull C., Fletcher C., Fujita K., Gariboldi M.,
 RA Guettich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohanski S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690 (2001).
 RN [9]
 RP PHOSPHORYLATION OF SER-515, AND MASS SPECTROMETRY.
 RC TISSUE=Erythrocytes;
 RX MEDLINE=97362284; PubMed=9211941;
 RA Gluckman J.F., Pavlovich J.G., Reich N.O.;
 RT "Peptide mapping of the murine DNA methyltransferase reveals a major
 RT phosphorylation site and the start of translation.";
 RL J. Biol. Chem. 272:17851-17857 (1997).
 RN [10]
 RP INTERACTION WITH HDAC1.
 RX MEDLINE=20082816; PubMed=10615135;
 RA Fuks F., Burgers W.A., Brehm A., Hughes-Davies L., Kouzarides T.;

RT "DNA methyltransferase Dnmt1 associates with histone deacetylase
 RT activity.";
 RL Nat. Genet. 24:88-91(2000).
 RP [11]
 RX INTERACTIONS WITH HDAC2 AND DNAP1.
 RX MEDLINE=20347709; PubMed=10888872;
 RA Rountree M.R., Bachman K.E., Baylín S.B.;
 RT "DNMT1 binds HDAC2 and a new co-repressor, DNAP1, to form a complex at
 RT replication foci.";
 RL Nat. Genet. 25:269-277(2000).
 RP [12]
 RX FUNCTION AND SUBCELLULAR LOCATION.
 RX MEDLINE=21185930; PubMed=11290321;
 RA Howell C.Y., Bestor T.H., Ding F., Latham K.E., Mertineit C.,
 RA Trasler J.M., Chaillet J.R.;
 RT "Genomic imprinting disrupted by a maternal effect mutation in the
 RT Dnmt1 gene.";
 RL Cell 104:829-838(2001).
 RP [13]
 RX ALLOSTERIC ACTIVATION.
 RX MEDLINE=21293215; PubMed=11399089;
 RA Patem M., Hermann A., Pradhan S., Jeltsch A.;
 RT "The activity of the murine DNA methyltransferase Dnmt1 is controlled
 RT by interaction of the catalytic domain with the N-terminal part of
 RT the enzyme leading to an allosteric activation of the enzyme after
 RT binding to methylated DNA.";
 RL J. Mol. Biol. 309:1189-1199(2001).
 RP [14]
 RX FUNCTION: Methylates CpG residues. Preferentially methylates
 CC hemimethylated DNA. It is responsible for maintaining methylation
 CC patterns established in development. Isoform 2, in oocytes, may
 CC provide maintenance methyltransferase activity specifically at
 CC imprinted loci during the fourth embryonic S phase. Mediates
 CC transcriptional repression by direct binding to HDAC2.
 CC CATALYTIC ACTIVITY: S-adenosyl-L-methionine + DNA = S-adenosyl-L-
 CC homocysteine + DNA containing 5-methylcytosine.
 CC ENZYME REGULATION: Allosterically regulated. The binding of 5-
 CC methylcytosine-containing DNA to the N-terminal parts of Dnmt1
 CC causes an allosteric activation of the catalytic domain by a
 CC direct interaction of its Zn-binding domain with the catalytic
 CC domain.
 CC SUBUNIT: Interacts with HDAC1 and with PCNA. Forms a complex with
 CC DNAP1 and HDAC2, with direct interaction.
 CC SUBCELLULAR LOCATION: Nuclear; it is nucleoplasmic through most of
 CC the cell cycle and associates with replication foci during S-
 CC phase. In germ cells: spermatogonia, preleptotene and leptotene
 CC spermatocytes all express high levels of nuclear protein, while
 CC the protein is not detected in pachytene spermatocytes, despite
 CC the fact they expressed high levels of mRNA. In females, the
 CC protein is not detected in non-growing oocytes, in contrast to the
 CC detectable in nuclei but accumulates to very high levels first
 CC throughout the cytoplasm. At the time of ovulation, all the
 CC protein is cytoplasmic and is actively associated with the oocyte
 CC cortex. After fecundation, in the preimplantation embryo, the
 CC protein remains cytoplasmic and after implantation, it is
 CC exclusively nuclear in all tissue types. Isoform 2 is sequestered
 CC in the cytoplasm of maturing oocytes and of preimplantation
 CC embryos, except for the 8-cell stage, while isoform 1 is
 CC exclusively nuclear.
 CC ALTERNATIVE PRODUCTS: 2 isoforms, 1/long form (shown here) and
 CC 2/short form; are produced by alternative splicing.
 CC TISSUE SPECIFICITY: Isoform 1 is expressed in embryonic stem cells
 CC and in somatic tissues. Isoform 2 is expressed in oocytes,
 CC preimplantation embryos, testis and in skeletal muscle during
 CC myogenesis.
 CC DEVELOPMENTAL STAGE: In germ cells, it is present at high levels
 CC in spermatogonia and spermatocytes until the pachytene stage,
 CC where it falls to undetectable levels. The transient drop at the
 CC pachytene stage coincides with the disappearance of the 5.2 kb
 CC mRNA and the accumulation of a larger 6.0 kb mRNA. Oocytes
 CC accumulate very large amounts of Dnmt1 protein during the growth
 CC phase.
 CC MISCELLANEOUS: There are three 5' exons, one specific to the

CC oocyte (1c), one specific to the pachytene spermatocyte and also
 CC found in skeletal muscle (1b) and one found in somatic cells (1a).
 CC Three different mRNAs can be produced which give rise to two
 CC different translation products: isoform 1 (mRNAs-1a) and isoform 2
 CC (mRNAs-1b or -1c).
 CC -1- SIMILARITY: BELONGS TO THE C5-METHYLTTRANSFERASE FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 BAH DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 CXXC-TYPE ZINC FINGER.
 CC -----
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 CC DR EMBL; X14805; CAA32910.1; -;
 CC DR EMBL; AF175432; AAF97695.1; -;
 CC DR EMBL; AF162282; AAF19352.1; -;
 CC DR EMBL; AF175431; AAF60965.1; -;
 CC DR EMBL; AF175412; AAF60965.1; JOINED.
 CC DR EMBL; AF175413; AAF60965.1; JOINED.
 CC -----
 CC Query Match 2.0%; Score 8; DB 1; Length 1620;
 CC Best local Similarity 100.0%; Pred. No. 14;
 CC Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC -----
 CC Qy 4 PALSPAG 11
 CC |||||
 CC Db 11 PALSPAG 18
 CC -----
 CC RESULT 12
 CC ID DNMT1_RAT STANDARD; PRT; 1622 AA.
 CC AC G92330; G9WTX3; P70487; G9WU57; G9R252;
 CC DT 15-JUN-2002 (Rel. 41, Created)
 CC DT 15-JUN-2002 (Rel. 41, Last sequence update)
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
 CC DE DNA (cytosine-5)-methyltransferase 1 (EC 2.1.1.37) (Dnmt1) (DNA
 CC methyltransferase I) (DNA MTase RnoIP) (MCRTP) (M.RnoIP).
 CC GN DNMT1.
 CC OS Rattus norvegicus (Rat).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC OX NCBI_TaxID=10116;
 CC RN [1]
 CC RP SEQUENCE FROM N.A. (ISOFORM 0).
 CC RC SPRAIN=Sprague-Dawley; TISSUE=Brain, and Placenta;
 CC RX MEDLINE=99097263; PubMed=9878564;
 CC RA Kimura H., Takeda T., Tanaka S., Ogawa T., Shiota K.;
 CC RT "Expression of rat DNA (cytosine-5) methyltransferase (DNA MTase) in
 CC RT rodent trophoblast giant cells: molecular cloning and characterization
 CC RT of rat DNA MTase.";
 CC RL Biochem. Biophys. Res. Commun. 253:495-501(1998).
 CC RN [2]
 CC RP SEQUENCE OF 1-144 FROM N.A. (ISOFORMS 0 AND 8).
 CC RC TISSUE=Brain;
 CC RA Deng J., Szyf M.;
 CC RT "Multiple N-terminal isoforms of DNA (cytosine-5)-methyltransferase
 CC RT in vivo.";
 CC RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 CC RN [3]
 CC RP SEQUENCE OF 17-356 FROM N.A., AND IN VITRO BINDING TO ANNEXIN V.
 CC RC SPRAIN=Wistar; TISSUE=Brain;
 CC RX MEDLINE=96301899; PubMed=8667030;
 CC RA Ohsawa K., Imai Y., Ito D., Kohsaka S.;
 CC RT "Molecular cloning and characterization of annexin V-binding proteins
 CC RT with highly hydrophilic peptide structure.";
 CC RL J. Neurochem. 67:89-97(1996).
 CC RN [4]
 CC RP SEQUENCE OF 1169-1517 FROM N.A. (ISOFORMS 0; 1; 2; 3; 4; 5; 6 AND 7).

SQ SEQUENCE 126 AA; 13270 MW; 59610E786B9C4F60 CRC64;
 Query Match 1.7%; Score 7; DB 1; Length 126;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 333 RFGISPS 339
 |||||
 Db 110 RFGISPS 116

RESULT 14
 EX3 HAEIN
 ID EX3 HAEIN STANDARD; PRT; 267 AA.
 AC P43318;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Exodeoxyribonuclease III (EC 3.1.11.2) (Exonuclease III) (EXO III).
 GN XTHA OR H10041.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Haemophilus.
 NC NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Rd / KW20 / ATCC 51907;
 RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 Scott J.D., Shiley R., Liu L.-I., Glodek A., Kelley J.M.,
 Widman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 Fine L.D., Fritchman J.L., Fuhmann J.L., Geoghagen N.S.M.,
 Ghem C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 Venter J.C.;
 RA "Whole-genome random sequencing and assembly of Haemophilus influenzae
 Rd.";
 RT Science 269:496-512 (1995).
 CC -1- FUNCTION: MAJOR APURINIC-APYRIMIDINIC ENDONUCLEASE OF E. COLI. IT
 REMOVES THE DAMAGED DNA AT CYTOSINES AND GUANINES BY CLEAVING ON
 CC THE 3' SIDE OF THE AP SITE BY A BETA-ELIMINATION REACTION
 CC (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Degradation of double-stranded DNA. It acts
 CC progressively in a 3'-to 5'-direction, releasing nucleoside 5'-
 CC phosphates.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE AP/EXO FAMILY OF DNA REPAIR ENZYMES.
 CC -----
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 CC -----
 CC EMBL: U32689; AAC21719.1; -.
 DR HSSP: P09030; IAKO.
 DR TIGR: H10041; -.
 DR InterPro: IPR000097; Apendonclse1.
 DR InterPro: IPR004442; Exonase III.
 DR InterPro: IPR004808; ExoIII xth.
 DR InterPro: IPR005135; Exo_endo_phos.
 DR Pfam: PF03372; Exo_endo_phos; 1.
 DR TIGRFAMs: TIGR00195; exoDnase_III; 1.
 DR TIGRFAMs: TIGR00633; xth; 1.
 DR PROSITE: PS00726; AP_NUCLEASE_F1_1; 1.
 DR PROSITE: PS00727; AP_NUCLEASE_F1_2; 1.
 DR PROSITE: PS00728; AP_NUCLEASE_F1_3; 1.
 KM Hydrolyase; Exonuclease; DNA repair; Complete proteome.
 FT METAL 34 MAGNESIUM OR MANGANESE (BY SIMILARITY).

FT ACT_SITE 259 259 GENERAL BASE (BY SIMILARITY).
 SQ SEQUENCE 267 AA; 31025 MW; 6B3ADE465A1E347C CRC64;
 Query Match 1.7%; Score 7; DB 1; Length 267;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 76 YRSKGF 82
 |||||
 Db 215 YRSKGF 221

RESULT 15
 EX3 ECOLI
 ID EX3 ECOLI STANDARD; PRT; 268 AA.
 AC P09030;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Exodeoxyribonuclease III (EC 3.1.11.2) (Exonuclease III) (EXO III) (AP
 DE endonuclease VI).
 GN XTHA OR XTH OR B1749.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 NC NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=8908066; PubMed=3049539;
 RA Saporito S.M., Smith-White B.J., Cunningham R.P.;
 RT "Nucleotide sequence of the xth gene of Escherichia coli K-12.";
 RL J. Bacteriol. 170:4542-4547 (1988).
 CC [2]
 CC SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RA Wurst H., Hoheisel J.D., Pohl F.M.;
 RL Submitted (NOV-1988) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=9742617; PubMed=9278503;
 RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glaesner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474 (1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97251357; PubMed=9097039;
 RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
 RA Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M.,
 RA Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,
 RA Motomura K., Nakade S., Nakamura Y., Nishimoto H., Nishio Y.,
 RA Oshima T., Saito N., Sampei G., Seki Y., Sivasubraman S.,
 RA Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,
 RA Yamamoto Y., Horichi T.;
 RT "A 570-Kb DNA sequence of the Escherichia coli K-12 genome
 RT corresponding to the 28.0-40.1 min region on the linkage map.";
 RL DNA Res. 3:363-377 (1996).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RX MEDLINE=95191690; PubMed=7885481;
 RA Mol C.D., Kuo C.-F., Thayer M.W., Cunningham R.P., Tainer J.A.;
 RT "Structure and function of the multifunctional DNA-repair enzyme
 RT exonuclease III.";
 RL Nature 374:381-386 (1995).
 RN [6]
 RP CHARACTERIZATION.
 RX MEDLINE=97105903; PubMed=8948651;
 RA Shida T., Noda M., Sekiguchi J.;

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RT "Cleavage of single- and double-stranded DNAs containing an abasic
RT residue by Escherichia coli exonuclease III (Ap endonuclease VI).";
RL Nucleic Acids Res. 24:4572-4576(1996).
CC -!- FUNCTION: MAJOR APURINIC-APYRIMIDINIC ENDONUCLEASE OF E. COLI. IT
CC REMOVES THE DAMAGED DNA AT CYTOSINES AND GUANINES BY CLEAVING ON
CC THE 3' SIDE OF THE AP SITE BY A BETA-ELIMINATION REACTION. IT
CC EXHIBITS 3',5'-EXONUCLEASE, 3'-PHOSPHOMONESTERASE, 3'-REPAIR
CC DIESTERASE AND RIBONUCLEASE H ACTIVITIES.
CC -!- CATALYTIC ACTIVITY: Degradation of double-stranded DNA. It acts
CC progressively in a 3'-to 5'-direction, releasing nucleoside 5'-
CC phosphates.
CC -!- SUBUNIT: MONOMER.
CC -!- SIMILARITY: BELONGS TO THE AP/EXO A FAMILY OF DNA REPAIR ENZYMES.
CC -----
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DR EMBL; X13002; CAA31424.1; -.
DR EMBL; M22592; AAA24767.1; -.
DR EMBL; AE000270; AAC74819.1; -.
DR EMBL; D90818; BAA15540.1; -.
DR EMBL; D90819; BAA15544.1; -.
DR PIR; A11839; NCECX3.
DR PIR; S03102; S03102.
DR PDB; 1AKO; 20-AUG-97.
DR SWISS-2DPAGE; P09030; COLI.
DR ECO2DBASE; G028.2; 6TH EDITION.
DR EcoGene; EG11073; xChA.
DR InterPro; IPR000097; Apendonc1se1.
DR InterPro; IPR004442; ExoDNase_III.
DR InterPro; IPR004608; ExoIII_xCh.
DR InterPro; IPR005135; Exo_endo_phos.
DR Pfam; PF03372; Exo_endo_phos; 1.
DR TIGRFAMs; TIGR00195; exoDNase_III; 1.
DR TIGRFAMs; TIGR00633; xCh; 1.
DR PROSITE; PS00726; AP_NUCLEASE_F1_1; 1.
DR PROSITE; PS00727; AP_NUCLEASE_F1_2; 1.
DR PROSITE; PS00728; AP_NUCLEASE_F1_3; 1.
KW Hydrolase; Nuclease; Exonuclease; DNA repair; Multifunctional enzyme;
KW 3D-structure; Complete proteome.
FT METAL 34 34 MAGNESIUM OR MANGANESE.
FT SITE 153 153 IMPORTANT FOR SUBSTRATE RECOGNITION.
FT ACT_SITE 259 259 GENERAL BASE.
FT CONFLICT 49 50 KL -> NV (IN REF. 1).
SQ SEQUENCE 268 AA; 30969 MW; 09E0E263DCF38634 CRC64;

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Query Match 1.7%; Score 7; DB 1; Length 268;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 76 YRSKGF 82
| | | | |
Db 215 YRSKGF 221

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Search completed: April 1, 2003, 11:51:46
Job time : 28 secs

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OM protein - protein search, using sw model

Run on: April 1, 2003, 11:49:45 ; Search time 88 Seconds

(without alignments)
950.626 Million cell updates/sec

Title: US-09-668-314C-2_COPY_63_468

Perfect score: 406
Sequence: 1 ALEPALASPAGANFLAMVD.....STEDVASNCVPAQSLSEPLL 406

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacterioplasmid:*
17: sp_archaeoplasmid:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	389	95.8	439	4	Q9H2V8
2	316	77.8	396	4	Q9NZL1
3	266	65.5	468	4	Q9NZL2
4	59	14.5	514	11	Q9JUL8
5	38	9.4	255	11	Q9RIP7
6	12	3.0	432	4	Q9BYB9
7	12	3.0	457	4	Q9BYC0
8	12	3.0	476	4	Q9BYC1
9	12	3.0	532	4	Q9YUS1
10	9	2.2	213	4	Q9PUD2
11	9	2.2	266	11	Q9CUD5
12	8	2.0	96	10	Q9M8Y6
13	8	2.0	159	16	Q9CP14
14	8	2.0	241	16	Q9LOR0
15	8	2.0	244	5	Q8WQY9
16	8	2.0	254	16	Q983Z3

17	8	2.0	287	10	Q9SH24	Q9SH24 arabidopsis
18	8	2.0	309	16	Q9RXF5	Q9RXF5 deinococcus
19	8	2.0	313	16	Q8Z5W7	Q8Z5W7 salmoneilla
20	8	2.0	327	3	P78849	P78849 schizosacch
21	8	2.0	333	16	Q8ZNV8	Q8ZNV8 salmoneilla
22	8	2.0	341	6	Q46495	Q46495 bos taurus
23	8	2.0	342	2	Q68868	Q68868 synechococc
24	8	2.0	352	17	Q9YER7	Q9YER7 aeropyrum p
25	8	2.0	366	10	Q8S1T9	Q8S1T9 oryza sativ
26	8	2.0	449	10	Q9S9K4	Q9S9K4 arabidopsis
27	8	2.0	451	10	Q9LGF1	Q9LGF1 oryza sativ
28	8	2.0	471	11	Q91XR7	Q91XR7 rattus norv
29	8	2.0	472	4	Q96PQ4	Q96PQ4 homo sapien
30	8	2.0	472	4	Q8WUX1	Q8WUX1 homo sapien
31	8	2.0	473	5	Q9VEE0	Q9VEE0 drosophila
32	8	2.0	474	5	Q8SQZ9	Q8SQZ9 encephalito
33	8	2.0	476	4	Q9LUT8	Q9LUT8 homo sapien
34	8	2.0	482	2	Q8RMG9	Q8RMG9 acetobacter
35	8	2.0	504	4	Q996Z4	Q996Z4 homo sapien
36	8	2.0	504	11	Q9JH29	Q9JH29 rattus norv
37	8	2.0	505	11	Q9DCP2	Q9DCP2 mus musculu
38	8	2.0	505	11	Q9DIL8	Q9DIL8 mus musculu
39	8	2.0	548	16	Q8Z2N7	Q8Z2N7 salmoneilla
40	8	2.0	548	16	Q8XB42	Q8XB42 escherichia
41	8	2.0	548	16	Q8ZKY4	Q8ZKY4 salmoneilla
42	8	2.0	592	5	Q9VTS5	Q9VTS5 drosophila
43	8	2.0	612	5	Q8T0E6	Q8T0E6 drosophila
44	8	2.0	637	10	Q8Z612	Q8Z612 arabidopsis
45	8	2.0	671	17	Q8TUA8	Q8TUA8 methanogarc
46	8	2.0	682	16	Q8XVM2	Q8XVM2 ralsonia s
47	8	2.0	904	16	Q9HUM7	Q9HUM7 pseudomonas
48	8	2.0	953	3	Q8X027	Q8X027 neurospora
49	8	1.7	32	16	Q98AB6	Q98AB6 rhizobium 1
50	8	1.7	84	17	Q8TMB3	Q8TMB3 methanopyru
51	8	1.7	85	2	Q9AP00	Q9AP00 burkholderi
52	8	1.7	86	2	Q9WKF8	Q9WKF8 rhodococcus
53	8	1.7	86	8	Q9S786	Q9S786 diatrocica
54	8	1.7	86	8	Q9S778	Q9S778 diatrocica
55	8	1.7	86	8	Q9S787	Q9S787 diatrocica
56	8	1.7	92	16	Q98JG3	Q98JG3 rhizobium 1
57	8	1.7	103	2	Q9ZEH7	Q9ZEH7 enterococcu
58	8	1.7	107	3	Q8XIT7	Q8XIT7 pholiota na
59	8	1.7	112	5	Q9VLE8	Q9VLE8 drosophila
60	8	1.7	115	2	P73231	P73231 rhodospirill
61	8	1.7	119	11	Q9OXI4	Q9OXI4 rattus norv
62	8	1.7	123	15	Q9YV02	Q9YV02 human immun
63	8	1.7	123	15	Q9YU25	Q9YU25 human immun
64	8	1.7	131	16	Q98QNI	Q98QNI mycoplasma
65	8	1.7	141	16	Q9KCU3	Q9KCU3 bacillus ha
66	8	1.7	150	16	Q8XKV6	Q8XKV6 clostridium
67	8	1.7	160	16	Q98K01	Q98K01 rhizobium 1
68	8	1.7	180	16	P71704	P71704 mycobacteri
69	8	1.7	187	8	Q03012	Q03012 mollugo ver
70	8	1.7	197	2	Q9WM61	Q9WM61 streptococ
71	8	1.7	206	10	Q9LSK3	Q9LSK3 arabidopsis
72	8	1.7	206	10	Q9LSK2	Q9LSK2 arabidopsis
73	8	1.7	206	16	Q8UB19	Q8UB19 agrobacteri
74	8	1.7	210	2	Q9XCJ9	Q9XCJ9 streptococ
75	8	1.7	218	2	Q9XCK5	Q9XCK5 streptococ
76	8	1.7	235	2	Q9XCK9	Q9XCK9 streptococ
77	8	1.7	235	16	Q9GRU0	Q9GRU0 chlamydia p
78	8	1.7	235	16	Q9Z742	Q9Z742 chlamydia p
79	8	1.7	240	11	Q9DIA3	Q9DIA3 mus musculu
80	8	1.7	241	16	Q9PIK3	Q9PIK3 chlamydia m
81	8	1.7	241	16	Q84728	Q84728 chlamydia t
82	8	1.7	244	16	Q8YUHO	Q8YUHO bruceella m
83	8	1.7	249	2	Q8VWJ4	Q8VWJ4 pseudomonas
84	8	1.7	253	2	Q9L4V7	Q9L4V7 streptococ
85	8	1.7	253	5	Q61709	Q61709 caenorhabdi
86	8	1.7	254	16	Q9A3X5	Q9A3X5 caulobacter
87	8	1.7	255	10	Q43406	Q43406 brasica ol
88	8	1.7	257	2	Q69217	Q69217 azotobacter
89	8	1.7	264	2	Q9JRS5	Q9JRS5 actinobacti

90	1.7	267	2	005382	005382 actinobacil	163	7	1.7	387	6	09GMV8	09gmY8 sorex ungui
91	1.7	267	2	066261	066261 actinobacil	164	7	1.7	387	6	046496	046496 bos taurus
92	1.7	267	5	09VHH4	09vhh4 drosophila	165	7	1.7	388	6	046524	046524 felis silve
93	1.7	267	16	09HMB2	09hmb2 pseudomonas	166	7	1.7	389	3	09Y775	09Y775 candida tro
94	1.7	267	16	09CMW2	09cmw2 pasteurella	167	7	1.7	389	6	09MYK3	09myK3 sus scrofa
95	1.7	268	16	08XD5	08xd5 escherichia	168	7	1.7	389	6	09MYK2	09myK2 sus scrofa
96	1.7	269	4	09EFW5	09efw5 mycoplasma	169	7	1.7	390	6	09GK10	09gk10 camelus dro
97	1.7	269	4	09UKP1	09ukp1 homo sapien	170	7	1.7	396	13	093428	093428 chionodraco
98	1.7	270	16	P1638	P1638 mycobacteri	171	7	1.7	398	16	09RW70	09rw70 deinococcus
99	1.7	270	16	09F509	09f509 vibrio chol	172	7	1.7	399	13	093458	093458 podarcus si
100	1.7	272	2	09RH18	09rh18 actinobacil	173	7	1.7	407	17	09HJF2	09hjf2 thermoplaem
101	1.7	281	2	093045	093045 clostridium	174	7	1.7	413	3	014413	014413 pichia angu
102	1.7	289	11	08R256	08r256 mus musculu	175	7	1.7	413	16	08RG42	08rg42 fusobacteri
103	1.7	289	12	09QAI8	09qai8 murid herpe	176	7	1.7	416	16	0987L1	0987L1 rhizobium i
104	1.7	291	16	09KMY5	09kmy5 vibrio chol	177	7	1.7	416	16	08ZHB5	08zhb5 yersinia pe
105	1.7	302	16	052882	052882 rhizobium m	178	7	1.7	419	10	094HM8	094hm8 oryza sativ
106	1.7	306	16	08ZRU1	08zru1 salmonella	179	7	1.7	423	2	09EZP6	09ezp6 streptococ
107	1.7	306	16	08Z9G7	08z9g7 salmonella	180	7	1.7	434	16	08ZIK4	08zik4 yersinia pe
108	1.7	306	16	08X9Y6	08x9y6 escherichia	181	7	1.7	437	16	09ZU00	09zU00 rhizobium m
109	1.7	319	5	09N3J6	09n3j6 caenorhabdi	182	7	1.7	438	10	08W347	08w347 oryza sativ
110	1.7	319	16	09CMU4	09cmu4 pasteurella	183	7	1.7	441	17	08TW66	08tw66 methanopyru
111	1.7	319	16	08YDM9	08ydm9 brucella me	184	7	1.7	449	17	08TWG3	08twg3 methanopyru
112	1.7	320	2	08KH54	08khs4 leptospira	185	7	1.7	450	5	060589	060589 plasmodium
113	1.7	320	2	09LS86	09ls86 leptospira	186	7	1.7	450	5	076565	076565 plasmodium
114	1.7	320	2	048546	048546 leptospira	187	7	1.7	450	5	076565	076565 plasmodium
115	1.7	320	16	09JXR6	09jxr6 neisseria m	188	7	1.7	451	16	08RHG6	08rhg6 fusobacteri
116	1.7	320	16	09JMS6	09jms6 neisseria m	189	7	1.7	452	10	09LI73	09li73 aradidopsis
117	1.7	322	5	09N3J7	09n3j7 caenorhabdi	190	7	1.7	460	4	09H8M0	09h8m0 homo sapien
118	1.7	325	16	092TJ8	092tj8 rhizobium m	191	7	1.7	461	10	09FUL9	09ful9 zea mays (m
119	1.7	326	16	08Y0J4	08y0j4 ralsconia s	192	7	1.7	470	11	099LK8	099lk8 mus musculu
120	1.7	327	16	09ZWF7	09zwf7 rhizobium m	193	7	1.7	473	4	096A99	096a99 homo sapien
121	1.7	331	16	09I561	09i561 pseudomonas	194	7	1.7	484	2	092911	092911 magnetospir
122	1.7	333	2	09XAT5	09xat5 rhizobium i	195	7	1.7	484	10	038934	038934 aradidopsis
123	1.7	333	16	08ZEG7	08zeg7 yersinia pe	196	7	1.7	486	13	08OGX2	08ogx2 brachydanio
124	1.7	335	5	0965L5	0965l5 caenorhabdi	197	7	1.7	491	16	08U9P9	08u9p9 agrobacteri
125	1.7	336	10	065453	065453 aradidopsis	198	7	1.7	491	17	09HN17	09hn17 halobacteri
126	1.7	339	16	08XXA2	08xxa2 ralsconia s	199	7	1.7	497	5	09GY92	09gy92 leishmania
127	1.7	341	6	002728	002728 ovis aries	200	7	1.7	504	10	09XFX3	09xfx3 cynara card
128	1.7	345	5	096439	096439 leishmania	201	7	1.7	505	10	09FRW6	09frw6 nepenthes a
129	1.7	345	16	09RRR0	09rrr0 lacnoccocus	202	7	1.7	506	10	039311	039311 brassica na
130	1.7	345	16	08Z359	08z359 salmonella	203	7	1.7	506	10	040140	040140 lycopersico
131	1.7	345	16	08UKA3	08uka3 agrobacteri	204	7	1.7	506	10	063390	063390 aradidopsis
132	1.7	346	6	002729	002729 ovis aries	205	7	1.7	507	10	09FRW7	09frw7 nepenthes a
133	1.7	346	16	09CHK6	09chk6 lactococcus	206	7	1.7	508	10	0948P0	0948p0 glycyne max
134	1.7	347	16	08ZOK4	08zok4 anabaena sp	207	7	1.7	508	10	09XEC4	09xec4 aradidopsis
135	1.7	353	2	P70901	P70901 borrelia he	208	7	1.7	510	10	09S6Z1	09s6z1 heliantus
136	1.7	354	5	09GXX7	09gxx7 boophilus m	209	7	1.7	510	16	099WR2	099wr2 staphylococ
137	1.7	358	10	P70899	P70899 borrelia he	210	7	1.7	512	10	004593	004593 aradidopsis
138	1.7	358	2	09FRW5	09frw5 nepenthes a	211	7	1.7	513	10	08VYL3	08vyl3 aradidopsis
139	1.7	360	2	P70905	P70905 borrelia he	212	7	1.7	514	10	09FRW9	09frw9 nepenthes a
140	1.7	361	16	092S90	092s90 rhizobium m	213	7	1.7	514	10	09FRW9	09frw9 streptococ
141	1.7	366	2	P70900	P70900 borrelia he	214	7	1.7	525	16	099ZJ0	099zj0 streptococ
142	1.7	367	16	098JF1	098jf1 rhizobium i	215	7	1.7	526	2	093N65	093n65 coxiella bu
143	1.7	368	16	08UDJ2	08udj2 agrobacteri	216	7	1.7	540	5	096Z14	096z14 plasmodium
144	1.7	371	2	09EZH2	09ezh2 streptococ	217	7	1.7	541	4	08TBY2	08tby2 homo sapien
145	1.7	373	10	09SD30	09sd30 aradidopsis	218	7	1.7	544	12	041936	041936 murid herpe
146	1.7	373	10	P93031	P93031 aradidopsis	219	7	1.7	555	10	09C7N0	09c7n0 aradidopsis
147	1.7	374	6	09RTW0	09rtw0 bos taurus	220	7	1.7	559	10	09FKP2	09fkp2 aradidopsis
148	1.7	378	13	09PUP9	09pup9 pseudopleur	221	7	1.7	582	11	08VHU6	08vhu6 rattus norv
149	1.7	379	11	09UJX1	09ujx1 iatius norv	222	7	1.7	583	16	08RCR3	08rcr3 thermoaer
150	1.7	380	6	046492	046492 bos taurus	223	7	1.7	600	5	09U2N6	09u2n6 caenorhabdi
151	1.7	380	6	09RTW5	09rtw5 capra hircu	224	7	1.7	609	10	09AUY9	09auy9 aradidopsis
152	1.7	380	6	09RTV4	09rtv4 bos taurus	225	7	1.7	615	13	042565	042565 xenopus lae
153	1.7	380	6	002723	002723 ovis aries	226	7	1.7	626	16	09KX09	09kx09 vibrio chol
154	1.7	381	6	09GK11	09gk11 camelus dro	227	7	1.7	633	16	098LR9	098lr9 rhizobium i
155	1.7	382	13	09PRG9	09prg9 gallus gall	228	7	1.7	649	4	09H0T2	09hot2 homo sapien
156	1.7	383	13	09DEC3	09dec3 xenopus lae	229	7	1.7	659	12	066383	066383 dengue viru
157	1.7	384	13	091322	091322 rana catesch	230	7	1.7	674	4	094GB7	094gb7 oryza sativ
158	1.7	385	6	029080	029080 sus scrofa	231	7	1.7	682	16	09H917	09h917 homo sapien
159	1.7	386	6	09GMV7	09gmY7 rhinolophus	232	7	1.7	682	16	08ZJ57	08zj57 yersinia pe
160	1.7	386	6	09GMV6	09gmY6 canis famli	233	7	1.7	690	16	09KLU8	09kl86 vibrio chol
161	1.7	386	6	09RTW8	09rtw8 capra hircu	234	7	1.7	707	16	09CD82	09cd82 mycobacteri
162	1.7	387	6	09GMV9	09gmY9 suncus murti	235	7	1.7	709	5	022548	022548 caenorhabdi

236	7	1.7	711	5	Q24205	Q24205 drosophila	309	6	1.5	62	5	P82170	P82170 locusta mig
237	7	1.7	722	3	Q10668	Q10668 schizosacch	310	6	1.5	64	8	Q36146	Q36146 thamnophis
238	7	1.7	732	10	Q94H45	Q94H45 oryza sativ	311	6	1.5	65	16	Q9K2D5	Q9K2D5 chlamydia p
239	7	1.7	784	16	Q8YAJ5	Q8YAJ5 listeria mo	312	6	1.5	67	16	Q9Z7S6	Q9Z7S6 listeria in
240	7	1.7	802	10	Q38802	Q38802 arabidopsis	313	6	1.5	69	10	Q9AUF7	Q9AUF7 brassica na
241	7	1.7	813	10	Q9LDT8	Q9LDT8 oryza sativ	314	6	1.5	70	10	Q9AUF6	Q9AUF6 brassica na
242	7	1.7	854	5	Q9NDZ8	Q9NDZ8 leishmania	315	6	1.5	70	10	Q9AUF5	Q9AUF5 brassica ol
243	7	1.7	873	2	Q9S4K0	Q9S4K0 streptococc	316	6	1.5	70	10	Q9AUF4	Q9AUF4 brassica ol
244	7	1.7	880	16	Q9A1M8	Q9A1M8 streptococc	317	6	1.5	71	2	Q9PCW3	Q9PCW3 escherichia
245	7	1.7	887	5	Q194Z8	Q194Z8 caenorhabdi	318	6	1.5	72	10	Q96618	Q96618 arabidopsis
246	7	1.7	893	10	Q8S615	Q8S615 oryza sativ	319	6	1.5	72	12	Q8VB96	Q8VB96 white spot
247	7	1.7	907	16	Q9LZ48	Q9LZ48 streptomyce	320	6	1.5	73	4	Q93067	Q93067 homo sapien
248	7	1.7	912	16	Q9K3Y2	Q9K3Y2 streptomyce	321	6	1.5	73	8	Q9XQK3	Q9XQK3 plism sativ
249	7	1.7	923	2	Q9S3T2	Q9S3T2 streptococc	322	6	1.5	73	8	Q35148	Q35148 neoridia ery
250	7	1.7	933	16	Q8XE39	Q8XE39 escherichia	323	6	1.5	73	16	Q9A2N3	Q9A2N3 caulobacter
251	7	1.7	934	11	Q924X9	Q924X9 mus musculu	324	6	1.5	74	16	Q8Y2X8	Q8Y2X8 ralatonia s
252	7	1.7	939	16	Q8YOR3	Q8YOR3 anabaena sp	325	6	1.5	75	2	Q9EY27	Q9EY27 photobacter
253	7	1.7	967	2	Q54123	Q54123 staphylococ	326	6	1.5	75	2	P94765	P94765 erwinia chr
254	7	1.7	968	2	Q9F848	Q9F848 streptomyce	327	6	1.5	76	8	Q48083	Q48083 eryx latari
255	7	1.7	991	4	Q15043	Q15043 homo sapien	328	6	1.5	77	8	Q99364	Q99364 elaphe ruf
256	7	1.7	1015	2	Q93T50	Q93T50 streptococc	329	6	1.5	77	8	Q9Z2V7	Q9Z2V7 elaphe ruf
257	7	1.7	1015	4	Q14572	Q14572 homo sapien	330	6	1.5	77	10	Q9X1X4	Q9X1X4 oryza sativ
258	7	1.7	1027	2	Q93T51	Q93T51 streptococc	331	6	1.5	78	8	Q36087	Q36087 thamnophis
259	7	1.7	1039	16	Q9KEQ8	Q9KEQ8 bacillus ha	332	6	1.5	78	8	Q36143	Q36143 thamnophis
260	7	1.7	1042	4	Q9H4G6	Q9H4G6 homo sapien	333	6	1.5	79	6	Q29452	Q29452 bos taurus
261	7	1.7	1130	4	Q9H1V5	Q9H1V5 homo sapien	334	6	1.5	79	16	Q25333	Q25333 helicobacte
262	7	1.7	1131	16	Q9H1V5	Q9H1V5 anabaena sp	335	6	1.5	80	2	Q70028	Q70028 streptomyce
263	7	1.7	1133	17	Q96KX7	Q96KX7 sulfolobus	336	6	1.5	80	2	Q9R6M8	Q9R6M8 agrobacteri
264	7	1.7	1142	16	Q97J24	Q97J24 clostridium	337	6	1.5	80	8	Q99365	Q99365 elaphe bima
265	7	1.7	1236	2	Q9UPA4	Q9UPA4 rhodocyclus	338	6	1.5	80	10	Q49028	Q49028 giracilaria
266	7	1.7	1269	5	Q43993	Q43993 dictyosteli	339	6	1.5	81	8	Q99362	Q99362 elaphe taen
267	7	1.7	1324	10	Q94CQ7	Q94CQ7 oryza sativ	340	6	1.5	81	8	Q99370	Q99370 dinodon ruf
268	7	1.7	1330	6	Q97961	Q97961 vulpes vulp	341	6	1.5	81	8	Q99371	Q99371 dinodon ruf
269	7	1.7	1379	5	Q9VNG9	Q9VNG9 drosophila	342	6	1.5	81	8	Q99372	Q99372 zaocys dhun
270	7	1.7	1379	5	Q9TY11	Q9TY11 drosophila	343	6	1.5	81	8	Q99373	Q99373 zaocys dhun
271	7	1.7	1411	2	Q9AJ93	Q9AJ93 actinomyces	344	6	1.5	81	8	Q99374	Q99374 ptyas kotto
272	7	1.7	1429	4	Q9Y5T6	Q9Y5T6 homo sapien	345	6	1.5	81	8	Q99375	Q99375 ptyas kotto
273	7	1.7	1433	11	Q07563	Q07563 mus musculu	346	6	1.5	81	8	Q36138	Q36138 thamnophis
274	7	1.7	1437	5	Q9G051	Q9G051 dictyosteli	347	6	1.5	81	8	Q9Z2X5	Q9Z2X5 zaocys dhun
275	7	1.7	1630	16	Q8RHH7	Q8RHH7 fusobacteri	348	6	1.5	81	8	Q9Z2X1	Q9Z2X1 elaphe taen
276	7	1.7	1866	5	Q9NKU5	Q9NKU5 leishmania	349	6	1.5	81	12	Q55445	Q55445 sindbis vir
277	7	1.7	1937	2	Q8RJZ2	Q8RJZ2 eligmarella	350	6	1.5	81	12	Q55447	Q55447 sindbis vir
278	7	1.7	2014	5	Q22774	Q22774 caenorhabdi	351	6	1.5	81	12	Q55448	Q55448 sindbis vir
279	7	1.7	2025	10	Q9SHK4	Q9SHK4 arabidopsis	352	6	1.5	81	12	Q9W8F2	Q9W8F2 sindbis vir
280	7	1.7	2042	5	Q9W1C5	Q9W1C5 drosophila	353	6	1.5	81	16	Q9PA00	Q9PA00 xyella fas
281	7	1.7	2554	5	Q9NKR1	Q9NKR1 leishmania	354	6	1.5	82	12	Q55446	Q55446 sindbis vir
282	7	1.7	2813	4	Q96JF6	Q96JF6 homo sapien	355	6	1.5	83	4	Q9H3B2	Q9H3B2 homo sapien
283	7	1.7	2813	4	Q8WXQ6	Q8WXQ6 homo sapien	356	6	1.5	84	8	Q36106	Q36106 thamnophis
284	7	1.7	2817	4	Q96P79	Q96P79 homo sapien	357	6	1.5	85	5	Q9W5T0	Q9W5T0 drosophila
285	7	1.7	2894	17	Q58791	Q58791 methanococc	358	6	1.5	85	8	Q48086	Q48086 eryx latari
286	6	1.5	15	3	Q9UR72	Q9UR72 trichoderma	359	6	1.5	85	17	Q9HJF0	Q9HJF0 thermoplaem
287	6	1.5	19	10	Q9S956	Q9S956 zea mays (m	360	6	1.5	88	8	Q36141	Q36141 thamnophis
288	6	1.5	22	11	Q9QWB6	Q9QWB6 mus sp. sgp	361	6	1.5	88	16	Q25107	Q25107 helicobacte
289	6	1.5	24	9	Q9T0Q7	Q9T0Q7 bacterioph	362	6	1.5	88	16	Q92K13	Q92K13 rhizobium m
290	6	1.5	25	12	Q9WMG7	Q9WMG7 sigma viru	363	6	1.5	88	16	Q9F2U8	Q9F2U8 streptomyce
291	6	1.5	30	7	Q31234	Q31234 mus musculu	364	6	1.5	89	8	Q36122	Q36122 thamnophis
292	6	1.5	35	8	Q9SA09	Q9SA09 synaphobran	365	6	1.5	89	16	Q9CHR8	Q9CHR8 lactococcus
293	6	1.5	39	5	Q16984	Q16984 acheta dome	366	6	1.5	90	8	Q36745	Q36745 epicrates s
294	6	1.5	40	10	Q9SSK6	Q9SSK6 arabidopsis	367	6	1.5	90	8	Q8WE07	Q8WE07 sanzinia ma
295	6	1.5	40	16	Q8VU52	Q8VU52 mycobacteri	368	6	1.5	90	8	Q8WE06	Q8WE06 boa constri
296	6	1.5	45	6	Q9GK71	Q9GK71 bos taurus	369	6	1.5	90	8	Q8WE05	Q8WE05 candaia bib
297	6	1.5	46	11	Q9RLN8	Q9RLN8 mus musculu	370	6	1.5	90	8	Q8WE04	Q8WE04 candaia car
298	6	1.5	46	11	Q9WVP4	Q9WVP4 mus apretus	371	6	1.5	90	8	Q8WE03	Q8WE03 candaia car
299	6	1.5	46	11	Q9WTK9	Q9WTK9 mus musculu	372	6	1.5	90	8	Q8WE02	Q8WE02 candaia car
300	6	1.5	49	2	Q9EVP1	Q9EVP1 escherichia	373	6	1.5	90	8	Q8WE01	Q8WE01 candaia car
301	6	1.5	52	16	Q9A041	Q9A041 streptococc	374	6	1.5	90	8	Q8W7U6	Q8W7U6 candaia bib
302	6	1.5	54	4	Q13807	Q13807 homo sapien	375	6	1.5	90	8	Q8W7N8	Q8W7N8 candaia asp
303	6	1.5	56	2	P97248	P97248 escherichia	376	6	1.5	90	8	Q8W7N7	Q8W7N7 candaia asp
304	6	1.5	58	4	Q969L1	Q969L1 homo sapien	377	6	1.5	90	8	Q8W7N6	Q8W7N6 candaia asp
305	6	1.5	59	16	Q9L720	Q9L720 caulobacter	378	6	1.5	90	13	Q91063	Q91063 jordanelia
306	6	1.5	60	3	Q12711	Q12711 trichoderma	379	6	1.5	90	13	Q90XU1	Q90XU1 acipenser s
307	6	1.5	60	9	Q38467	Q38467 bacterioph	380	6	1.5	90	13	Q90X15	Q90X15 amia calva
308	6	1.5	61	2	Q52860	Q52860 bacillus su	381	6	1.5	90	16	Q9K3G8	Q9K3G8 streptomyce

382	6	1.5	92	2	052631	052631 escherichia	455	6	1.5	103	8	09TAZ6	09TAZ6 agkistrodon
383	6	1.5	92	2	052632	052632 escherichia	456	6	1.5	103	8	09TAZ5	09TAZ5 ovophis mon
384	6	1.5	92	8	036123	036123 thiamophis	457	6	1.5	103	8	09TAZ4	09TAZ4 trimeresu
385	6	1.5	93	13	091251	091251 profundulus	458	6	1.5	103	8	09TAZ3	09TAZ3 trimeresu
386	6	1.5	93	17	08TWE6	08TWE6 methanophyru	459	6	1.5	103	10	08ST73	08ST73 oryza sativ
387	6	1.5	94	8	036145	036145 thiamophis	460	6	1.5	103	13	090224	090224 aplocheilic
388	6	1.5	94	8	036094	036094 thiamophis	461	6	1.5	103	13	090312	090312 crenichthys
389	6	1.5	95	2	049154	049154 methylolact	462	6	1.5	103	13	090191	090191 zoogeomelicu
390	6	1.5	95	8	036000	036000 thiamophis	463	6	1.5	103	16	098P21	098P21 rhizobium 1
391	6	1.5	95	8	035147	035147 meridia ery	464	6	1.5	104	6	029169	029169 sus scrofa
392	6	1.5	95	15	09INC6	09INC6 human immun	465	6	1.5	104	13	090242	090242 aplocheilic
393	6	1.5	96	8	036001	036001 thiamophis	466	6	1.5	104	13	091536	091536 xenotoca ei
394	6	1.5	96	11	08RA01	08RA01 ratcus norv	467	6	1.5	105	16	08TH98	08TH98 bruceia me
395	6	1.5	96	12	08QP44	08QP44 dengue viru	468	6	1.5	106	8	09BA26	09BA26 crocatus ho
396	6	1.5	96	15	038190	038190 human immun	469	6	1.5	106	8	09BA26	09BA26 crocatus ho
397	6	1.5	97	8	036051	036051 thiamophis	470	6	1.5	106	12	09YK02	09YK02 dengue viru
398	6	1.5	97	8	036019	036019 thiamophis	471	6	1.5	107	2	005626	005626 streptomyce
399	6	1.5	97	8	036021	036021 thiamophis	472	6	1.5	107	5	P91196	P91196 caenorhabdi
400	6	1.5	97	8	036029	036029 thiamophis	473	6	1.5	107	17	0979E7	0979E7 thermoplas
401	6	1.5	97	8	035983	035983 thiamophis	474	6	1.5	109	5	024148	024148 drosophila
402	6	1.5	97	15	09YX65	09YX65 human immun	475	6	1.5	109	9	08SCS1	08SCS1 pseudomonas
403	6	1.5	98	5	08SYX2	08SYX2 drosophila	476	6	1.5	109	12	09WUG7	09WUG7 dengue viru
404	6	1.5	98	8	036077	036077 thiamophis	477	6	1.5	109	16	09Z007	09Z007 rhizobium m
405	6	1.5	98	8	035982	035982 thiamophis	478	6	1.5	111	4	09H383	09H383 homo sapien
406	6	1.5	98	8	021564	021564 sigmoidon oc	479	6	1.5	112	10	09SEF33	09SEF33 arabidopsis
407	6	1.5	98	8	036028	036028 thiamophis	480	6	1.5	112	10	09LYY2	09LYY2 arabidopsis
408	6	1.5	98	9	080282	080282 xanthomonas	481	6	1.5	112	16	08Z6U5	08Z6U5 salmonella
409	6	1.5	99	8	036124	036124 thiamophis	482	6	1.5	113	11	08R0E4	08R0E4 mus musculu
410	6	1.5	99	8	08G435	08G435 thiamophis	483	6	1.5	113	12	09YJT5	09YJT5 atelrine her
411	6	1.5	99	8	036024	036024 thiamophis	484	6	1.5	113	16	09KB10	09KB10 bacillus ha
412	6	1.5	99	12	073557	073557 lassa virus	485	6	1.5	114	2	09RBK0	09RBK0 mycobacteri
413	6	1.5	99	12	071241	071241 human immun	486	6	1.5	114	5	09Y063	09Y063 xanthomonas
414	6	1.5	99	16	092Y38	092Y38 rhizobium m	487	6	1.5	114	5	09SUI8	09SUI8 trichinella
415	6	1.5	99	16	08YYN5	08YYN5 anabaena sp	488	6	1.5	114	5	09SUI8	08WGS5 oryza sativ
416	6	1.5	100	8	08TEP8	08TEP8 natrrix natr	489	6	1.5	114	10	08W0G5	09YFA7 aeropyrum p
417	6	1.5	100	8	09TEP7	09TEP7 elapne long	490	6	1.5	114	17	09YFA7	048070 eryx colubr
418	6	1.5	100	8	036144	036144 thiamophis	491	6	1.5	115	8	048070	09A712 aradidopsi
419	6	1.5	100	8	036025	036025 thiamophis	492	6	1.5	115	10	09A7H2	09A7H2 coryllus ave
420	6	1.5	100	8	036027	036027 thiamophis	493	6	1.5	115	10	09AMM2	09AMM2 oryza sativ
421	6	1.5	100	8	036003	036003 thiamophis	494	6	1.5	116	16	09PBU5	09PBU5 streptomyce
422	6	1.5	100	8	035150	035150 meridia fas	495	6	1.5	116	17	08ZYX8	08ZYX8 pyrobaculum
423	6	1.5	100	12	091FS4	091FS4 chilo tride	496	6	1.5	117	5	09NGU5	09NGU5 sarcophaga
424	6	1.5	100	13	090393	090393 cyprinodon	497	6	1.5	117	10	09WY32	08W335 retama raet
425	6	1.5	101	2	046552	046552 bacteroides	498	6	1.5	118	10	09FY12	09FY12 aradidopsi
426	6	1.5	101	8	036083	036083 thiamophis	499	6	1.5	119	8	063527	063527 dicrococliu
427	6	1.5	101	17	09Y9N7	09Y9N7 aeropyrum p	500	6	1.5	119	8	048061	048061 eptacraes s
428	6	1.5	102	8	08G1Z1	08G1Z1 thiamophis	501	6	1.5	119	8	048069	048069 eryx colubr
429	6	1.5	102	8	09G1W2	09G1W2 thiamophis	502	6	1.5	120	5	08TA28	08TA28 heterodera
430	6	1.5	102	8	09G1V3	09G1V3 thiamophis	503	6	1.5	120	9	08SCW5	08SCW5 pseudomonas
431	6	1.5	102	8	09G1T7	09G1T7 thiamophis	504	6	1.5	121	2	09AMU8	09AMU8 bradyrhizob
432	6	1.5	102	8	036078	036078 thiamophis	505	6	1.5	121	4	08MUE8	08MUE8 homo sapien
433	6	1.5	102	8	036022	036022 thiamophis	506	6	1.5	121	10	08RYC6	08RYC6 arabidopsis
434	6	1.5	102	8	036023	036023 thiamophis	507	6	1.5	121	16	09A1R0	09A1R0 streptococc
435	6	1.5	102	8	09B8P0	09B8P0 philodryas	508	6	1.5	121	16	09L2K6	09L2K6 streptomyce
436	6	1.5	102	8	09B8N9	09B8N9 philodryas	509	6	1.5	122	8	09TEC5	09TEC5 eptacraes f
437	6	1.5	102	8	09B8N8	09B8N8 philodryas	510	6	1.5	122	8	09TEC6	09TEC6 eptacraes f
438	6	1.5	102	8	09B8N7	09B8N7 philodryas	511	6	1.5	122	8	048074	048074 eryx elegans
439	6	1.5	102	8	09B8N6	09B8N6 philodryas	512	6	1.5	122	12	09WUG6	09WUG6 dengue viru
440	6	1.5	102	8	09B8N3	09B8N3 tropidodrya	513	6	1.5	123	8	048018	048018 boa constri
441	6	1.5	102	8	09B8N1	09B8N1 oxyrinopus g	514	6	1.5	123	8	09TEC7	09TEC7 boa constri
442	6	1.5	102	8	09G436	09G436 thiamophis	515	6	1.5	123	8	048021	048021 boa constri
443	6	1.5	102	8	09G434	09G434 thiamophis	516	6	1.5	123	8	048022	048022 boa constri
444	6	1.5	102	8	09G432	09G432 thiamophis	517	6	1.5	123	8	048115	048115 thiamophis
445	6	1.5	102	16	08X798	08X798 escherichia	518	6	1.5	123	8	048020	048020 boa constri
446	6	1.5	103	8	09TB05	09TB05 azemiops fe	519	6	1.5	123	12	09YK01	09YK01 dengue viru
447	6	1.5	103	8	09TB04	09TB04 agkistrodon	520	6	1.5	123	17	09HMY9	09HMY9 halobacteri
448	6	1.5	103	8	09TB03	09TB03 agkistrodon	521	6	1.5	124	17	08TNS0	08TNS0 methanosaic
449	6	1.5	103	8	09TB02	09TB02 glyoxydus br	522	6	1.5	125	6	09NOC6	09NOC6 macaca fasc
450	6	1.5	103	8	09TB01	09TB01 agkistrodon	523	6	1.5	125	8	09S822	09S822 lachesis mu
451	6	1.5	103	8	09TB00	09TB00 glyoxydus st	524	6	1.5	125	10	08S007	08S007 oryza sativ
452	6	1.5	103	8	09TAZ9	09TAZ9 glyoxydus sa	525	6	1.5	125	16	08UGX4	08UGX4 agriobacteri
453	6	1.5	103	8	09TAZ8	09TAZ8 glyoxydus sh	526	6	1.5	126	10	09LPK9	09LPK9 arabidopsis
454	6	1.5	103	8	09TAZ7	09TAZ7 glyoxydus st	527	6	1.5	127	2	093RNI	093RNI listeria mo

528	6	1.5	128	8	Q95722	Q95722 agkistrodon	601	6	1.5	146	16	Q92943	Q92943 chlamydia p
529	6	1.5	128	12	Q98279	Q98279 molluscum c	602	6	1.5	146	16	Q8RAL2	Q8RAL2 thermoaer
530	6	1.5	128	12	Q9YK03	Q9YK03 dengue viru	603	6	1.5	146	17	Q97XK6	Q97XK6 sulfolobus
531	6	1.5	129	10	Q93X29	Q93X29 nicotiana t	604	6	1.5	147	5	Q8SUJ4	Q8SUJ4 enccephalto
532	6	1.5	129	16	Q98R21	Q98R21 mycoplasma	605	6	1.5	147	17	Q9HKK9	Q9HKK9 thermoplasm
533	6	1.5	129	16	Q8YF69	Q8YF69 bruceella me	606	6	1.5	148	9	Q38345	Q38345 lactococcus
534	6	1.5	131	8	Q95733	Q95733 glycydus ha	607	6	1.5	148	12	Q11391	Q11391 rheus papi
535	6	1.5	131	12	Q8QPNO	Q8QPNO dengue viru	608	6	1.5	148	12	Q11394	Q11394 rheus papi
536	6	1.5	131	12	Q8QPM9	Q8QPM9 dengue viru	609	6	1.5	148	12	Q11400	Q11400 rheus papi
537	6	1.5	131	12	Q8QPM8	Q8QPM8 dengue viru	610	6	1.5	148	16	Q9XWR8	Q9XWR8 thermoga
538	6	1.5	131	12	Q8QPM7	Q8QPM7 dengue viru	611	6	1.5	148	16	Q92X98	Q92X98 rhizobium m
539	6	1.5	131	12	Q8QPM6	Q8QPM6 dengue viru	612	6	1.5	149	16	Q8U7V3	Q8U7V3 agrobacteri
540	6	1.5	131	12	Q8QPM5	Q8QPM5 dengue viru	613	6	1.5	149	17	Q976D8	Q976D8 sulfolobus
541	6	1.5	131	15	Q80675	Q80675 human immun	614	6	1.5	150	9	Q94MW6	Q94MW6 bacterioph
542	6	1.5	131	15	Q80677	Q80677 human immun	615	6	1.5	150	12	Q11396	Q11396 rheus papi
543	6	1.5	131	15	Q80679	Q80679 human immun	616	6	1.5	150	12	Q11397	Q11397 rheus papi
544	6	1.5	131	17	Q97VX9	Q97VX9 sulfolobus	617	6	1.5	150	12	Q11398	Q11398 rheus papi
545	6	1.5	132	8	Q9G100	Q9G100 arctica isl	618	6	1.5	150	16	Q98WK9	Q98WK9 rhizobium 1
546	6	1.5	132	8	Q9GAB4	Q9GAB4 arctica isl	619	6	1.5	150	16	Q981T3	Q981T3 rhizobium 1
547	6	1.5	132	8	Q9GAB3	Q9GAB3 arctica isl	620	6	1.5	150	17	Q97B14	Q97B14 thermoplasm
548	6	1.5	132	16	Q927V7	Q927V7 listeria in	621	6	1.5	151	2	Q91475	Q91475 lactococcus
549	6	1.5	132	16	Q8YAB5	Q8YAB5 streptomyce	622	6	1.5	151	5	Q8WOP7	Q8WOP7 anopheles g
550	6	1.5	132	16	Q50489	Q50489 caulobacter	623	6	1.5	151	10	Q9FM68	Q9FM68 oryza sativ
551	6	1.5	133	16	Q9A2K3	Q9A2K3 escherichia	624	6	1.5	151	16	Q9CHT0	Q9CHT0 lactococcus
552	6	1.5	133	2	Q47122	Q47122 escherichia	625	6	1.5	151	17	Q9HSW0	Q9HSW0 halobacteri
553	6	1.5	134	12	Q39791	Q39791 dengue viru	626	6	1.5	152	2	Q8ROP5	Q8ROP5 thermus the
554	6	1.5	134	16	Q8UGT2	Q8UGT2 agrobacteri	627	6	1.5	152	8	Q48024	Q48024 candida asp
555	6	1.5	135	17	Q57837	Q57837 pyrococcus	628	6	1.5	152	8	Q48048	Q48048 epicrateae e
556	6	1.5	135	6	Q8WMG1	Q8WMG1 bubalus bub	629	6	1.5	152	8	Q48119	Q48119 ungalliphis
557	6	1.5	137	6	Q95MP6	Q95MP6 bos taurus	630	6	1.5	152	10	Q8VXP7	Q8VXP7 cicet retic
558	6	1.5	138	16	Q8XAK9	Q8XAK9 escherichia	631	6	1.5	152	16	Q9L222	Q9L222 streptomyce
559	6	1.5	138	17	Q9YBJ7	Q9YBJ7 aeropyrum p	632	6	1.5	152	17	Q9YG78	Q9YG78 aeropyrum p
560	6	1.5	139	17	Q30319	Q30319 archaeoglob	633	6	1.5	152	17	Q8TUD9	Q8TUD9 methanarc
561	6	1.5	140	4	Q9P1I9	Q9P1I9 homo sapien	634	6	1.5	153	4	Q8WY26	Q8WY26 homo sapien
562	6	1.5	141	10	Q98851	Q98851 guillardia	635	6	1.5	153	16	Q96GW3	Q96GW3 rhizobium 1
563	6	1.5	141	12	Q65260	Q65260 african swi	636	6	1.5	154	2	Q93PL4	Q93PL4 pseudomonas
564	6	1.5	141	16	Q8X325	Q8X325 escherichia	637	6	1.5	154	9	Q03959	Q03959 bacterioph
565	6	1.5	141	16	Q8YC88	Q8YC88 bruceella me	638	6	1.5	154	14	Q99126	Q99126 uncultured
566	6	1.5	142	2	Q47124	Q47124 escherichia	639	6	1.5	155	10	Q949A8	Q949A8 oryza sativ
567	6	1.5	142	12	Q919G1	Q919G1 blueberry r	640	6	1.5	155	16	Q8YED0	Q8YED0 bruceella me
568	6	1.5	142	16	Q9ABR1	Q9ABR1 rhizobium 1	641	6	1.5	155	17	Q9YB53	Q9YB53 aeropyrum p
569	6	1.5	142	16	Q8YHQ1	Q8YHQ1 bruceella me	642	6	1.5	156	2	Q9FSB0	Q9FSB0 agrobacteri
570	6	1.5	143	1	Q9CA58	Q9CA58 halobacteri	643	6	1.5	156	16	Q92P09	Q92P09 rhizobium m
571	6	1.5	143	2	Q9ZAG7	Q9ZAG7 streptococc	644	6	1.5	156	16	Q8XWJ5	Q8XWJ5 ralestonia s
572	6	1.5	143	3	Q9U9U5	Q9U9U5 schizosacch	645	6	1.5	157	10	Q9LTT7	Q9LTT7 arabidopsis
573	6	1.5	143	9	Q03935	Q03935 bacterioph	646	6	1.5	157	16	Q9KQD0	Q9KQD0 vibrio chol
574	6	1.5	143	16	Q8YVH3	Q8YVH3 ralestonia s	647	6	1.5	157	16	Q9HVR3	Q9HVR3 pseudomonas
575	6	1.5	143	16	Q8XV31	Q8XV31 ralestonia s	648	6	1.5	157	17	Q9YDV5	Q9YDV5 aeropyrum p
576	6	1.5	143	16	Q8RH81	Q8RH81 fusbacteri	649	6	1.5	157	17	Q8TXR0	Q8TXR0 methanopyru
577	6	1.5	144	12	Q11395	Q11395 rheus papi	650	6	1.5	158	5	Q9GQX4	Q9GQX4 plasmodium
578	6	1.5	144	16	Q9FBS3	Q9FBS3 streptomyce	651	6	1.5	158	5	Q9VK73	Q9VK73 drosophila
579	6	1.5	145	11	Q54878	Q54878 mus musculu	652	6	1.5	158	16	Q8XZB3	Q8XZB3 ralestonia s
580	6	1.5	145	12	Q72508	Q72508 sindbis vir	653	6	1.5	159	5	Q9N7I7	Q9N7I7 leishmania
581	6	1.5	145	12	Q72509	Q72509 sindbis vir	654	6	1.5	159	10	Q23429	Q23429 arabidopsis
582	6	1.5	145	12	Q72510	Q72510 sindbis vir	655	6	1.5	159	12	Q8QP46	Q8QP46 dengue viru
583	6	1.5	145	12	Q72511	Q72511 sindbis vir	656	6	1.5	159	16	Q9CCU6	Q9CCU6 mycobacteri
584	6	1.5	145	12	Q72512	Q72512 sindbis vir	657	6	1.5	159	16	Q9XAP5	Q9XAP5 streptomyce
585	6	1.5	145	12	Q72513	Q72513 sindbis vir	658	6	1.5	159	16	Q92S42	Q92S42 rhizobium m
586	6	1.5	145	12	Q72514	Q72514 sindbis vir	659	6	1.5	160	16	Q92KH6	Q92KH6 rhizobium m
587	6	1.5	145	12	Q72515	Q72515 sindbis vir	660	6	1.5	161	4	Q96FPH9	Q96FPH9 homo sapien
588	6	1.5	145	12	Q72516	Q72516 sindbis vir	661	6	1.5	161	10	Q90P59	Q90P59 oryza sativ
589	6	1.5	145	12	Q93005	Q93005 sindbis vir	662	6	1.5	161	12	Q90P59	Q90P59 cucumber gr
590	6	1.5	145	12	Q93006	Q93006 sindbis vir	663	6	1.5	162	5	Q24353	Q24353 drosophila 1
591	6	1.5	145	12	Q9WHL4	Q9WHL4 sindbis vir	664	6	1.5	162	16	Q98F42	Q98F42 rhizobium 1
592	6	1.5	145	12	Q9W9S2	Q9W9S2 sindbis vir	665	6	1.5	162	16	Q8U682	Q8U682 agrobacteri
593	6	1.5	145	12	Q9W883	Q9W883 sindbis vir	666	6	1.5	163	5	Q9Y199	Q9Y199 caenorhabdi
594	6	1.5	145	12	Q8QTH9	Q8QTH9 sindbis vir	667	6	1.5	163	6	Q95WPS	Q95WPS bos taurus
595	6	1.5	145	16	Q912X8	Q912X8 pseudomonas	668	6	1.5	163	12	Q94929	Q94929 rana tempor
596	6	1.5	145	17	Q9HKG7	Q9HKG7 thermoplasm	669	6	1.5	163	12	Q94927	Q94927 rana tempor
597	6	1.5	146	4	Q9HDK7	Q9HDK7 homo sapien	670	6	1.5	163	12	Q94925	Q94925 bufo marinu
598	6	1.5	146	11	Q9DCY8	Q9DCY8 mus musculu	671	6	1.5	163	12	Q94923	Q94923 bovine irido
599	6	1.5	146	11	Q9UT45	Q9UT45 mus musculu	672	6	1.5	163	12	Q94921	Q94921 bufo bufo u
600	6	1.5	146	16	Q8XUX6	Q8XUX6 clostridium	673	6	1.5	163	12	Q94919	Q94919 bufo bufo u

674	6	1.5	163	12	Q9J9Y7	Q9J9Y7 bufo bufo u	747	6	1.5	174	12	Q84937	Q84937 porcine rep
675	6	1.5	163	12	Q9J9Y5	Q9J9Y5 catfish lrl	748	6	1.5	174	12	Q84950	Q84950 porcine rep
676	6	1.5	163	12	Q9J9Y3	Q9J9Y3 bufo marinu	749	6	1.5	174	12	Q84953	Q84953 porcine rep
677	6	1.5	163	12	Q9J9Y1	Q9J9Y1 bufo marinu	750	6	1.5	174	12	Q70659	Q70659 porcine rep
678	6	1.5	163	12	Q9J9X9	Q9J9X9 doctor fish	751	6	1.5	174	12	Q70661	Q70661 porcine rep
679	6	1.5	163	12	Q9J9X7	Q9J9X7 epizootic h	752	6	1.5	174	12	Q70664	Q70664 porcine rep
680	6	1.5	163	12	Q9J9X5	Q9J9X5 frog virus	753	6	1.5	174	12	Q70667	Q70667 porcine rep
681	6	1.5	163	12	Q9J9X3	Q9J9X3 guppyfish 1	754	6	1.5	174	12	Q70670	Q70670 porcine rep
682	6	1.5	163	12	Q9J9X1	Q9J9X1 leptoactyl	755	6	1.5	174	12	Q70673	Q70673 porcine rep
683	6	1.5	163	12	Q9J9W9	Q9J9W9 bufo marinu	756	6	1.5	174	12	P89041	P89041 porcine rep
684	6	1.5	163	12	Q9J9W7	Q9J9W7 bufo marinu	757	6	1.5	174	12	Q9YLST	Q9YLST porcine rep
685	6	1.5	163	12	Q9J9W5	Q9J9W5 sheefish 1	758	6	1.5	174	12	Q90050	Q90050 porcine rep
686	6	1.5	163	12	Q9J9W3	Q9J9W3 tadpole ede	759	6	1.5	174	12	Q9YSG5	Q9YSG5 porcine rep
687	6	1.5	163	17	Q8RH43	Q8RH43 fusobacteri	760	6	1.5	174	12	Q9E8M4	Q9E8M4 porcine rep
688	6	1.5	163	17	Q9YG32	Q9YG32 aeropyrum p	761	6	1.5	174	12	Q99B00	Q99B00 porcine rep
689	6	1.5	164	2	005140	005140 proteus mir	762	6	1.5	174	12	Q98XX0	Q98XX0 porcine rep
690	6	1.5	164	2	08RIY8	08RIY8 xenorhabdus	763	6	1.5	174	12	Q88702	Q88702 porcine rep
691	6	1.5	164	16	Q9K0U4	Q9K0U4 vibrio chol	764	6	1.5	174	12	Q9YNY2	Q9YNY2 porcine rep
692	6	1.5	164	16	Q8ZG08	Q8ZG08 yersinia pe	765	6	1.5	174	12	Q88934	Q88934 porcine rep
693	6	1.5	164	16	Q8Z815	Q8Z815 salmonella	766	6	1.5	174	12	Q993U6	Q993U6 porcine rep
694	6	1.5	164	17	Q8TU01	Q8TU01 methanosarc	767	6	1.5	174	12	Q56259	Q56259 porcine rep
695	6	1.5	165	16	Q9BDG7	Q9BDG7 rhizobium 1	768	6	1.5	174	12	Q9WBR3	Q9WBR3 porcine rep
696	6	1.5	165	16	Q8UC24	Q8UC24 agrobacteri	769	6	1.5	174	12	Q55493	Q55493 porcine rep
697	6	1.5	166	16	Q9CN27	Q9CN27 pasteurella	770	6	1.5	174	12	Q9YWM6	Q9YWM6 porcine rep
698	6	1.5	166	16	Q9J005	Q9J005 streptomyce	771	6	1.5	174	12	Q57287	Q57287 porcine rep
699	6	1.5	167	2	Q93G69	Q93G69 escherichia	772	6	1.5	174	12	Q73563	Q73563 porcine rep
700	6	1.5	167	5	077278	077278 drosophila	773	6	1.5	174	12	Q8Q0W3	Q8Q0W3 porcine rep
701	6	1.5	167	5	Q9W414	Q9W414 drosophila	774	6	1.5	174	17	Q9YCC9	Q9YCC9 aeropyrum p
702	6	1.5	167	16	Q8XYV4	Q8XYV4 ralsstonia s	775	6	1.5	176	11	Q62195	Q62195 mus musculu
703	6	1.5	167	17	Q8TY65	Q8TY65 methanopyru	776	6	1.5	176	16	Q989C1	Q989C1 rhizobium 1
704	6	1.5	168	2	Q47123	Q47123 escherichia	777	6	1.5	177	8	Q9GB05	Q9GB05 trimeresuru
705	6	1.5	168	2	Q9GAZ8	Q9GAZ8 trimeresuru	778	6	1.5	177	16	Q8XV48	Q8XV48 ralsstonia s
706	6	1.5	168	10	Q9M444	Q9M444 ciccer ariet	779	6	1.5	178	2	Q44994	Q44994 bovine bu
707	6	1.5	168	16	Q9RRC6	Q9RRC6 deinococcus	780	6	1.5	178	5	Q45197	Q45197 caenorhabdi
708	6	1.5	169	12	Q91IT9	Q91IT9 hepatitis c	781	6	1.5	178	10	Q9SVD6	Q9SVD6 arabisdopsis
709	6	1.5	169	12	Q917S7	Q917S7 hepatitis c	782	6	1.5	178	11	Q922K0	Q922K0 mus musculu
710	6	1.5	169	12	Q917S6	Q917S6 hepatitis c	783	6	1.5	178	11	Q922K0	Q922K0 mus musculu
711	6	1.5	169	12	Q917S5	Q917S5 hepatitis c	784	6	1.5	178	16	Q9RNR3	Q9RNR3 streptomyce
712	6	1.5	169	16	Q9RWJ6	Q9RWJ6 deinococcus	785	6	1.5	179	2	Q9AKR3	Q9AKR3 ralsstonia m
713	6	1.5	169	16	Q8X5C9	Q8X5C9 escherichia	786	6	1.5	179	16	Q9RWM3	Q9RWM3 deinococcus
714	6	1.5	170	8	Q94XW9	Q94XW9 agkistrodon	787	6	1.5	180	5	Q20659	Q20659 caenorhabdi
715	6	1.5	170	8	Q94XW6	Q94XW6 crocatalus pu	788	6	1.5	181	10	Q9SG96	Q9SG96 arabisdopsis
716	6	1.5	170	10	Q9FVY3	Q9FVY3 oryza sativ	789	6	1.5	181	10	Q9UGF0	Q9UGF0 oryza sativ
717	6	1.5	170	17	Q9UX55	Q9UX55 sulfolobus	790	6	1.5	183	11	Q54877	Q54877 mus musculu
718	6	1.5	171	2	Q93CH4	Q93CH4 photobacter	791	6	1.5	183	12	Q92291	Q92291 dengue viru
719	6	1.5	171	10	Q9ZU47	Q9ZU47 arabisdopsis	792	6	1.5	183	12	Q9YKK0	Q9YKK0 dengue viru
720	6	1.5	171	10	Q9FVN9	Q9FVN9 arabisdopsis	793	6	1.5	183	12	Q9YJZ9	Q9YJZ9 dengue viru
721	6	1.5	171	10	Q9S1I5	Q9S1I5 arabisdopsis	794	6	1.5	183	12	Q9YJZ8	Q9YJZ8 dengue viru
722	6	1.5	171	12	Q9W868	Q9W868 porcine ade	795	6	1.5	183	12	Q9YJZ7	Q9YJZ7 dengue viru
723	6	1.5	171	12	Q91IT4	Q91IT4 hepatitis c	796	6	1.5	183	12	Q9W9N2	Q9W9N2 dengue viru
724	6	1.5	171	12	Q91IT2	Q91IT2 hepatitis c	797	6	1.5	183	16	Q9AK22	Q9AK22 streptomyce
725	6	1.5	171	12	Q91IS7	Q91IS7 hepatitis c	798	6	1.5	183	16	Q8RH71	Q8RH71 fusobacteri
726	6	1.5	171	12	Q91IS7	Q91IS7 hepatitis c	799	6	1.5	183	17	Q9YEB9	Q9YEB9 aeropyrum p
727	6	1.5	171	16	Q9A8T1	Q9A8T1 caulobacter	800	6	1.5	184	2	Q938D6	Q938D6 mycobacteri
728	6	1.5	171	16	Q8RBM2	Q8RBM2 thermoanaer	801	6	1.5	184	2	Q9XBS4	Q9XBS4 erwinia car
729	6	1.5	172	4	Q96QTO	Q96QTO homo sapien	802	6	1.5	184	8	Q9GAX3	Q9GAX3 agkistrodon
730	6	1.5	172	10	Q24126	Q24126 nicotiana t	803	6	1.5	185	4	Q9P0P2	Q9P0P2 homo sapien
731	6	1.5	172	10	Q9SHE9	Q9SHE9 arabisdopsis	804	6	1.5	185	4	Q9P0P1	Q9P0P1 homo sapien
732	6	1.5	172	10	Q9SHE9	Q9SHE9 arabisdopsis	805	6	1.5	185	4	Q9Y3R1	Q9Y3R1 homo sapien
733	6	1.5	172	12	Q99D34	Q99D34 porcine rep	806	6	1.5	185	4	Q9UT14	Q9UT14 homo sapien
734	6	1.5	172	16	Q8X934	Q8X934 escherichia	807	6	1.5	185	8	Q9TEC6	Q9TEC6 amorphilla s
735	6	1.5	172	17	Q96YU7	Q96YU7 sulfolobus	808	6	1.5	185	8	Q94XW3	Q94XW3 crocatalus wi
736	6	1.5	173	3	Q96TV7	Q96TV7 pleurotus o	809	6	1.5	185	11	Q9CMZ0	Q9CMZ0 mus musculu
737	6	1.5	173	5	Q95Y22	Q95Y22 leishmania	810	6	1.5	185	11	Q9JIB0	Q9JIB0 mus musculu
738	6	1.5	173	8	Q8SGV5	Q8SGV5 blitis nasac	811	6	1.5	186	4	Q9HD47	Q9HD47 homo sapien
739	6	1.5	173	12	Q55479	Q55479 porcine rep	812	6	1.5	186	8	Q94XW4	Q94XW4 crocatalus wi
740	6	1.5	173	12	Q85022	Q85022 porcine rep	813	6	1.5	186	8	Q8SFR21	Q8SFR21 actrodipsas
741	6	1.5	173	12	Q9DY96	Q9DY96 porcine rep	814	6	1.5	186	10	Q9FRD0	Q9FRD0 oryza sativ
742	6	1.5	173	16	Q91305	Q91305 pseudomonas	815	6	1.5	186	10	Q9FTI8	Q9FTI8 oryza sativ
743	6	1.5	174	2	Q49927	Q49927 mycobacteri	816	6	1.5	186	16	Q8YMW8	Q8YMW8 anabaena sp
744	6	1.5	174	12	Q89452	Q89452 porcine rep	817	6	1.5	186	16	Q8YK72	Q8YK72 anabaena sp
745	6	1.5	174	12	Q98V07	Q98V07 porcine rep	818	6	1.5	187	2	Q93UV3	Q93UV3 agrobacteri
746	6	1.5	174	12	Q88707	Q88707 porcine rep	819	6	1.5	187	2	Q939U5	Q939U5 rhodovulium

820	6	1.5	187	3	013565	013565 saccharomyc	893	6	1.5	199	8	094563	094563 atheris agu
821	6	1.5	187	9	08SC14	08SC14 bacterioph	894	6	1.5	199	8	094RL9	094RL9 bitis ariet
822	6	1.5	187	10	09FTK5	09FTK5 oryza sativ	895	6	1.5	199	8	094RL8	094RL8 bitis ariet
823	6	1.5	188	2	09FSD9	09FSD9 agrobacteri	896	6	1.5	199	8	094RL4	094RL4 bitis cornu
824	6	1.5	188	8	094XX0	094XX0 agkistrodon	897	6	1.5	199	8	094RL3	094RL3 bitis gabon
825	6	1.5	188	8	094XW8	094XW8 siistrurus m	898	6	1.5	199	8	094RL2	094RL2 bitis nasic
826	6	1.5	188	8	094XW7	094XW7 siistrurus r	899	6	1.5	199	8	094RL0	094RL0 bitis rhino
827	6	1.5	188	8	094XW5	094XW5 crotaurus ce	900	6	1.5	199	8	094RL9	094RL9 bitis worth
828	6	1.5	188	8	094XW1	094XW1 crotaurus to	901	6	1.5	199	8	094RL8	094RL8 cerastes ce
829	6	1.5	188	10	09SJW5	09SJW5 arabidopsis	902	6	1.5	199	8	094RL7	094RL7 cerastes ce
830	6	1.5	188	11	09CRA1	09CRA1 mus musculu	903	6	1.5	199	8	094RL8	094RL8 daboia russ
831	6	1.5	189	2	08VVE6	08VVE6 salmoneilla	904	6	1.5	199	8	094RH5	094RH5 eristicophi
832	6	1.5	189	10	065060	065060 picea maria	905	6	1.5	199	8	094RD7	094RD7 macrovipea
833	6	1.5	189	11	09WUP0	09WUP0 mus musculu	906	6	1.5	199	8	094RC9	094RC9 pseudoceras
834	6	1.5	190	8	09T2U6	09T2U6 sus scrofa	907	6	1.5	199	8	094RC1	094RC1 pseudoceras
835	6	1.5	190	11	09EOY7	09EOY7 mus musculu	908	6	1.5	199	8	094R66	094R66 vipera ammo
836	6	1.5	190	16	08YOA0	08YOA0 ralatonia s	909	6	1.5	199	8	094R62	094R62 vipera beru
837	6	1.5	191	5	09U9S6	09U9S6 drosophila	910	6	1.5	199	8	094R61	094R61 vipera niko
838	6	1.5	191	5	09U9S5	09U9S5 drosophila	911	6	1.5	199	8	094R60	094R60 vipera pala
839	6	1.5	191	5	09U9S4	09U9S4 drosophila	912	6	1.5	199	8	094R58	094R58 vipera seoa
840	6	1.5	191	5	09U9S3	09U9S3 drosophila	913	6	1.5	199	8	094P05	094P05 vipera beru
841	6	1.5	191	8	09G806	09G806 trimeresuru	914	6	1.5	199	12	065970	065970 cucumber ye
842	6	1.5	191	11	09D814	09D814 mus musculu	915	6	1.5	199	12	091051	091051 influenzavi
843	6	1.5	192	11	09DSM7	09DSM7 mus musculu	916	6	1.5	199	12	091050	091050 influenzavi
844	6	1.5	192	12	081420	081420 hepaticis c	917	6	1.5	199	12	09Q217	09Q217 influenzavi
845	6	1.5	192	16	098B25	098B25 rhizobium 1	918	6	1.5	199	12	09Q2P4	09Q2P4 influenzavi
846	6	1.5	194	8	09GB02	09GB02 trimeresuru	919	6	1.5	199	12	09Q205	09Q205 influenzavi
847	6	1.5	194	11	09CZK8	09CZK8 mus musculu	920	6	1.5	199	12	09Q203	09Q203 influenzavi
848	6	1.5	194	12	P89529	P89529 chickpea st	921	6	1.5	199	12	09Q201	09Q201 influenzavi
849	6	1.5	195	2	09Z1W7	09Z1W7 streptomyce	922	6	1.5	199	12	09Q1Z9	09Q1Z9 influenzavi
850	6	1.5	195	12	P89530	P89530 beet wester	923	6	1.5	199	12	09Q1Z7	09Q1Z7 influenzavi
851	6	1.5	195	16	050932	050932 borrelia bu	924	6	1.5	199	12	09Q1Z5	09Q1Z5 influenzavi
852	6	1.5	195	16	097KX0	097KX0 clostridium	925	6	1.5	199	12	09Q1Z3	09Q1Z3 influenzavi
853	6	1.5	195	16	08XGR5	08XGR5 ralatonia s	926	6	1.5	199	12	09Q1Z1	09Q1Z1 influenzavi
854	6	1.5	195	17	08THU5	08THU5 methanosarc	927	6	1.5	199	12	09Q1Y9	09Q1Y9 influenzavi
855	6	1.5	196	2	050257	050257 desulfovibr	928	6	1.5	199	12	09Q1Y7	09Q1Y7 influenzavi
856	6	1.5	196	5	Q23205	Q23205 caenorhabdi	929	6	1.5	199	12	08Q2I1	08Q2I1 influenzavi
857	6	1.5	196	11	Q9D599	Q9D599 mus musculu	930	6	1.5	199	12	08Q2I0	08Q2I0 influenzavi
858	6	1.5	196	16	Q9PGH0	Q9PGH0 chlamydia m	931	6	1.5	199	12	08Q2H9	08Q2H9 influenzavi
859	6	1.5	196	16	Q9LIU0	Q9LIU0 streptomyce	932	6	1.5	199	12	08Q2H8	08Q2H8 influenzavi
860	6	1.5	197	4	Q9NUP9	Q9NUP9 homo sapien	933	6	1.5	199	12	08Q2H7	08Q2H7 influenzavi
861	6	1.5	197	8	Q48035	Q48035 corallus ca	934	6	1.5	199	12	08Q2H6	08Q2H6 influenzavi
862	6	1.5	197	11	Q91WY7	Q91WY7 rattus norv	935	6	1.5	199	12	08Q2H5	08Q2H5 influenzavi
863	6	1.5	197	11	088952	088952 mus musculu	936	6	1.5	199	12	08Q2H4	08Q2H4 influenzavi
864	6	1.5	197	12	065880	065880 barley yell	937	6	1.5	199	12	08Q2H3	08Q2H3 influenzavi
865	6	1.5	197	17	09HIL9	09HIL9 thermoplasma	938	6	1.5	199	12	08Q2H2	08Q2H2 influenzavi
866	6	1.5	198	2	09FBA2	09FBA2 chirococcid	939	6	1.5	199	12	08Q2H1	08Q2H1 influenzavi
867	6	1.5	198	2	09FBA1	09FBA1 scytonema s	940	6	1.5	199	12	08Q2H0	08Q2H0 influenzavi
868	6	1.5	198	2	09FBA0	09FBA0 xenococcus	941	6	1.5	199	12	08Q2G9	08Q2G9 influenzavi
869	6	1.5	198	2	09FB96	09FB96 geitlerinem	942	6	1.5	199	12	08Q2G8	08Q2G8 influenzavi
870	6	1.5	198	2	09FB73	09FB73 nostoc musc	943	6	1.5	199	12	08Q2G7	08Q2G7 influenzavi
871	6	1.5	198	2	09FB72	09FB72 calochrix p	944	6	1.5	199	12	08Q2G6	08Q2G6 influenzavi
872	6	1.5	198	2	09FB54	09FB54 gloeobacter	945	6	1.5	199	12	08Q2G5	08Q2G5 influenzavi
873	6	1.5	198	8	09GAY3	09GAY3 trimeresuru	946	6	1.5	199	12	08Q2G4	08Q2G4 influenzavi
874	6	1.5	198	16	08XIF4	08XIF4 clostridium	947	6	1.5	199	12	08Q2G3	08Q2G3 influenzavi
875	6	1.5	199	8	09MDT4	09MDT4 elaphe dion	948	6	1.5	199	12	08Q2G2	08Q2G2 influenzavi
876	6	1.5	199	8	09MEC0	09MEC0 elaphe quat	949	6	1.5	199	12	08Q2G1	08Q2G1 influenzavi
877	6	1.5	199	8	09B1Z9	09B1Z9 macrovipea	950	6	1.5	199	16	09CPI9	09CPI9 influenzavi
878	6	1.5	199	8	09MJU0	09MJU0 elaphe none	951	6	1.5	199	16	097P31	097P31 influenzavi
879	6	1.5	199	8	09MJU9	09MJU9 elaphe long	952	6	1.5	200	6	098P54	098P54 pteropus gl
880	6	1.5	199	8	09MJU8	09MJU8 elaphe long	953	6	1.5	200	10	09M3U2	09M3U2 cucumis sat
881	6	1.5	199	8	09MJU7	09MJU7 elaphe pers	954	6	1.5	200	16	09KYP9	09KYP9 streptomyce
882	6	1.5	199	8	09MJU6	09MJU6 elaphe line	955	6	1.5	201	5	09B1P5	09B1P5 osteotragia
883	6	1.5	199	8	09MJU3	09MJU3 elaphe quat	956	6	1.5	201	8	09GAW9	09GAW9 trimeresuru
884	6	1.5	199	8	09MJU2	09MJU2 elaphe quat	957	6	1.5	202	8	09GAZ4	09GAZ4 trimeresuru
885	6	1.5	199	8	09MJU1	09MJU1 elaphe quat	958	6	1.5	202	9	09MBW1	09MBW1 bacterioph
886	6	1.5	199	8	09MJU0	09MJU0 elaphe situ	959	6	1.5	202	12	065841	065841 beet wester
887	6	1.5	199	8	09MJU9	09MJU9 elaphe situ	960	6	1.5	202	12	065842	065842 beet wester
888	6	1.5	199	8	094YA2	094YA2 adenorhinos	961	6	1.5	202	12	065837	065837 beet wester
889	6	1.5	199	8	094Y97	094Y97 atheris cer	962	6	1.5	202	12	065838	065838 beet wester
890	6	1.5	199	8	094Y96	094Y96 atheris chl	963	6	1.5	202	12	065839	065839 beet wester
891	6	1.5	199	8	094Y97	094Y97 atheris his	964	6	1.5	202	12	065840	065840 beet wester
892	6	1.5	199	8	094Y96	094Y96 atheris nit	965	6	1.5	202	12	065830	065830 beet wester

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966 6 1.5 202 12 065832 065832 beet wester
967 6 1.5 202 12 065833 065833 beet wester
968 6 1.5 202 12 065834 065834 beet wester
969 6 1.5 202 12 091AV9 091AV9 beet chloro
970 6 1.5 202 12 091AV5 091AV5 beet chloro
971 6 1.5 202 12 08V9K7 08V9K7 beet wester
972 6 1.5 202 12 089780 089780 beet wester
973 6 1.5 202 12 089780 089780 beet wester
974 6 1.5 202 16 08UC04 08UC04 agrobaacter
975 6 1.5 202 17 09YD86 09YD86 aeropyrum p
976 6 1.5 203 8 09GAX1 09GAX1 trimeresuru
977 6 1.5 203 10 09AYR8 09AYR8 cucumis sat
978 6 1.5 203 16 092S96 092S96 rhizobium m
979 6 1.5 204 11 09JLM3 09JLM3 rattus norv
980 6 1.5 204 12 083099 083099 latino viru
981 6 1.5 204 12 09XOY6 09XOY6 ranid herpe
982 6 1.5 205 2 044152 044152 acetobacter
983 6 1.5 205 8 09GB04 09GB04 trimeresuru
984 6 1.5 205 11 08V1B5 08V1B5 mus musculu
985 6 1.5 205 16 0981H8 0981H8 rhizobium 1
986 6 1.5 205 16 08ZKZ9 08ZKZ9 salmonella
987 6 1.5 205 16 08XES8 08XES8 escherichia
988 6 1.5 205 16 08XG06 08XG06 salmonella
989 6 1.5 206 10 09SWT7 09SWT7 hordeum vul
990 6 1.5 206 10 09STH2 09STH2 arabidopsis
991 6 1.5 206 11 099PR6 099PR6 cavia porce
992 6 1.5 206 16 098N56 098N56 rhizobium 1
993 6 1.5 206 16 099W14 099W14 staphylococ
994 6 1.5 206 16 08ZLY8 08ZLY8 salmonella
995 6 1.5 206 16 08Z3N3 08Z3N3 salmonella
996 6 1.5 206 17 0973W7 0973W7 sulfolobus
997 6 1.5 207 4 09HAP6 09HAP6 homo sapien
998 6 1.5 207 11 088951 088951 mus musculu
999 6 1.5 207 11 092252 092252 rattus norv
1000 6 1.5 207 16 09K558 09K558 bacillus ha

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ALIGNMENTS

RESULT 1

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Q9H2V8 PRELIMINARY; PRT; 439 AA.
ID Q9H2V8;
AC Q9H2V8;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE CDAL13.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PHOCHROMOCYTOMA;
RA Li Y., Huang Q., Peng, Y., Song H., Yu Y., Xu S., Ren S., Chen Z.,
  Han Z.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DDJ databases.
DR EMBL; AF212255; AAG41783.1; -.
DR HSSP; P00797; ZREN.
DR InterPro; IPR001461; Asproteaseal.
DR InterPro; IPR001969; Asprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 439 AA; 48275 MW; 02EC0E0E50F11602 CRC64;

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Query Match 95.8%; Score 389; DB 4; Length 439;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 18 MVNLIQDSDGRGYLLEMLIGTPPKQLILVDTGSSNFAVAGTPHPSYIDTYFDTERSSYTR 77
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Db 1 MVNLIQDSDGRGYLLEMLIGTPPKQLILVDTGSSNFAVAGTPHPSYIDTYFDTERSSYTR 60
QY 78 SKGFDVTVKYTGSGMTGFGVEDLVITIPKGFNTSLVNIATIFSESENFPLPGIKNNGLIGL 137
Db 61 SKGFDVTVKYTGSGMTGFGVEDLVITIPKGFNTSLVNIATIFSESENFPLPGIKNNGLIGL 120
QY 138 AVATLAKRSSLETFPDSLVLTQANI PVVFSQMCGAGLPVAGSGTNGSLVGGIIEPSLY 197
Db 121 AVATLAKRSSLETFPDSLVLTQANI PVVFSQMCGAGLPVAGSGTNGSLVGGIIEPSLY 180
QY 198 KGDITVPIKEWYVQIEILKLEIGQSINLDCENYADKAI VDSGTTLRLPQKVPDAV 257
Db 181 KGDITVPIKEWYVQIEILKLEIGQSINLDCENYADKAI VDSGTTLRLPQKVPDAV 240
QY 258 VEAVARASLIPEFDGFWTGSQGLACMTNSETPMGVFPKISITLBDENSSRSFRITILPOL 317
Db 241 VEAVARASLIPEFDGFWTGSQGLACMTNSETPMGVFPKISITLBDENSSRSFRITILPOL 300
QY 318 YIQPMWAGALNYECYRFGISPTNALVIGATVMEGFYVIFDRAQKRVGFAPASPCAETIAGA 377
Db 301 YIQPMWAGALNYECYRFGISPTNALVIGATVMEGFYVIFDRAQKRVGFAPASPCAETIAGA 360
QY 378 AVSEISGPFSTEDVANSNCVPAQSISEPTL 406
Db 361 AVSEISGPFSTEDVANSNCVPAQSISEPTL 389

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RESULT 2

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ID Q9NZL1 PRELIMINARY; PRT; 396 AA.
AC Q9NZL1;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Aspareryl protease.
GN BACE2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20422477; Pubmed=10965118;
RA Solans A., Estivill X., de La Luna S.;
RT "A new aspareryl protease on 21q22.3, BACE2, is highly similar to
  Alzheimer's amyloid precursor protein beta-secretase.";
RL Cyrogenet. Cell Genet. 89:177-184 (2000).
DR EMBL; AF188277; AAF35836.1; -.
DR HSSP; P00797; ZREN.
DR MEROPS; A01.041; -.
DR InterPro; IPR001461; Asproteaseal.
DR InterPro; IPR001969; Asprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_2.
SQ SEQUENCE 396 AA; 43013 MW; 5023A7AF391CEAC9 CRC64;

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Query Match 77.8%; Score 316; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ALEPLASPAANFLAVNDMLQDSDGRGYLLEMLIGTPPKQLILVDTGSSNFAVAGTP 60
Db 63 ALEPLASPAANFLAVNDMLQDSDGRGYLLEMLIGTPPKQLILVDTGSSNFAVAGTP 122
QY 61 HSYIDTYFDTERSSYTRSKGFDVTVKYTGSGMTGFGVEDLVITIPKGFNTSLVNIATIFE 120
Db 123 HSYIDTYFDTERSSYTRSKGFDVTVKYTGSGMTGFGVEDLVITIPKGFNTSLVNIATIFE 182
QY 121 SENFPLPGIKNNGLIGLAVATLAKRSSLETFPDSLVLTQANI PVVFSQMCGAGLPVAGS 180
Db 183 SENFPLPGIKNNGLIGLAVATLAKRSSLETFPDSLVLTQANI PVVFSQMCGAGLPVAGS 242

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QY 181 GTNGSLVGGIIEPSLYKGDWYTPKEWYQIIEILKLEIGGSLNDCERYNADKAIY 240
 DB 243 GTNGSLVGGIIEPSLYKGDWYTPKEWYQIIEILKLEIGGSLNDCERYNADKAIY 302
 QY 241 DSGTTLRLPKVFPVAVVEAVARASLIPEFSDGFWTGSQACWNTSETPWSYFPKISITL 300
 DB 303 DSGTTLRLPKVFPVAVVEAVARASLIPEFSDGFWTGSQACWNTSETPWSYFPKISITL 362
 QY 301 RDENSSRSFRITILPQ 316
 DB 363 RDENSSRSFRITILPQ 378

RESULT 3

Q9NZL2 PRELIMINARY; PRT; 468 AA.
 AC Q9NZL2; 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Aspartyl protease.
 GN BACE2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20422477; PubMed=10965118;
 RA Solans A., Estivill X., de La Luna S.;
 RT "A new aspartyl protease on 21q22.3, BACE2, is highly similar to
 RT Alzheimer's amyloid precursor protein beta-secretase.";
 DR Cyogenet. Cell Genet. 89:177-184 (2000).
 DR EMBL; AF188276; AAF35835.1;
 DR HSP; P00797; 2REN.
 DR MEROPS; A01.041; -.
 DR InterPro; IPR001461; Asproteasea1.
 DR InterPro; IPR001969; Asprotease_site.
 DR Pfam; PF00026; asp.1.
 DR PRINTS; PR00792; PEPsin.
 DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_2.
 KW Protease.
 SQ SEQUENCE 468 AA; 50324 MW; 717E0920126A0142 CRC64;

Query Match

Best Local Similarity 100.0%; Score 266; DB 4; Length 468;
 Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALEPALASPAGANFLAVNDLQDSDGRGYLEMLIGTPPQKLTIVDTGSSNFAVAGTP 60
 DB 63 ALEPALASPAGANFLAVNDLQDSDGRGYLEMLIGTPPQKLTIVDTGSSNFAVAGTP 122
 QY 61 HSYIDTYDTRSSSTYRSKGFDTYKYQGSWTVGSDLVTPKGFNTSLVNIATIFE 120
 DB 123 HSYIDTYDTRSSSTYRSKGFDTYKYQGSWTVGSDLVTPKGFNTSLVNIATIFE 182
 QY 121 SENFPLPKIKNGILGLAVATLAKSSSLTFPPDSLVQANIPNPFNSMOMGAGLPVAGS 180
 DB 183 SENFPLPKIKNGILGLAVATLAKSSSLTFPPDSLVQANIPNPFNSMOMGAGLPVAGS 242
 QY 181 GTNGSLVGGIIEPSLYKGDWYTPKEWYQIIEILKLEIGGSLNDCERYNADKAIY 240
 DB 243 GTNGSLVGGIIEPSLYKGDWYTPKEWYQIIEILKLEIGGSLNDCERYNADKAIY 302
 QY 241 DSGTTLRLPKVFPVAVVEAVARASL 266
 DB 303 DSGTTLRLPKVFPVAVVEAVARASL 328

RESULT 4

Q9JUL8 PRELIMINARY; PRT; 514 AA.
 ID Q9JUL8

AC Q9JUL8; 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Aspartyl protease 1.
 GN BACE2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Choi D.K., Sugano S., Sakaki Y.;
 RT "Molecular characterization of the mouse Aspi gene, a homolog of the
 RT human Aspi (Down Syndrome Region aspartyl protease).";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF216310; AAF36599.1;
 DR HSP; P32329; 1YFS.
 DR MEROPS; A01.041; -.
 DR MGD; MGI:1860440; Bace2.
 DR InterPro; IPR001461; Asproteasea1.
 DR InterPro; IPR001969; Asprotease_site.
 DR Pfam; PF00026; asp.1.
 DR PRINTS; PR00792; PEPsin.
 DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_2.
 KW Protease.
 SQ SEQUENCE 514 AA; 55799 MW; A70725F2C1DF5B47 CRC64;

Query Match

Best Local Similarity 14.5%; Score 59; DB 11; Length 514;
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 FSMOMCGALPVAGSGTNGSLVGGIIEPSLYKGDWYTPKEWYQIIEILKLEIGG 224
 DB 224 FSMOMCGALPVAGSGTNGSLVGGIIEPSLYKGDWYTPKEWYQIIEILKLEIGG 282

RESULT 5

Q9RI17 PRELIMINARY; PRT; 255 AA.
 AC Q9RI17; 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Aspartyl protease (Fragment).
 GN BACE2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Accarino M., Fumagalli P., Taramelli R., Ottolenghi S.;
 RT "Cloning of a gene from chromosome 21 Down Region encoding a potential
 RT transmembrane protease.";
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF051150; AAD45964.1;
 DR MEROPS; A01.041; -.
 DR MGD; MGI:1860440; Bace2.
 DR InterPro; IPR001461; Asproteasea1.
 DR InterPro; IPR001969; Asprotease_site.
 DR PRINTS; PR00792; PEPsin.
 DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
 KW Protease.
 FT NON_TER 1
 SQ SEQUENCE 255 AA; 28685 MW; 53DE317815996D63 CRC64;

Query Match

Best Local Similarity 9.4%; Score 38; DB 11; Length 255;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 LINDCREYNADKAIVDSGTTLRLPKVFPVAVVEAVAR 263
 LINDCREYNADKAIVDSGTTLRLPKVFPVAVVEAVAR

Db 25 INLDREYNADKAIVDSTGLRLPQKVDVAVAVAR 62

RESULT 6

Q9BYB9 ID Q9BYB9 PRELIMINARY; PRT; 432 AA.
AC Q9BYB9; DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Beta-site APP cleaving enzyme I-432.
GN BACE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RX MEDLINE=21408467; PubMed=11516562;
RA Tanahashi H., Tabira T.;
RT "Three novel alternatively spliced isoforms of the human beta-site APP
cleaving enzyme (BACE) and their effect on amyloid beta-peptide
production.";
RL Neurosci. Lett. 307:9-12(2001).
DR EMBL; AB050438; BAB40933.1; -.
DR HSSP; P32329; IYPS.
DR InterPro; IPR001461; AsproteaseA1.
DR InterPro; IPR001969; Asprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPSIN.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN 1.
SQ SEQUENCE 432 AA; 48212 MW; 96FC81E6F0ED01B CRC64;

Query Match 3.0%; Score 12; DB 4; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.0017;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 ILVDTGSSNFAV 56
Db 90 ILVDTGSSNFAV 101

RESULT 7

Q9BYC0 ID Q9BYC0 PRELIMINARY; PRT; 457 AA.
AC Q9BYC0; DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Beta-site APP cleaving enzyme I-457 (Beta-site APP cleaving enzyme
type C).
GN BACE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RX MEDLINE=21408467; PubMed=11516562;
RA Tanahashi H., Tabira T.;
RT "Three novel alternatively spliced isoforms of the human beta-site APP
cleaving enzyme (BACE) and their effect on amyloid beta-peptide
production.";
RL Neurosci. Lett. 307:9-12(2001).
GN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=EXOCRINE PANCREAS;
RA Zaccaretti D., De Pietri Tonelli D., Schurbus R.;
RT "New beta-site APP cleaving enzyme isoform (BACE-1C) obtained from
human pancreas.";
RN Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.

DR EMBL; AB050437; BAB40932.1; -.
DR EMBL; AF338817; AAK38375.1; -.
DR HSSP; P32329; IYPS.
DR InterPro; IPR001461; AsproteaseA1.
DR InterPro; IPR001969; Asprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPSIN.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN 1.
SQ SEQUENCE 457 AA; 51068 MW; C794C9A9E85FE7A2 CRC64;

Query Match 3.0%; Score 12; DB 4; Length 457;
Best Local Similarity 100.0%; Pred. No. 0.0017;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 ILVDTGSSNFAV 56
Db 90 ILVDTGSSNFAV 101

RESULT 8

Q9BYC1 ID Q9BYC1 PRELIMINARY; PRT; 476 AA.
AC Q9BYC1; DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Beta-site APP cleaving enzyme I-476.
GN BACE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RX MEDLINE=21408467; PubMed=11516562;
RA Tanahashi H., Tabira T.;
RT "Three novel alternatively spliced isoforms of the human beta-site APP
cleaving enzyme (BACE) and their effect on amyloid beta-peptide
production.";
RL Neurosci. Lett. 307:9-12(2001).
DR EMBL; AB050436; BAB40931.1; -.
DR HSSP; P32329; IYPS.
DR InterPro; IPR001461; AsproteaseA1.
DR InterPro; IPR001969; Asprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPSIN.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN 1.
SQ SEQUENCE 476 AA; 52907 MW; 6C8C87F8A953AF66 CRC64;

Query Match 3.0%; Score 12; DB 4; Length 476;
Best Local Similarity 100.0%; Pred. No. 0.0018;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 ILVDTGSSNFAV 56
Db 90 ILVDTGSSNFAV 101

RESULT 9

Q9ULS1 ID Q9ULS1 PRELIMINARY; PRT; 532 AA.
AC Q9ULS1; DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE KIAA1149 protein (Fragment).
GN KIAA1149.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

```

RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=20033618; PubMed=10574461;
RA Hirosewa M., Nagase T., Ishikawa K., Kikuno R., Nomura N., Ohara O.;
RT "Characterization of cDNA clones selected by the Genemart analysis
RL from size-fractionated cDNA libraries from human brain.";
DR DNA Res. 6:329-336(1999);
DR EMBL; AB032975; BAA86463.2; -
DR HSP; P56272; IAM5; -
DR MEROPS; A01.004; -
DR InterPro; IPR001461; Asproteaseal.
DR InterPro; IPR001969; Asprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
FT NON TER 1
SQ SEQUENCE 532 AA; 58720 MW; 98B135D0D5FBD2E8 CRC64;

Query Match 3.0%; Score 12; DB 4; Length 532;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 ILVDTGSSNFAV 56
DB 121 ILVDTGSSNFAV 132

RESULT 10
Q9P0D2 PRELIMINARY; PRT; 213 AA.
AC Q9P0D2;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE HSPC104 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CORD BLOOD;
RA Zhang Q.H., Ye M., Zhou J., Shen Y., Wu X.Y., Guan Z.Q., Wang L.,
RA Fan H.Y., Mao Y.F., Dai M., Huang Q.H., Chen S.J., Chen Z.;
RT "Human partial CDS cloned from cd34+ stem cells.";
RL Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF61367; AAF28927.1; -
DR InterPro; IPR001461; Asproteaseal.
DR Pfam; PF00026; asp; 1.
FT NON TER 1
SQ SEQUENCE 213 AA; 24338 MW; EC9D3FA31CFA835C CRC64;

Query Match 2.2%; Score 9; DB 4; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 308 SFRITLIPQ 316
DB 119 SFRITLIPQ 127

RESULT 11
Q9CUN5 PRELIMINARY; PRT; 266 AA.
AC Q9CUN5;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Beta-site APP cleaving enzyme (Fragment).
GN BACE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=BRAIN;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Komoto H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamada I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Scandali F., Suzuki R., Tomita M., Wagner L., Mashio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshew-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohseuki S.,
RA Hasehizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK014390; BAB29317.1; -
DR MEROPS; A01.004; -
DR MGD; MGI:1346542; Bace.
DR InterPro; IPR001461; Asproteaseal.
DR Pfam; PF00026; asp; 1.
FT NON TER 1
SQ SEQUENCE 266 AA; 30201 MW; B913FDA8ADAB4238 CRC64;

Query Match 2.2%; Score 9; DB 11; Length 266;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 308 SFRITLIPQ 316
DB 121 SFRITLIPQ 129

RESULT 12
Q9M8Y6 PRELIMINARY; PRT; 96 AA.
AC Q9M8Y6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE T6K12.8 protein.
GN T6K12.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_Taxid=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV; COLUMBIA;
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,
RA Ranning C.M., Koo H., Fujii C.Y., Uteback T.R., Barnstead M.E.,
RA Bowman C.L., White O., Niernan W.C., Fraser C.M.;
RT "Arabidopsis thaliana chromosome III BAC T6K12 genomic sequence.";
RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AC016829; AAF26784.1; -
DR SQU SEQUENCE 96 AA; 10847 MW; DCD06B55060EDA2 CRC64;

Query Match 2.0%; Score 8; DB 10; Length 96;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 99 DLVTIPKG 106

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Db 66 DLVTIPKG 73

RESULT 13

09CPL4 ID 09CPL4 PRELIMINARY; PRT; 159 AA.
 AC 09CPL4;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Lrp.
 GN LRP OR PM0254.
 OS Pasteurella multocida.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 CC Pasteurella;
 CX NCBI_TaxID=747;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=PM70;
 RX MEDLINE=21145866; PubMed=11248100;
 RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittem T.S., Kapur V.;
 RL "Complete genomic sequence of Pasteurella multocida Pm70.";
 CC Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
 CC -1- SIMILARITY: BELONGS TO THE ASNC FAMILY OF TRANSCRIPTIONAL
 CC REGULATORS.
 DR EMBL; AE006060; AAK02338.1; -;
 DR InterPro; IPR000485; ASNC_trans_reg.
 DR Pfam; PF01037; ASNC_trans_reg; 1.
 DR PRINTS; PR00033; HTASNC.
 DR SMART; SM00344; HTH_ASNC; 1.
 DR PROSITE; PS00519; HTH_ASNC_FAMILY; 1.
 KW DNA-binding; Transcription regulation; Complete proteome.
 SQ SEQUENCE 159 AA; 18085 MW; 45A5FE4CC7F874D CRC64;

Query Match 2.0%; Score 8; DB 16; Length 159;
 Best Local Similarity 100.0%; Pred. No. 9.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 243 GTTLRLP 250
 Db 129 GTTLRLP 136

RESULT 14

09LORO ID 09LORO PRELIMINARY; PRT; 241 AA.
 AC 09LORO;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Putative lipoprotein.
 GN SC04231 OR SCD8A.04C.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 CC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
 CX NCBI_TaxID=1902;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Seeger K.J., Harris D.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Cerdano A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN (3)
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RX MEDLINE=97000351; PubMed=8843436;
 RA Redenbach M., Kieser H.M., Denapalte D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for

RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 RN (4)

RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
 RA Warren T., Wietorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 RT coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 DR EMBL; AL160331; CAB7325.1; -;
 DR InterPro; IPR000531; TonB_boxC.
 DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
 KW Lipoprotein.
 SQ SEQUENCE 241 AA; 23517 MW; C42774C407869AB5 CRC64;

Query Match 2.0%; Score 8; DB 16; Length 241;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 184 GGSILVIG 191
 Db 112 GGSILVIG 119

RESULT 15

08WOY9 ID 08WOY9 PRELIMINARY; PRT; 244 AA.
 AC 08WOY9;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Aspartate protease (Fragment).
 GN App.
 OS Aphrocallistes vastus.
 OC Eukaryota; Metazoa; Porifera; Hexactinellida; Hexasterophora;
 CC Lysacinosida; Rossellidae; Aphrocallistes.
 CX NCBI_TaxID=83887;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Mueller W.E.G., Mueller I.M., Grebenjuk V.A.;
 RT "Umecetazoa: Origin and evolution of the common ancestor of Metazoa";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ304863; CAC83293.1; -;
 DR InterPro; IPR001461; Aspartatease1.
 DR InterPro; IPR001969; Aspartatease_site.
 DR InterPro; IPR000055; HTHARAC.
 DR Pfam; PF000026; asp; 1.
 DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
 DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
 KW Protease.
 FT NON TER 244
 SQ SEQUENCE 244 AA; 26366 MW; 653690261E0E4C7 CRC64;

Query Match 2.0%; Score 8; DB 15; Length 244;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 50 GGSNFAVA 57
 Db 53 GGSNFAVA 60

Search completed: April 1, 2003, 11:53:26
 Job time : 107 secs

GenCore version 5.1.4 PJ 4578
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OM protein - protein search, using sw model

Run on: April 1, 2003, 11:21:58 ; Search time 39 Seconds
(without alignments)
1769,842 Million cell updates/sec

Title: US-09-668-314C-2
Perfect score: 2687
Sequence: 1 MGALRALPLPLAQLMLRA.....RPRDPEVNDSSLRHHRWK 518

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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 - 21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
 - 22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
 - 23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2687	100.0	518	19 AAM61362	Aspartic proteinase
2	2687	100.0	518	20 AAY41774	Human PRO852, prote
3	2687	100.0	518	20 AAY22239	Human CSP56, aspar
4	2687	100.0	518	20 AAY13799	Human aspartyl pro
5	2687	100.0	518	21 AAB44270	Human PRO852 (UNO4
6	2687	100.0	518	21 AAY88424	Human aspartyl pro
7	2687	100.0	518	22 AAY10628	Human aspartyl pro
8	2687	100.0	518	22 AAY10656	Human Asp 1 protei
9	2687	100.0	518	22 AAU29059	Human PRO polypept
10	2687	100.0	518	22 AAE06858	Human aspartyl pro

11	2687	100.0	518	22 AAU06602	Human Aspartyl pro
12	2687	100.0	518	22 AAU07201	Human aspartyl pro
13	2687	100.0	518	22 AAE02580	Human aspartyl pro
14	2687	100.0	518	22 AAE02608	Human Aspartyl pro
15	2687	100.0	518	22 ABB78589	Human Asp-1 protei
16	2687	100.0	518	23 ABB78617	Human Asp-1delatM
17	2687	100.0	518	23 ABB06531	Human aspartyl pro
18	2687	100.0	518	23 ABB07453	Human BACE2 amino
19	2506	93.3	481	22 AAG75592	Human colon cancer
20	2437	90.7	475	22 AAE10657	Secreted recombin
21	2437	90.7	475	22 AAE02609	Human secreted asp
22	2437	90.7	475	23 ABB78618	Secreted recombin
23	2395	89.1	514	22 AAB84204	Amino acid sequenc
24	2293	85.3	439	23 ABB80365	Human polypeptide
25	2207	82.1	423	22 AAE04796	Human aspartyl pro
26	2184	81.3	423	22 ABB88479	Human membrane or
27	2124	79.0	413	22 AAE10658	Acid-processed hu-
28	2124	79.0	413	22 AAE02610	Human acid-process
29	2124	79.0	413	23 ABB78619	Asp-1delatM(his)6
30	1794	66.8	355	22 AAB93925	Human protein sequ
31	1187	44.2	501	21 AAY94769	Rat beta-secretase
32	1186.5	44.2	501	22 AAB84948	Mouse aspartic sec
33	1185	44.1	501	21 AAY94768	Murine beta-secret
34	1185	44.1	501	21 AAB84267	Murine aspartyl pr
35	1185	44.1	501	22 AAE10631	Murine aspartyl pr
36	1185	44.1	501	22 AAE06861	Murine aspartyl pr
37	1185	44.1	501	22 AAU06605	Mouse aspartyl pro
38	1185	44.1	501	22 AAU07204	Mouse aspartyl pro
39	1185	44.1	501	22 AAE02583	Murine aspartyl pr
40	1185	44.1	501	23 ABB78592	Mouse Asp-2(a) pro
41	1178.5	43.9	501	21 AAY94767	Human beta-secreta
42	1178.5	43.9	501	21 AAB07896	Amino acid sequenc
43	1178.5	43.9	509	23 AAM52697	FLAG-tagged human
44	1175	43.7	488	22 AAB65572	Human memapsin 2
45	1175	43.7	488	22 AAB61334	Memapsin 2 protein

ALIGNMENTS

RESULT 1
AAW61362 standard; Protein; 518 AA.

AC AAW61362;
25-SEP-1998 (first entry)
Aspartic proteinase ASP1.
ASPL: Aspartic proteinase; Alzheimer's disease; cancer; melanoma.
OS Homo sapiens.
PN EP848062-A2.
PD 17-JUN-1998.

PF 01-DEC-1997; 97EP-0309648.
PR 14-DEC-1996; 96GB-0026022.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PI (SMIK) SMITHKLINE BEECHAM PLC.
PI Chapman CG, Evans JR, Powell DJ, Southan C;
DR WPI; 1998-314477/28.
DR N-PSDB; AAV27962.

New isolated polynucleotide encodes Aspartic protease polypeptide -
used to diagnosis, treat and vaccinate against Alzheimer's disease,
cancer and melanoma

6.98 published
Fousell
100%

XX Claim 11; Page 7; 19pp; English.
XX The human ASP1 protein is structurally related to other proteins of the
CC Aspartic protease family. ASP 1 polypeptides and polynucleotides can
CC be used to diagnose, treat and vaccinate against Alzheimer's disease,
CC cancer and melanoma.
XX
SQ Sequence 518 AA;
Query Match 100.0%; Score 2687; DB 19; Length 518;
Best local similarity 100.0%; Pred. No. 3e-231;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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D 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLMLIGTPPOKLQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTFPDRSSSTRSKGFDVTVKYTGSGWTGFGVEDLVITPKGFNTSFLVNIATI 180
D 121 TPHSYIDTFPDRSSSTRSKGFDVTVKYTGSGWTGFGVEDLVITPKGFNTSFLVNIATI 180
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D 181 FESSEFPLPGIKWNGILGLAVATLAKPSSLETFPDSLVTOANINVSQMCGAGLPVA 240
QY 241 GSGTNGSLVIGIEPSLYKGIWYTPIKEWYQIIEIKLIGGOSINLDCREYNADKA 300
D 241 GSGTNGSLVIGIEPSLYKGIWYTPIKEWYQIIEIKLIGGOSINLDCREYNADKA 300
QY 301 IVDSGTTLRLPQKVFDAVEAVASLIPESDGFMTGSQLACWTNSETPWSYFKISI 360
D 301 IVDSGTTLRLPQKVFDAVEAVASLIPESDGFMTGSQLACWTNSETPWSYFKISI 360
QY 361 YLRDSSRSRFTITLPLQYIOPMMGAGINVCYRFGISPSNNAIVIGATWEGFYVFD 420
D 361 YLRDSSRSRFTITLPLQYIOPMMGAGINVCYRFGISPSNNAIVIGATWEGFYVFD 420
QY 421 RAQKVGFAFASCAIAGAASEISGFSTEDVASCVAQSLSEPIILIVSYALMSYCG 480
D 421 RAQKVGFAFASCAIAGAASEISGFSTEDVASCVAQSLSEPIILIVSYALMSYCG 480
QY 481 ALLVLIVLLIPRCORRRDPEVNDSSLVRRHWK 518
D 481 ALLVLIVLLIPRCORRRDPEVNDSSLVRRHWK 518
RESULT 2
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ID AA41714 standard; Protein; 518 AA.
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XX AA41714;
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XX 07-DEC-1999 (first entry)
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XX Human PRO852 protein sequence.
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XX Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
XX probe; blood coagulation disorder; cancer; cellular adhesion disorder;
XX secreted protein; transmembrane protein.
XX
XX Homo sapiens.
XX
XX OS
XX PN WO9946281-A2.
XX PD 16-SEP-1999.
XX PF 08-MAR-1999; 99WO-US05028.
XX

PR 10-MAR-1998; 98US-0077450.
PR 11-MAR-1998; 98US-0077632.
PR 11-MAR-1998; 98US-0077641.
PR 11-MAR-1998; 98US-0077649.
PR 12-MAR-1998; 98US-0077791.
PR 13-MAR-1998; 98US-0078004.
PR 17-MAR-1998; 98US-0040220.
PR 20-MAR-1998; 98US-0078886.
PR 20-MAR-1998; 98US-0078919.
PR 20-MAR-1998; 98US-0078936.
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PR 25-MAR-1998; 98US-0079254.
PR 26-MAR-1998; 98US-0079656.
PR 27-MAR-1998; 98US-0079663.
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PR 27-MAR-1998; 98US-0079786.
PR 30-MAR-1998; 98US-0079920.
PR 30-MAR-1998; 98US-0079923.
PR 31-MAR-1998; 98US-0080105.
PR 31-MAR-1998; 98US-0080107.
PR 31-MAR-1998; 98US-0080165.
PR 31-MAR-1998; 98US-0080194.
PR 01-APR-1998; 98US-0080327.
PR 01-APR-1998; 98US-0080328.
PR 01-APR-1998; 98US-0080333.
PR 01-APR-1998; 98US-0080334.
PR 08-APR-1998; 98US-0081049.
PR 08-APR-1998; 98US-0081070.
PR 08-APR-1998; 98US-0081071.
PR 09-APR-1998; 98US-0081195.
PR 09-APR-1998; 98US-0081203.
PR 09-APR-1998; 98US-0081229.
PR 15-APR-1998; 98US-0081817.
PR 15-APR-1998; 98US-0081838.
PR 15-APR-1998; 98US-0081952.
PR 15-APR-1998; 98US-0081955.
PR 21-APR-1998; 98US-0082568.
PR 21-APR-1998; 98US-0082569.
PR 22-APR-1998; 98US-0082700.
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PR 23-APR-1998; 98US-0082767.
PR 23-APR-1998; 98US-0082796.
PR 27-APR-1998; 98US-0083336.
PR 28-APR-1998; 98US-0083332.
PR 29-APR-1998; 98US-0083392.
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PR 29-APR-1998; 98US-0083545.
PR 29-APR-1998; 98US-0083554.
PR 29-APR-1998; 98US-0083558.
PR 29-APR-1998; 98US-0083559.
PR 30-APR-1998; 98US-0083742.
PR 05-MAY-1998; 98US-0084366.
PR 06-MAY-1998; 98US-0084414.
PR 06-MAY-1998; 98US-0084441.
PR 07-MAY-1998; 98US-0084598.
PR 07-MAY-1998; 98US-0084600.
PR 07-MAY-1998; 98US-0084627.
PR 07-MAY-1998; 98US-0084637.
PR 07-MAY-1998; 98US-0084639.
PR 07-MAY-1998; 98US-0084640.
PR 07-MAY-1998; 98US-0084643.
PR 13-MAY-1998; 98US-0085323.
PR 13-MAY-1998; 98US-0085339.
PR 13-MAY-1998; 98US-0085339.
PR 15-MAY-1998; 98US-0085573.
PR 15-MAY-1998; 98US-0085579.
PR 15-MAY-1998; 98US-0085580.

3.98

PR 15-MAY-1998; 98US-0085582.
 PR 15-MAY-1998; 98US-0085689.
 PR 15-MAY-1998; 98US-0085697.
 PR 15-MAY-1998; 98US-0085700.
 PR 15-MAY-1998; 98US-0085704.
 PR 18-MAY-1998; 98US-0086023.
 PR 22-MAY-1998; 98US-0086392.
 PR 22-MAY-1998; 98US-0086414.
 PR 22-MAY-1998; 98US-0086430.
 PR 22-MAY-1998; 98US-0086486.
 PR 28-MAY-1998; 98US-0087098.
 PR 28-MAY-1998; 98US-0087106.
 PR 28-MAY-1998; 98US-0087208.
 PR 30-JUL-1998; 98US-0094651.
 PR 11-SEP-1998; 98US-0100038.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
 XX
 XX WPI; 1999-551358/46.
 DR N-PSDB; AAZ34056.
 XX
 PT New secreted and transmembrane polypeptides and their polynucleotides,
 PT useful for treating blood coagulation disorders, cancers and cellular
 PT adhesion disorders -
 XX
 PS Claim 12; Fig 73; 530pp; English.
 XX
 CC The present invention describes secreted and transmembrane polypeptides
 CC and their polynucleotides. The nucleotide sequences are useful as
 CC sources of probes, primers, for chromosome mapping, and for generation
 CC of antisense sequences. They can also be used to create transgenic
 CC animals. The proteins can be used to treat a variety of diseases and
 CC disorders, depending on their function. Diseases that may be treated
 CC include blood coagulation disorders, cancers and cellular adhesion
 CC disorders. They may also be used to raise antibodies. AAZ33891 to
 CC AAZ34338, and AAY41685 to AAY41774 represent polynucleotide and
 CC polypeptide sequence given in the exemplification of the present
 CC invention.
 CC
 CC
 SQ Sequence 518 AA;
 Query Match 100.0%; Score 2687; DB 20; Length 518;
 Best Local Similarity 100.0%; Pred. No. 3e-231;
 Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGALARALLPLAQLWILRAAPBLAPFTLPLRVAATNRVVAFTPGPTPAERHADGL 60
 DB 1 MGALARALLPLAQLWILRAAPBLAPFTLPLRVAATNRVVAFTPGPTPAERHADGL 60
 QY 61 ALALEPALASAGANFLAMVDNIOGDSGRGYLEMLIGTPPOKQLIVDTGSSNFAVAG 120
 DB 61 ALALEPALASAGANFLAMVDNIOGDSGRGYLEMLIGTPPOKQLIVDTGSSNFAVAG 120
 QY 121 TPHSYIDTYFPTERRSSTYRSKGFDTVTKYTOGSMWTFVGEDLVITIPKGFNTSFLVNIATI 180
 DB 121 TPHSYIDTYFPTERRSSTYRSKGFDTVTKYTOGSMWTFVGEDLVITIPKGFNTSFLVNIATI 180
 QY 181 FESNPFPLPGIKMNGIILGLAVATLAKPSSSLETFFDSLVTQANIPNVSMQCGAGLPLVA 240
 DB 181 FESNPFPLPGIKMNGIILGLAVATLAKPSSSLETFFDSLVTQANIPNVSMQCGAGLPLVA 240
 QY 241 GSGNGSGSIVIGTIEPSLYKGDIVWTPIKEMWYQIETLKIEIGOSNLDCRENNADKA 300
 DB 241 GSGNGSGSIVIGTIEPSLYKGDIVWTPIKEMWYQIETLKIEIGOSNLDCRENNADKA 300
 QY 301 IVDGTTLLRLPQKVFDAVVAARASLIPFSDGFTGSQLACWTNSETPMSYFPKISI 360
 DB 301 IVDGTTLLRLPQKVFDAVVAARASLIPFSDGFTGSQLACWTNSETPMSYFPKISI 360
 QY 361 YLRDENSRSRFRITTLPOLYIQPMAGALNCEYRFGISPTNALVIGATWMEGFYI 420

DB 361 YLRDENSRSRFRITTLPOLYIQPMAGALNCEYRFGISPTNALVIGATWMEGFYI 420
 QY 421 RAOKRVGFAPCAEIAAASVSEISGFSTEDVANSVCVPAQSLSEPLIMVSYALMSVCG 480
 DB 421 RAOKRVGFAPCAEIAAASVSEISGFSTEDVANSVCVPAQSLSEPLIMVSYALMSVCG 480
 QY 481 ALLVLVLLLPFCORRRPRDEPVNDESSLVHRMK 518
 DB 481 ALLVLVLLLPFCORRRPRDEPVNDESSLVHRMK 518
 RESULT 3
 AAY22239
 ID AAY22239 standard; Protein; 518 AA.
 XX
 AC AAY22239;
 XX
 DT 20-SEP-1999 (first entry)
 XX
 DE Human CSP56, aspartyl-type protease, protein sequence.
 XX
 KW Metastatic marker protein; human; cancer metastasis; breast cancer;
 KW colon cancer; diagnosis; therapy; tumour; metastatic potential;
 KW CSP56; aspartyl-type protease.
 XX
 OS Homo sapiens.
 XX
 PN NO9934004-A2
 XX
 XX 08-JUL-1999.
 PD
 XX 24-DEC-1998; 98WO-US27608.
 PF
 XX 31-DEC-1997; 97US-0070112.
 PR
 XX (CHIR) CHIRON CORP.
 PA
 XX Glese K, Xin H;
 PI
 XX WPI; 1999-430248/36.
 DR N-PSDB; AAX84708.
 DR
 XX
 PT New polynucleotides associated with cancer metastasis
 PT
 PS Claim 4; Page 78-80; 80pp; English.
 XX
 CC This sequence represents a polypeptide of the invention, and is
 CC an aspartyl-type protease, designated CSP56. The polynucleotides (PNS) of
 CC the invention encode metastatic marker protein variants. The PNS and
 CC polypeptides can be used as markers for cancer metastasis. The products
 CC can be used for identifying metastatic tissue or metastatic potential of
 CC a tissue, e.g. breast or colon tissue. They can also be used for
 CC screening test compounds for the ability to suppress the metastatic
 CC potential of a tumour. The products can be used for developing products
 CC for the therapy of cancers, particularly breast or colon cancer.
 CC
 CC
 SQ Sequence 518 AA;
 Query Match 100.0%; Score 2687; DB 20; Length 518;
 Best Local Similarity 100.0%; Pred. No. 3e-231;
 Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGALARALLPLAQLWILRAAPBLAPFTLPLRVAATNRVVAFTPGPTPAERHADGL 60
 DB 1 MGALARALLPLAQLWILRAAPBLAPFTLPLRVAATNRVVAFTPGPTPAERHADGL 60
 QY 61 ALALEPALASAGANFLAMVDNIOGDSGRGYLEMLIGTPPOKQLIVDTGSSNFAVAG 120
 DB 61 ALALEPALASAGANFLAMVDNIOGDSGRGYLEMLIGTPPOKQLIVDTGSSNFAVAG 120
 QY 121 TPHSYIDTYFPTERRSSTYRSKGFDTVTKYTOGSMWTFVGEDLVITIPKGFNTSFLVNIATI 180
 DB 121 TPHSYIDTYFPTERRSSTYRSKGFDTVTKYTOGSMWTFVGEDLVITIPKGFNTSFLVNIATI 180

QY 181 FESENFPLPGIKMNGIILGLAVATLAKPSSSLETFPDSLVTQANI PNVSQMCGAGLPVA 240
 DB 181 FESENFPLPGIKMNGIILGLAVATLAKPSSSLETFPDSLVTQANI PNVSQMCGAGLPVA 240
 QY 241 GSGTNGSLVIGIEPSLYKGDWYTPIKEWYQIEILKLEIGGQSLNDCREYNADKA 300
 DB 241 GSGTNGSLVIGIEPSLYKGDWYTPIKEWYQIEILKLEIGGQSLNDCREYNADKA 300
 QY 301 IVDGTTLLRLPQKVPFAVEAVARASLIPEFSDGFWTGSQACWTNSETPMWSYFPKISI 360
 DB 301 IVDGTTLLRLPQKVPFAVEAVARASLIPEFSDGFWTGSQACWTNSETPMWSYFPKISI 360
 QY 361 YLRDENSRSRFRITILPOLYIOPMMGAGLNEYCYRFGISPTNALVIGATWEGFYIIFD 420
 DB 361 YLRDENSRSRFRITILPOLYIOPMMGAGLNEYCYRFGISPTNALVIGATWEGFYIIFD 420
 QY 421 RAQKRVGFAPSPCAEIIAGAAVSEISGPFSTEDVASCNCPAQSLEPILIMIVSYALMSVCG 480
 DB 421 RAQKRVGFAPSPCAEIIAGAAVSEISGPFSTEDVASCNCPAQSLEPILIMIVSYALMSVCG 480
 QY 481 AILLVLIVLILPFCORRPRDPEVNDSSLVHRWK 518
 DB 481 AILLVLIVLILPFCORRPRDPEVNDSSLVHRWK 518

RESULT 4

AA13799
 ID AA13799 standard; Protein: 518 AA.

AC AA13799;

DT 21-SEP-1999 (first entry)

DE Human aspartyl protease, CSP56.

KW CSP56; human, aspartyl protease; diagnosis; neoplasia; tumour;
 KM breast tumour; colon tumour.

OS Homo sapiens.

FN WO9933963-A1.

PD 08-JUL-1999.

PE 14-DEC-1998; 98WO-US26547.

PR 31-DEC-1997; 97US-0070112.

XX (CHIR) CHIRON CORP.

XX Giese KW, Xin H;

XX WPI; 1999-430240/36.

XX DR N-PSDB; AAX89297.

XX PT Human CSP56 protein for diagnosis of neoplasia

XX PS Claim 2; Fig 2A; 51pp; English.

XX This represents a human CSP56 protein, a novel aspartyl protease. The

CC CSP56 protein can be used in methods for diagnosing neoplasia, for

CC determining the metastatic potential of a tumor, and for screening test

CC compounds for the ability to suppress the metastatic potential of a

CC tumour. The tumours are preferably from breast or colon.

XX Sequence 518 AA;

QY 1 MGALARALLPLLAQWLRAAPBLAPAPPTLPLRVAATAATNRVVAPTPGPTAERRHADGL 60

DB 1 MGALARALLPLLAQWLRAAPBLAPAPPTLPLRVAATAATNRVVAPTPGPTAERRHADGL 60
 QY 61 ALALEPALASPAGANFLAMVDNLQSGRGYIEMILIGTPPQQLIVDTGSSNFAVAG 120
 DB 61 ALALEPALASPAGANFLAMVDNLQSGRGYIEMILIGTPPQQLIVDTGSSNFAVAG 120
 QY 121 TPHSYIDTYPEDTERSSSTYRSKGFDTVKYTOGSWTGVEGDELVTIIPKGFNTSFLVNIATI 180
 DB 121 TPHSYIDTYPEDTERSSSTYRSKGFDTVKYTOGSWTGVEGDELVTIIPKGFNTSFLVNIATI 180
 QY 181 FESENFPLPGIKMNGIILGLAVATLAKPSSSLETFPDSLVTQANI PNVSQMCGAGLPVA 240
 DB 181 FESENFPLPGIKMNGIILGLAVATLAKPSSSLETFPDSLVTQANI PNVSQMCGAGLPVA 240
 QY 241 GSGTNGSLVIGIEPSLYKGDWYTPIKEWYQIEILKLEIGGQSLNDCREYNADKA 300
 DB 241 GSGTNGSLVIGIEPSLYKGDWYTPIKEWYQIEILKLEIGGQSLNDCREYNADKA 300
 QY 301 IVDGTTLLRLPQKVPFAVEAVARASLIPEFSDGFWTGSQACWTNSETPMWSYFPKISI 360
 DB 301 IVDGTTLLRLPQKVPFAVEAVARASLIPEFSDGFWTGSQACWTNSETPMWSYFPKISI 360
 QY 361 YLRDENSRSRFRITILPOLYIOPMMGAGLNEYCYRFGISPTNALVIGATWEGFYIIFD 420
 DB 361 YLRDENSRSRFRITILPOLYIOPMMGAGLNEYCYRFGISPTNALVIGATWEGFYIIFD 420
 QY 421 RAQKRVGFAPSPCAEIIAGAAVSEISGPFSTEDVASCNCPAQSLEPILIMIVSYALMSVCG 480
 DB 421 RAQKRVGFAPSPCAEIIAGAAVSEISGPFSTEDVASCNCPAQSLEPILIMIVSYALMSVCG 480
 QY 481 AILLVLIVLILPFCORRPRDPEVNDSSLVHRWK 518
 DB 481 AILLVLIVLILPFCORRPRDPEVNDSSLVHRWK 518

RESULT 5

AA44270
 ID AA44270 standard; Protein: 518 AA.

AC AA44270;

DT 08-FEB-2001 (first entry)

DE Human PRO852 (UNQ418) protein sequence SEQ ID NO:196.

KW Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;

KM expressed sequence tag; detection; cancer.

OS Homo sapiens.

FN WO200053756-A2.

PD 14-SEP-2000.

PE 18-FEB-2000; 2000WO-US04341.

PR 08-MAR-1999; 99WO-US05028.

PR 12-MAR-1999; 99US-0123957.

PR 21-MAR-1999; 99US-0126773.

PR 21-APR-1999; 99US-0130232.

PR 28-APR-1999; 99US-0131445.

PR 14-MAY-1999; 99US-0134287.

PR 23-JUN-1999; 99US-0141037.

PR 26-JUL-1999; 99US-0145698.

PR 29-OCT-1999; 99US-0162506.

PR 30-NOV-1999; 99WO-US28313.

PR 02-DEC-1999; 99WO-US28551.

PR 16-DEC-1999; 99WO-US30095.

PR 30-DEC-1999; 99WO-US31243.

PR 30-DEC-1999; 99WO-US31274.

PR 05-JAN-2000; 2000WO-US00219.

06-JAN-2000; 2000MO-US00277.
 PR 06-JAN-2000; 2000MO-US00376.
 XX
 PA (GERTH) GENENTECH INC.
 XX
 PI Aeshkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Filvarolf E, Fong S, Gao W, Gether H, Gertlisen ME;
 PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
 PI Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
 PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WJ;
 XX
 DR WPI; 2000-611443/58.
 DR N-PSDB; AAC78500.
 XX
 PT Novel PRO polypeptides and polynucleotides used in detection methods,
 PT to target bioactive molecules to specific cells, and to modulate
 PT cellular activities -
 XX
 PS
 XX Claim 12; Fig 73; 636pp; English.
 XX
 CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed
 CC sequence tag) sequences which encode secreted or transmembrane PRO
 CC polypeptides. The PRO polynucleotides and polypeptides have cytosolic
 CC activity. The polynucleotides and polypeptides can be used for detecting
 CC the presence of PRO polypeptides in samples, for linking bioactive
 CC molecules to cells and for modulating biological activities of cells,
 CC using the polypeptides for specific targeting. The polypeptide targeting
 CC can be used to kill the target cells, e.g. for the treatment of cancers.
 CC The polypeptide pairs provide specific targeting of bioactive molecules
 CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
 CC the isolation of the PRO polynucleotide sequences.
 XX
 SQ Sequence 518 AA;
 Query Match 100.0%; Score 2687; DB 21; Length 518;
 Best Local Similarity 100.0%; Pred. No. 3e-231;
 Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGALARALLPLQLQWLLRAAPELAPAPFTLLPRLVAATNRVAPTPGPGPARHADGL 60
 DB 1 MGALARALLPLQLQWLLRAAPELAPAPFTLLPRLVAATNRVAPTPGPGPARHADGL 60
 QY 61 ALALEPALASPAGANFLAMVDNIOGDSGRGYLEMLIGTPPKQLIIVDTGSSNFAVAG 120
 DB 61 ALALEPALASPAGANFLAMVDNIOGDSGRGYLEMLIGTPPKQLIIVDTGSSNFAVAG 120
 QY 121 TPHSYIDYPTERTSSSTRSGKGFVTVKYTGSGTGVGVEDLVITIPKGFNTSFLVNIATI 180
 DB 121 TPHSYIDYPTERTSSSTRSGKGFVTVKYTGSGTGVGVEDLVITIPKGFNTSFLVNIATI 180
 QY 181 FESNFFLPGLKMGIIIGLAAYATLAKPSSSLPTFDSLVTOANIPNVFSMOMCGAGLPVA 240
 DB 181 FESNFFLPGLKMGIIIGLAAYATLAKPSSSLPTFDSLVTOANIPNVFSMOMCGAGLPVA 240
 QY 241 GSGTNGSLVIGIEPLSYKGDIVWTPKIEWYQIEILKLEIGGOSINLDCREYNADKA 300
 DB 241 GSGTNGSLVIGIEPLSYKGDIVWTPKIEWYQIEILKLEIGGOSINLDCREYNADKA 300
 QY 301 IVDGTTLLRLPKQVFDVAVAVASLIPERSDGFMTGSOLACTNSETPWSYFPKISI 360
 DB 301 IVDGTTLLRLPKQVFDVAVAVASLIPERSDGFMTGSOLACTNSETPWSYFPKISI 360
 QY 361 YLRBENSRSRFRITILPOLYIOPMMGAGLANEYCFRFGISPTSNALVIGATWEGYVIFD 420
 DB 361 YLRBENSRSRFRITILPOLYIOPMMGAGLANEYCFRFGISPTSNALVIGATWEGYVIFD 420
 QY 421 RAQRVGFPAAPCAEIIAGAAVSEISGPESTDVASCNPAOSLSEPLIMVSYALMSVCG 480
 DB 421 RAQRVGFPAAPCAEIIAGAAVSEISGPESTDVASCNPAOSLSEPLIMVSYALMSVCG 480
 QY 481 AILVLVLLLPCCORRRPDPPEVNDSSLVHRMK 518
 DB 481 AILVLVLLLPCCORRRPDPPEVNDSSLVHRMK 518

RESULT 6
 AAY88424
 ID AAY88424 standard; Protein; 518 AA.
 XX
 AC AAY88424;
 XX
 DT 03-AUG-2000 (first entry)
 XX
 DE Human aspartyl protease 1 (Asp1) amino acid sequence.
 XX
 KW Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 1;
 KW Alzheimer's disease; beta secretase site.
 OS Homo sapiens.
 XX
 EN WO200017369-A2.
 XX
 PD 30-MAR-2000.
 XX
 PF 23-SEP-1999; 99MO-US20881.
 XX
 PR 24-SEP-1998; 98US-0101594.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 PI Gurney ME, Bienkowski MJ, Heinrikson RL, Parodi LA, Yan R;
 DR WPI; 2000-303209/26.
 DR N-PSDB; AAA15661.
 XX
 PT New enzyme designated human aspartase useful in research into
 PT the beta secretase site to produce amyloid beta peptide
 PS
 XX Claim 54; Fig 1; 183pp; English.
 CC This sequence represents the human aspartyl protease amino acid sequence.
 CC The invention relates to a protease capable of cleaving the beta
 CC secretase site of amyloid precursor protein (APP). The protease contains
 CC a sequence encoding the amino acid sequence DTG and a sequence encoding
 CC DSG or DTG separated by 100-300 amino acids. When mutated the APP gene
 CC causes an autosomal dominant form of Alzheimer's disease. APP localises
 CC to the cell surface membrane and have a single C-terminal transmembrane
 CC domain. Proteolytic processing of APP produces the amyloid beta protein,
 CC which is possibly very important in Alzheimer's disease. The invention
 CC includes a nucleotide sequence encoding the protease, a vector containing
 CC the nucleotide sequence, and a cell line comprising the vector. Methods
 CC for screening for inhibitors of beta secretase activity are also given in
 CC the invention. The human aspartase protein and nucleotide sequences and
 CC the methods for identifying inhibitors of the protease, are useful in the
 CC treatment of and research in to Alzheimer's disease.
 XX
 SQ Sequence 518 AA;
 Query Match 100.0%; Score 2687; DB 21; Length 518;
 Best Local Similarity 100.0%; Pred. No. 3e-231;
 Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGALARALLPLQLQWLLRAAPELAPAPFTLLPRLVAATNRVAPTPGPGPARHADGL 60
 DB 1 MGALARALLPLQLQWLLRAAPELAPAPFTLLPRLVAATNRVAPTPGPGPARHADGL 60
 QY 61 ALALEPALASPAGANFLAMVDNIOGDSGRGYLEMLIGTPPKQLIIVDTGSSNFAVAG 120
 DB 61 ALALEPALASPAGANFLAMVDNIOGDSGRGYLEMLIGTPPKQLIIVDTGSSNFAVAG 120
 QY 121 TPHSYIDYPTERTSSSTRSGKGFVTVKYTGSGTGVGVEDLVITIPKGFNTSFLVNIATI 180
 DB 121 TPHSYIDYPTERTSSSTRSGKGFVTVKYTGSGTGVGVEDLVITIPKGFNTSFLVNIATI 180
 QY 181 FESNFFLPGLKMGIIIGLAAYATLAKPSSSLPTFDSLVTOANIPNVFSMOMCGAGLPVA 240
 DB 181 FESNFFLPGLKMGIIIGLAAYATLAKPSSSLPTFDSLVTOANIPNVFSMOMCGAGLPVA 240

```

DB 181 FESNFPLPGIKMNGIIGLAVALAKPSSLETFFDSLVTOANI PNVSQMCGAGLPVA 240
QY 241 GSGTNGSLVIGIEPSLYKGDIVYTPKEMWYQIETLKIEIGGSLNLCREYNADKA 300
DB 241 GSGTNGSLVIGIEPSLYKGDIVYTPKEMWYQIETLKIEIGGSLNLCREYNADKA 300
QY 301 IVDGTTLLRLPQKVPDAVAVARASLIPEFSDGFWTGSQACWTSNSETWMSYFPKISI 360
DB 301 IVDGTTLLRLPQKVPDAVAVARASLIPEFSDGFWTGSQACWTSNSETWMSYFPKISI 360
QY 361 YLRDENSRSFRITILPOLYIQPMGAGLNEYCYRFGISPSSTNALVIGATWMEGFYVIFD 420
DB 361 YLRDENSRSFRITILPOLYIQPMGAGLNEYCYRFGISPSSTNALVIGATWMEGFYVIFD 420
QY 421 RAQKRVGFAASPACAEIAGAAVSEISGPSTEDVASCNCPAOSLSPELITWISYALMSVCG 480
DB 421 RAQKRVGFAASPACAEIAGAAVSEISGPSTEDVASCNCPAOSLSPELITWISYALMSVCG 480
QY 481 AILVLVILVLLPFCQRRPDPPEVNDSSLVHRMK 518
DB 481 AILVLVILVLLPFCQRRPDPPEVNDSSLVHRMK 518

```

RESULT 7
AAE10628
ID AAE10628 standard; Protein: 518 AA.

```

XX 10-DEC-2001 (first entry)
XX Human aspartyl protease 1 (hu-Asp1) protein.
XX
XX Human; aspartyl protease 1; Asp1; amyloid precursor protein; APP;
XX Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
XX amyloid plaque; neuronal loss; proteolytic; neurotrophic; neuroprotective;
XX chromosome 21.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..20
XX FT /label= Signal_peptide
XX FT 21..518
XX FT /note= "Mature human aspartyl protease 1"
XX FT Domain 469..492
XX FT /label= Transmembrane_domain
XX
XX GB2357767-A.
XX
XX 04-JUL-2001.
XX
XX 22-SEP-2000; 2000GB-0023315.
XX
XX 23-SEP-1999; 99US-0155493.
XX 23-SEP-1999; 99US-0404133.
XX 23-SEP-1999; 99WO-US20881.
XX 13-OCT-1999; 99US-0416901.
XX 06-DEC-1999; 99US-0169232.
XX
XX (PHAA ) PHARMACIA & UPJOHN CO.
XX
XX Bienkowski MJ, Gurney M;
XX
XX WPI; 2001-444208/48.
XX
XX N-PSDB; AAD17864.
XX
XX
XX Polypeptide comprising fragments of human aspartyl protease with
XX amyloid precursor protein processing activity and alpha-secretase
XX activity, for identifying modulators useful in treating Alzheimer's
XX disease -
XX

```

PS Claim 36; Fig 1; 187bp; English.

XX The patent discloses human aspartyl protease 1 (hu-Asp1) or modified
 CC Asp1 proteins which lack transmembrane domain or amino terminal
 CC domain or cytoplasmic domain and retains alpha-secretase activity
 CC and amyloid protein precursor (APP) processing activity. The proteins
 CC of the invention are useful for assaying hu-Asp1 alpha-secretase
 CC activity, which in turn is useful for identifying modulators of
 CC hu-Asp1 alpha-secretase activity, where modulators that increase
 CC hu-Asp1 alpha-secretase activity are useful for treating Alzheimer's
 CC disease (AD) which causes progressive dementia with consequent
 CC formation of amyloid plaques, neurofibrillary tangles, gliosis and
 CC neuronal loss. Hu-Asp1 protease substrate is useful for assaying
 CC hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein with
 CC the substrate under acidic conditions and determining the level of
 CC hu-Asp1 proteolytic activity. The present sequence is Asp1 protein
 CC from human. Asp1 gene is localized on chromosome 21.

XX Sequence 518 AA;

Query Match 100.0%; Score 2687; DB 22; Length 518;

Best Local Similarity 100.0%; Pred. No. 3e-231;

Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MGALARALLPPLAQWLLRAAPELAPFTILRVAAATNRVVAFTPGPTARRHADGL 60
DB 1 MGALARALLPPLAQWLLRAAPELAPFTILRVAAATNRVVAFTPGPTARRHADGL 60
QY 61 ALALEPALASPAGANFLAWDNIGDSGRGYTEMIGTPPOKQLIIVDTGSSNFAVAG 120
DB 61 ALALEPALASPAGANFLAWDNIGDSGRGYTEMIGTPPOKQLIIVDTGSSNFAVAG 120
QY 121 TPHSYIDYFPTERSSTYRSKGFDTVTKYTGQSWTGFVGEDLVTIYPKGFNTSFLVNIATI 180
DB 121 TPHSYIDYFPTERSSTYRSKGFDTVTKYTGQSWTGFVGEDLVTIYPKGFNTSFLVNIATI 180
QY 181 FESNFPLPGIKMNGIIGLAVALAKPSSLETFFDSLVTOANI PNVSQMCGAGLPVA 240
DB 181 FESNFPLPGIKMNGIIGLAVALAKPSSLETFFDSLVTOANI PNVSQMCGAGLPVA 240
QY 241 GSGTNGSLVIGIEPSLYKGDIVYTPKEMWYQIETLKIEIGGSLNLCREYNADKA 300
DB 241 GSGTNGSLVIGIEPSLYKGDIVYTPKEMWYQIETLKIEIGGSLNLCREYNADKA 300
QY 301 IVDGTTLLRLPQKVPDAVAVARASLIPEFSDGFWTGSQACWTSNSETWMSYFPKISI 360
DB 301 IVDGTTLLRLPQKVPDAVAVARASLIPEFSDGFWTGSQACWTSNSETWMSYFPKISI 360
QY 361 YLRDENSRSFRITILPOLYIQPMGAGLNEYCYRFGISPSSTNALVIGATWMEGFYVIFD 420
DB 361 YLRDENSRSFRITILPOLYIQPMGAGLNEYCYRFGISPSSTNALVIGATWMEGFYVIFD 420
QY 421 RAQKRVGFAASPACAEIAGAAVSEISGPSTEDVASCNCPAOSLSPELITWISYALMSVCG 480
DB 421 RAQKRVGFAASPACAEIAGAAVSEISGPSTEDVASCNCPAOSLSPELITWISYALMSVCG 480
QY 481 AILVLVILVLLPFCQRRPDPPEVNDSSLVHRMK 518
DB 481 AILVLVILVLLPFCQRRPDPPEVNDSSLVHRMK 518

```

RESULT 8
AAE10656
ID AAE10656 standard; Protein: 518 AA.

```

XX 10-DEC-2001 (first entry)
XX Human-Asp 1 protein lacking TM domain and containing (His) 6 tag.
XX
XX Human; aspartyl protease 1; Asp1; amyloid precursor protein; APP;
XX Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
XX

```

KM amyloid plaque; neuronal loss; proteolytic; neurotropic; neuroprotective.
 XX Homo sapiens.
 OS Synthetic.
 XX GB357767-A.
 PN
 XX
 XX 04-JUL-2001.
 PD
 XX
 XX 22-SEP-2000; 2000GB-0023315.
 PF
 XX 23-SEP-1999; 99US-0155493.
 PR 23-SEP-1999; 99US-0404133.
 PR 23-SEP-1999; 99MO-US20881.
 PR 13-OCT-1999; 99US-0416901.
 PR 06-DEC-1999; 99US-0169232.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 XX Bienkowskaki MJ, Gurney M;
 PI
 XX WPI; 2001-444208/48.
 DR
 XX
 XX
 PT Polypeptide comprising fragments of human aspartyl protease with
 PT amyloid precursor protein processing activity and alpha-secretase
 PT activity, for identifying modulators useful in treating Alzheimer's
 PT disease -
 XX
 XX Example 14; Page 155-156; 187pp; English.
 PS
 XX The patent discloses human aspartyl protease 1 (hu-Asp1) or modified
 CC Asp1 proteins which lack transmembrane domain or amino terminal
 CC domain or cytoplasmic domain and retains alpha-secretase activity
 CC and amyloid protein precursor (APP) processing activity. The proteins
 CC of the invention are useful for assaying hu-Asp1 alpha-secretase
 CC activity, which in turn is useful for identifying modulators of
 CC hu-Asp1 alpha-secretase activity, where modulators that increase
 CC hu-Asp1 alpha-secretase activity are useful for treating Alzheimer's
 CC disease (AD) which causes progressive dementia with consequent
 CC formation of amyloid plaques, neurofibrillary tangles, gliosis and
 CC neuronal loss. Hu-Asp1 protease substrate is useful for assaying
 CC hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein with
 CC the substrate under acidic conditions and determining the level of
 CC hu-Asp1 proteolytic activity. The present sequence is human Asp 1
 CC protein lacking a transmembrane (TM) domain and containing (His)6
 CC tag. This sequence is generated from human Asp 1 protein by the
 CC deletion of its C-terminal TM domain and addition of hexa-histidine
 CC tag at its C-terminus.
 CC
 XX
 XX Sequence 518 AA;
 SQ
 Query Match 100.0%; Score 2687; DB 22; Length 518;
 Best Local Similarity 100.0%; Pred. No. 3e-231;
 Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 241 GSGTNGSLVIGIBPSLYKDIWTPPIKEEMYYQIEILKLEIGGSLINDCREYNADKA 300
 Qy 301 IVDSGTTLRLPQKVFADVAEVARASLIPEFSDGFWTGSOLACMTSETPMSYFPKISI 360
 Db 301 IVDSGTTLRLPQKVFADVAEVARASLIPEFSDGFWTGSOLACMTSETPMSYFPKISI 360
 Qy 361 YLRDENSRSRFRITILPOLYIQPMWAGLNEYCYRFGISPSSTNALVIGATWEGFFYVIFD 420
 Db 361 YLRDENSRSRFRITILPOLYIQPMWAGLNEYCYRFGISPSSTNALVIGATWEGFFYVIFD 420
 Qy 421 RAQKRVGFPAAPCAEIAAGAAVSEISGPFSTEDVASCNCPAQSISEPTIMIVSYALMSVCG 480
 Db 421 RAQKRVGFPAAPCAEIAAGAAVSEISGPFSTEDVASCNCPAQSISEPTIMIVSYALMSVCG 480
 Qy 481 ALLVLVILLLPPRCORRPDPPEVNDSESLVHRMK 518
 Db 481 ALLVLVILLLPPRCORRPDPPEVNDSESLVHRMK 518
 RESULT 9
 ID AAU29059
 AAU29059 standard; Protein; 518 AA.
 XX
 AC AAU29059;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human PRO polypeptide sequence #36.
 XX
 KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
 KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WC200168848-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 28-FEB-2001; 2001WO-US06520.
 XX
 XX 01-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 03-MAR-2000; 2000US-187202P.
 PR 05-MAR-2000; 2000US-186968P.
 PR 14-MAR-2000; 2000US-189320P.
 PR 14-MAR-2000; 2000US-189328P.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 21-MAR-2000; 2000US-190828P.
 PR 21-MAR-2000; 2000US-191007P.
 PR 21-MAR-2000; 2000US-191048P.
 PR 21-MAR-2000; 2000US-191314P.
 PR 28-MAR-2000; 2000US-192655P.
 PR 29-MAR-2000; 2000US-193032P.
 PR 29-MAR-2000; 2000US-193053P.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 04-APR-2000; 2000US-194449P.
 PR 04-APR-2000; 2000US-194647P.
 PR 11-APR-2000; 2000US-195975P.
 PR 11-APR-2000; 2000US-196000P.
 PR 11-APR-2000; 2000US-196187P.
 PR 11-APR-2000; 2000US-196690P.
 PR 11-APR-2000; 2000US-196820P.
 PR 18-APR-2000; 2000US-198121P.
 PR 18-APR-2000; 2000US-198585P.
 PR 25-APR-2000; 2000US-199397P.
 PR 25-APR-2000; 2000US-199550P.
 PR 25-APR-2000; 2000US-199654P.
 PR 03-MAY-2000; 2000US-201516P.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.

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PR 02-JUN-2000; 2000WO-US15264.
PR 05-JUN-2000; 2000US-209832P.
PR 28-JUN-2000; 2000WO-US02710.
PR 22-AUG-2000; 2000US-0644848.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
XX
XX (GERTH ) GENENTECH INC.
XX
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
XX MPI: 2001-602746/68.
XX N-PSDB; AAS45960.
XX
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumours, such as prostate and breast tumours, in mammals and
PT to screen for modulators of the compounds -
XX
XX Claim 11; Fig 72; 774pp: English.
XX
XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
CC The PRO polypeptides and their associated nucleic acids can be used to
CC detect the presence of a tumour in a mammal by comparing the level of
CC expression of a PRO polypeptide in a test sample of cells from the animal
CC and a control sample of normal cells, whereby a higher level of
CC expression in the test sample indicates the presence of a tumour in the
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC and rabbits but are preferably human. The polypeptides can be used to
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC when contacted with it. A specific polypeptide can be used to stimulate
CC the proliferation or differentiation of chondrocyte cells. The PRO
CC proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders.
XX
XX Sequence 518 AA:
XX
XX Query Match 100.0%; Score 2687; DB 22; Length 518;
XX Best Local Similarity 100.0%; Pred. No. 3e-231;
XX Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MGALRALLLPLLAQWLLFAAPBLAPAPPTLLPRVAAANRVVAPPPGCTPAERHADDL 60
XX 1 MGALRALLLPLLAQWLLFAAPBLAPAPPTLLPRVAAANRVVAPPPGCTPAERHADDL 60
XX
XX 61 ALALEPALASPAGANFLMVDNLQSGRGYYLEMLIGTPPOKQIILVDTGSSNFAVAG 120
XX 61 ALALEPALASPAGANFLMVDNLQSGRGYYLEMLIGTPPOKQIILVDTGSSNFAVAG 120
XX
XX 121 TPHSYIDTYFDTERSSSTYRSKGFDTVTKTQGSWTGFEVEDLVTIPKGFNTSFLVNIATI 180
XX 121 TPHSYIDTYFDTERSSSTYRSKGFDTVTKTQGSWTGFEVEDLVTIPKGFNTSFLVNIATI 180
XX
XX 121 TPHSYIDTYFDTERSSSTYRSKGFDTVTKTQGSWTGFEVEDLVTIPKGFNTSFLVNIATI 180
XX 121 TPHSYIDTYFDTERSSSTYRSKGFDTVTKTQGSWTGFEVEDLVTIPKGFNTSFLVNIATI 180
XX
XX 181 FESSENFELPGIKWNGILGLATLAPSSSLTEFPDSLVTONIPNVFSMOMCGAGLPPVA 240
XX 181 FESSENFELPGIKWNGILGLATLAPSSSLTEFPDSLVTONIPNVFSMOMCGAGLPPVA 240
XX
XX 181 FESSENFELPGIKWNGILGLATLAPSSSLTEFPDSLVTONIPNVFSMOMCGAGLPPVA 240
XX 181 FESSENFELPGIKWNGILGLATLAPSSSLTEFPDSLVTONIPNVFSMOMCGAGLPPVA 240
XX
XX 241 GSGTNGGSLVGLGIEPSLTKGDIWYPIREBMYYOIEIKLEIGGOSLNDCEHYADXA 300
XX 241 GSGTNGGSLVGLGIEPSLTKGDIWYPIREBMYYOIEIKLEIGGOSLNDCEHYADXA 300
XX
XX 241 GSGTNGGSLVGLGIEPSLTKGDIWYPIREBMYYOIEIKLEIGGOSLNDCEHYADXA 300
XX 241 GSGTNGGSLVGLGIEPSLTKGDIWYPIREBMYYOIEIKLEIGGOSLNDCEHYADXA 300
XX
XX 301 IYDSGTTLLRLPQKVDVAVEAVARASLIPEFSDGFWTSQOLACWNSETPMSYFPKISI 360
XX 301 IYDSGTTLLRLPQKVDVAVEAVARASLIPEFSDGFWTSQOLACWNSETPMSYFPKISI 360
XX
XX 361 YRDENSSSFRITLIPOLIYOPMGAGLNYECYRFGISBPNALVIGATWEGFVIYD 420
XX 361 YRDENSSSFRITLIPOLIYOPMGAGLNYECYRFGISBPNALVIGATWEGFVIYD 420
XX
XX 361 YRDENSSSFRITLIPOLIYOPMGAGLNYECYRFGISBPNALVIGATWEGFVIYD 420
XX 361 YRDENSSSFRITLIPOLIYOPMGAGLNYECYRFGISBPNALVIGATWEGFVIYD 420

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XX 421 RAQKRVGFASPCAEIAGAVSEISGFSTEDVNASNCVPAQSLSEPIIMTVSALMSVCG 480
XX 421 RAQKRVGFASPCAEIAGAVSEISGFSTEDVNASNCVPAQSLSEPIIMTVSALMSVCG 480
XX
XX 481 AILVLVLLPLPRCORPRPDEPVNVNDESLVHRMK 518
XX 481 AILVLVLLPLPRCORPRPDEPVNVNDESLVHRMK 518
XX
XX 481 AILVLVLLPLPRCORPRPDEPVNVNDESLVHRMK 518
XX 481 AILVLVLLPLPRCORPRPDEPVNVNDESLVHRMK 518
XX
XX
XX RESULT 10
XX AAE06858
XX ID AAE06858 standard; Protein; 518 AA.
XX
XX AAE06858;
XX
XX 23-OCT-2001 (first entry)
XX
XX Human aspartyl protease 1 (Hu-Asp1) protein.
XX
XX Human; aspartyl protease 1; Asp 1; beta-amyloid precursor protein; APP;
XX beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
XX neurofibrillary tangle; neuronal loss; amyloid-beta peptide; neurotropic;
XX neuroprotective; antisense therapy; gene therapy; chromosome 21.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..20
XX Protein /label=Signal_peptide
XX /note="Mature human aspartyl protease 1 (Hu-Asp1)"
XX Domain 465..492
XX /label=Transmembrane_domain
XX
XX WC200150829-A2.
XX
XX 19-JUL-2001.
XX
XX 09-MAY-2001; 2001WO-IB00799.
XX
XX 09-MAY-2001; 2001WO-IB00799.
XX
XX (BIEN/) BIENKOWSKI M J.
XX (GURN/) GURNEY M E.
XX (HEIN/) HEINRIKSON R L.
XX (PARO/) PARODI L A.
XX (YANR/) YAN R.
XX
XX Blenkowski MO, Gurney ME, Heinrichson RL, Parodi LA, Yan R;
XX MPI: 2001-483072/52.
XX N-PSDB; AAD13020.
XX
XX Novel purified polypeptide comprising fragment of mammalian aspartyl
XX protease 2, lacking Asp2 transmembrane domain and retaining beta
XX secretase activity of Asp2 useful for identifying inhibitors of Asp2
XX activity
XX
XX Example 2; Fig 1; 185pp: English.
XX
XX The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
XX precursor protein (APP) isoforms and their corresponding DNA molecules.
XX Human aspartyl proteases can act as beta-secretase proteases useful for
XX treating Alzheimer's disease. APP isoforms are useful for identifying
XX modulators of amyloid-beta peptide production, for use in designing
XX therapeutics for the treatment and prevention of Alzheimer's disease,
XX dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
XX and neuronal loss. APP isoforms are also used in methods for identifying
XX inhibitors and modulators of human Asp2 activity. The invention relates
XX to a method for identifying agents that modulate the activity of human
XX aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
XX as a means to screen in cellular assays for the inhibitors of beta- and

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|||||
Db 361 YLRDENSRSFRITILPOLYIQPMGAGLNVCEYRFGISPSSTNALVIGATWEGFYIFD 420
Oy 421 RAQKRVGFPAASPCAEIAGAAVSEISGPFSTEDVASCNCPAQSLEPILMIVSYALMSVCG 480
Db 421 RAQKRVGFPAASPCAEIAGAAVSEISGPFSTEDVASCNCPAQSLEPILMIVSYALMSVCG 480
Oy 481 AILVLIVLILLLPFRQRRPRDPEVYNDESSLVHRHWK 518
Db 481 AILVLIVLILLLPFRQRRPRDPEVYNDESSLVHRHWK 518

RESULT 12
AAU07201
ID AAU07201 standard; Protein; 518 AA.
XX
AC AAU07201;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human aspartyl protease 1 (Asp-1).
XX
KW Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;
KM aspartyl protease 2; Asp2; amyloid protein precursor; APP;
KM beta-secretase; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN MO200149097-A2.
XX
PD 12-JUL-2001.
XX
PE 09-MAY-2001; 2001MO-IB00797.
XX
PR 09-MAY-2001; 2001MO-IB00797.
XX
PA (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (VANR/) VAN R.
XX
PI Bienkowski MJ, Gurney ME, Heinrichson RL, Parodi LA, Van R;
XX
DR WPI: 2001-502548/55.
XX
DR N-PSDB; AAS11701.
XX
PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
XX
XX activity -
XX
XX Example 2; Fig 1; 185bp; English.
XX
XX
CC The invention relates to a novel purified polypeptide comprising a
CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
CC and the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. Also included is an isoform of amyloid protein precursor (APP)
CC comprising the amino acid sequence of a APP or its fragment containing
CC an APP cleavage site recognizable by a mammalian beta-secretase, and
CC further comprising two lysine residues at the carboxyl terminus of the
CC amino acid sequence of the mammalian APP or APP fragment. The
CC polypeptides are used for assaying for modulators of beta-secretase
CC activity; identifying agents that inhibit the APP processing activity
CC of human Asp2 aspartyl protease (Hu-Asp2); identifying agents that
CC modulate the activity of Asp2; and for reducing cellular production of
CC amyloid beta (Abeta) from APP. Agents identified by the above methods
CC are useful for treating Alzheimer's disease; and for identifying
CC modulators of amyloid-beta (Abeta) peptide production, for use in
CC designing therapeutics for the treatment or prevention of Alzheimer's
CC disease. Probes and primers derived from Asp nucleic acid sequences
CC are useful for detecting Hu-Asp nucleic acids in in vitro assays and in
```

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CC Northern and Southern blots. The present sequence represents the
CC amino acid sequence of human Asp-1.
XX
SQ Sequence 518 AA;
Query Match 100.0%; Score 2687; DB 22; Length 518;
Best Local Similarity 100.0%; Pred. No. 3e-231;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 MGALRALILPLQLQWILRAPELAPAPFTLPLRAAATNRVVAPTPGPGTAPARRHADGL 60
Db 1 MGALRALILPLQLQWILRAPELAPAPFTLPLRAAATNRVVAPTPGPGTAPARRHADGL 60
Oy 61 ALALEPALASPAGANFLAWVDNLQDSDGRGYLEMLIGTPPOKQLILVDTGSSNFAVAG 120
Db 61 ALALEPALASPAGANFLAWVDNLQDSDGRGYLEMLIGTPPOKQLILVDTGSSNFAVAG 120
Oy 121 TPHSYIDTYFDTERSSSTYRSKGFVTVYKYGWTFGVGEDLVITIPKGFNTSELVNATI 180
Db 121 TPHSYIDTYFDTERSSSTYRSKGFVTVYKYGWTFGVGEDLVITIPKGFNTSELVNATI 180
Oy 181 FESSEFPLPGIKMGIIGLAATLAKPSSLETFPDSLVTOANI PNYSMQMGAGLPVA 240
Db 181 FESSEFPLPGIKMGIIGLAATLAKPSSLETFPDSLVTOANI PNYSMQMGAGLPVA 240
Oy 241 GSGTNGSLVVGGLIEPSLYKGDWYTPIKEEMYYQIEILKLEIGQSILNDCREYNADKA 300
Db 241 GSGTNGSLVVGGLIEPSLYKGDWYTPIKEEMYYQIEILKLEIGQSILNDCREYNADKA 300
Oy 301 IVDSGTLLRLPQKVFDAVAVARASLIPFSGFWTGSQLAQWNTSETWMSYFPKISI 360
Db 301 IVDSGTLLRLPQKVFDAVAVARASLIPFSGFWTGSQLAQWNTSETWMSYFPKISI 360
Oy 361 YLRDENSRSFRITILPOLYIQPMGAGLNVCEYRFGISPSSTNALVIGATWEGFYIFD 420
Db 361 YLRDENSRSFRITILPOLYIQPMGAGLNVCEYRFGISPSSTNALVIGATWEGFYIFD 420
Oy 421 RAQKRVGFPAASPCAEIAGAAVSEISGPFSTEDVASCNCPAQSLEPILMIVSYALMSVCG 480
Db 421 RAQKRVGFPAASPCAEIAGAAVSEISGPFSTEDVASCNCPAQSLEPILMIVSYALMSVCG 480
Oy 481 AILVLIVLILLLPFRQRRPRDPEVYNDESSLVHRHWK 518
Db 481 AILVLIVLILLLPFRQRRPRDPEVYNDESSLVHRHWK 518

RESULT 13
AAE02580
ID AAE02580 standard; Protein; 518 AA.
XX
AC AAE02580;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human aspartyl protease 1 (Asp 1).
XX
KW Human; alpha-secretase; amyloid precursor protein; APP; therapy;
KW Alzheimer's disease; antialzheimer's; aspartyl protease 1; Asp 1;
KW beta-secretase; chromosome 21.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH Peptide 1..20
FT /label= Signal_peptide
FT Peptide 22..62
FT /label= Asp_1_prepropeptide
FT Peptide 23..62
FT /label= Asp_1_propeptide
FT Protein 63..518
FT /label= Mature human Asp 1 protein
FT /note= "Specifically claimed"
FT Active-site 87..89
```

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FT Active-site /label= Active_site_1
FT 110..113
FT /label= Active_site_2
FT Active-site 303..305
FT /label= Active_site_3
FT 469..492
FT Domain /label= Transmembrane_domain
FT 493..518
FT /label= Cytoplasmic_domain
FT Region 497..518
FT /note= "Peptide #1"
XX
XX WO200123533-A2.
XX
XX 05-APR-2001.
XX
XX 22-SEP-2000; 2000WO-US26080.
XX
XX 23-SEP-1999; 99US-0155493.
XX 23-SEP-1999; 99WO-US20881.
XX 13-OCT-1999; 99US-0416901.
XX 06-DEC-1999; 99US-0169232.
XX
XX (PHAA ) PHARMACIA & UPJOHN CO.
XX
XX Gurney M, Bienkowski MJ;
XX
XX WPI; 2001-290516/30.
XX
XX N-PSDB; AAD06738.
XX
XX
XX Enzymes that cleave the alpha-secretase site of the amyloid precursor
XX protein, useful for the treatment of Alzheimer's disease -
XX
XX Claim 29; Fig 1; 189pp; English.
XX
XX The present invention relates to enzymes for cleaving the alpha-
XX secretase site of the amyloid precursor protein (APP) and methods of
XX identifying those enzymes. The methods may be used to identify enzymes
XX that may be used to cleave the alpha-secretase cleavage site of the APP
XX protein. The enzymes may be used to treat or modulate the progress of
XX Alzheimer's disease. The present sequence is human aspartyl protease 1
XX (Asp1). Asp1 has alpha-secretase protease and beta-secretase
XX protease activities. Asp1 gene is located on chromosome 21.
XX
XX
XX Sequence 518 AA;
XX
XX Query Match 100.0%; Score 2687; DB 22; Length 518;
XX Best Local Similarity 100.0%; Pred. No. 3e-231;
XX Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVVAFTPGPTPAERHADGL 60
XX
XX 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVVAFTPGPTPAERHADGL 60
XX
XX 61 ALALEPALASPAGANFLAMVDNIQDSGRGYLEMLIGTPPOKLIIVDTGSSNFAVAG 120
XX
XX 61 ALALEPALASPAGANFLAMVDNIQDSGRGYLEMLIGTPPOKLIIVDTGSSNFAVAG 120
XX
XX 121 TPHSYIDVYPTERSSTRSGKGFVTVYKTGSGTGFGEEDLVITPKGFNTSFLVNIAITI 180
XX
XX 121 TPHSYIDVYPTERSSTRSGKGFVTVYKTGSGTGFGEEDLVITPKGFNTSFLVNIAITI 180
XX
XX 181 FESNFPLPGIKMNGIILGAYATLAKPSSLETFFDSLVTOANIPNVSMQCGAGLVA 240
XX
XX 181 FESNFPLPGIKMNGIILGAYATLAKPSSLETFFDSLVTOANIPNVSMQCGAGLVA 240
XX
XX 241 GSGTNGSGLVIGIEPLSYKGDIVYTPIKEWYQIIEITLKEIGSGSINTLDCREYNADKA 300
XX
XX 241 GSGTNGSGLVIGIEPLSYKGDIVYTPIKEWYQIIEITLKEIGSGSINTLDCREYNADKA 300
XX
XX 301 IVDSTTLRLTPQKVFDAVVAVASLIPESDGFMTGSQLACTNSETPWSYFPKIKSI 360
XX
XX 301 IVDSTTLRLTPQKVFDAVVAVASLIPESDGFMTGSQLACTNSETPWSYFPKIKSI 360

```

```

QY 361 YLRDENSRSFRITILPOLYIQPMGAGLNYECYRFGISPESTNALVIGATYMEGFFYIFD 420
DB 361 YLRDENSRSFRITILPOLYIQPMGAGLNYECYRFGISPESTNALVIGATYMEGFFYIFD 420
QY 421 RAQKRVGFPAAPCAEIAAGANVSEISGPFSTDVASCNCPAOSISEPILMIVSYALMSVCG 480
DB 421 RAQKRVGFPAAPCAEIAAGANVSEISGPFSTDVASCNCPAOSISEPILMIVSYALMSVCG 480
QY 481 ALLVLIVLILLLPFCORPRDPEVYNDESSLVHRMK 518
DB 481 ALLVLIVLILLLPFCORPRDPEVYNDESSLVHRMK 518

RESULT 14
ID AAE02608
XX AAE02608 standard; Protein; 518 AA.
XX
XX AAE02608;
XX
XX 10-AUG-2001 (first entry)
XX
XX Human Aspartyl protease-1 (Asp-1) deltatm (His)6 protein.
XX
XX Human; alpha-secretase; amyloid precursor protein; APP; therapy;
XX Alzheimer's disease; antialzheimer's; aspartyl protease 1; Asp1;
XX beta-secretase; Asp-1 deltatm (His)6 protein.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX WO200123533-A2.
XX
XX 05-APR-2001.
XX
XX 22-SEP-2000; 2000WO-US26080.
XX
XX 23-SEP-1999; 99US-0155493.
XX 23-SEP-1999; 99WO-US20881.
XX 13-OCT-1999; 99US-0416901.
XX 06-DEC-1999; 99US-0169232.
XX
XX (PHAA ) PHARMACIA & UPJOHN CO.
XX
XX Gurney M, Bienkowski MJ;
XX
XX WPI; 2001-290516/30.
XX
XX Enzymes that cleave the alpha-secretase site of the amyloid precursor
XX protein, useful for the treatment of Alzheimer's disease -
XX
XX Example 14; Page 183-184; 189pp; English.
XX
XX The present invention relates to enzymes for cleaving the alpha-
XX secretase site of the amyloid precursor protein (APP) and methods of
XX identifying those enzymes. The methods may be used to identify enzymes
XX that may be used to cleave the alpha-secretase cleavage site of the APP
XX protein. The enzymes may be used to treat or modulate the progress of
XX Alzheimer's disease. The present sequence is human Aspartyl protease-1
XX (Asp-1) deltatm (His)6 protein which is used for the expression of
XX pre-pro-human-Aspartyl protease 1 (Asp1). This protein is obtained by
XX replacing C-terminal transmembrane and cytoplasmic domains with a
XX hexahistidine purification tag in the human Aspartyl protease 1.
XX
XX
XX Sequence 518 AA;
XX
XX Query Match 100.0%; Score 2687; DB 22; Length 518;
XX Best Local Similarity 100.0%; Pred. No. 3e-231;
XX Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVVAFTPGPTPAERHADGL 60
XX
XX 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVVAFTPGPTPAERHADGL 60

```

QY 61 ALALEPALASPAGANFLAMVDNLQDGRGYLEMLIGTPPKQILIVDTGSSNFAVAG 120
 DB 61 ALALEPALASPAGANFLAMVDNLQDGRGYLEMLIGTPPKQILIVDTGSSNFAVAG 120
 QY 121 TPHSYIDTYFPTERSSTYRSKGFDTVVKYQGSWTFVGEDLVITPKGFNTSFLVNIAIT 180
 DB 121 TPHSYIDTYFPTERSSTYRSKGFDTVVKYQGSWTFVGEDLVITPKGFNTSFLVNIAIT 180
 QY 181 FESSENFPLPGIKMNGILGLAVATLAKPSSSLETFPDSLVTOANIPNVSMQCGALPVA 240
 DB 181 FESSENFPLPGIKMNGILGLAVATLAKPSSSLETFPDSLVTOANIPNVSMQCGALPVA 240
 QY 241 GSGTNGSVLVGIEPSPSYKGDIVWTPPIKEEMYYQIEILKLEIGGQSLNLDCEYNADKA 300
 DB 241 GSGTNGSVLVGIEPSPSYKGDIVWTPPIKEEMYYQIEILKLEIGGQSLNLDCEYNADKA 300
 QY 301 IVDSGTTLRLPQKVFDAVAVASASLIPFSDGFWTGSQACWNTSETPMSYFPKXISI 360
 DB 301 IVDSGTTLRLPQKVFDAVAVASASLIPFSDGFWTGSQACWNTSETPMSYFPKXISI 360
 QY 361 YLRDENSRSRFRITTLPPQYIOPMMGAGINYECCYRFGISPSSTNALVIGATWEGFYVIFD 420
 DB 361 YLRDENSRSRFRITTLPPQYIOPMMGAGINYECCYRFGISPSSTNALVIGATWEGFYVIFD 420
 QY 421 RAQKRVGFAPASCACIAGAASEISGPSTEDVASCNCPAOSLSBPILMIVSYALMSVCG 480
 DB 421 RAQKRVGFAPASCACIAGAASEISGPSTEDVASCNCPAOSLSBPILMIVSYALMSVCG 480
 QY 481 ALLVLIVLILLLPFRQRRPRDPEVNDSSIVRRHMK 518
 DB 481 ALLVLIVLILLLPFRQRRPRDPEVNDSSIVRRHMK 518

RESULT 15

ABR78589
 ID ABR78589 standard; Protein; 518 AA.
 XX
 AC ABR78589;
 DT 16-JUL-2002 (first entry)
 DE Human Asp-1 protein sequence SEQ ID NO:2.
 KW Human; Asp-1; Asp-2; aspartyl protease; enzyme; Alzheimer's disease;
 KM proteolytic; chromosome 21.
 OS Homo sapiens.
 FN GB2367060-A.
 PD 27-MAR-2002.
 PF 29-OCT-2001; 2001GB-0025934.
 PR 23-SEP-1999; 99US-155493P.
 PR 23-SEP-1999; 99US-0404133.
 PR 13-OCT-1999; 99MO-US20881.
 PR 06-DEC-1999; 99US-0416901.
 PR 22-SEP-2000; 2000GB-0023315.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 PI Bienkowski MJ, Gurney M;
 DR WPI, 2002-396337/43.
 DR N-PSDB; ABL52456.
 XX Human aspartyl protease 1 substrates useful in assays to detect
 PT aspartyl protease activity, e.g. for the diagnosis of Alzheimer's
 XX disease -

PS Claim 7; Fig 1; 182pp; English.

XX The present invention describes a human aspartyl protease 1 (hu-Asp1)
 CC substrate (I) which comprises a peptide of no more than 50 amino acids,
 CC and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
 CC Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1
 CC proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with
 CC (I) under acidic conditions; and (b) determining the level of hu-Asp1
 CC proteolytic activity; (2) a purified polynucleotide (II) comprising a
 CC nucleotide sequence that hybridises under stringent conditions to the
 CC non-coding strand complementary to a defined 1804 nucleotide sequence
 CC (see ABL52456) where the nucleotide sequence encodes a polypeptide having
 CC Asp1 proteolytic activity and lacks nucleotides encoding a transmembrane
 CC domain; (3) a purified polynucleotide (III) comprising a sequence that
 CC hybridises under stringent conditions to (II) (the nucleotide sequence
 CC encodes a polypeptide further lacking a pro-peptide domain corresponding
 CC to amino acids 23-62 of hu-Asp1 (see ABR78589)); (4) a vector (IV)
 CC comprising (III) or (III'); and (5) a host cell (V) transformed or
 CC transfected with (III), (III') and/or (IV). The hu-Asp1 protease
 CC substrate (I) may be used as an enzyme substrate in assays to detect
 CC aspartyl protease activity, (II) and therefore diagnose diseases
 CC associated with aberrant hu-Asp1 expression and activity such as
 CC Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while
 CC hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
 CC sequence represents hu-Asp1 from the present invention.

XX Sequence 518 AA;

Query Match 100.0%; Score 2687; DB 23; Length 518;
 Best Local Similarity 100.0%; Pred. No. 3e-231;
 Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 61 ALALEPALASPAGANFLAMVDNLQDGRGYLEMLIGTPPKQILIVDTGSSNFAVAG 120
 QY 121 TPHSYIDTYFPTERSSTYRSKGFDTVVKYQGSWTFVGEDLVITPKGFNTSFLVNIAIT 180
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 DB 361 YLRDENSRSRFRITTLPPQYIOPMMGAGINYECCYRFGISPSSTNALVIGATWEGFYVIFD 420
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 DB 421 RAQKRVGFAPASCACIAGAASEISGPSTEDVASCNCPAOSLSBPILMIVSYALMSVCG 480
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 DB 481 ALLVLIVLILLLPFRQRRPRDPEVNDSSIVRRHMK 518

Search completed: April 1, 2003, 11:32:23
 Job time : 42 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 1, 2003, 11:31:43 ; Search time 16 Seconds

(without alignments)
952.567 Million cell updates/sec

Title: US-09-668-314C-2

Perfect score: 2687
Sequence: 1 MGALARALLPLLAQWLRA.....RPRDEYVNDSSLVRHRWK 518

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

- 1: Issued_Patents_AA.*
- 2: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfilest.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2687	100.0	518	3 US-08-999-723-2	Sequence 2, Appli
2	2687	100.0	518	4 US-09-434-427-2	Sequence 2, Appli
3	2687	100.0	518	4 US-09-548-372D-2	Sequence 2, Appli
4	2687	100.0	518	4 US-09-548-367D-2	Sequence 2, Appli
5	2395	89.1	514	4 US-09-717-432-2	Sequence 2, Appli
6	2395	89.1	514	4 US-09-912-484-2	Sequence 2, Appli
7	1186.5	44.2	501	4 US-09-713-158-2	Sequence 2, Appli
8	1185	44.1	501	4 US-09-548-372D-8	Sequence 8, Appli
9	1185	44.1	501	4 US-09-548-367D-8	Sequence 8, Appli
10	1178.5	43.9	501	4 US-09-548-372D-4	Sequence 4, Appli
11	1178.5	43.9	501	4 US-09-548-367D-4	Sequence 4, Appli
12	1172.5	43.6	501	4 US-09-009-191-2	Sequence 2, Appli
13	1160.5	43.2	774	4 US-09-009-191-4	Sequence 2, Appli
14	1139	42.4	453	4 US-09-548-372D-30	Sequence 30, Appli
15	1139	42.4	453	4 US-09-548-372D-30	Sequence 30, Appli
16	1139	42.4	459	4 US-09-548-372D-32	Sequence 32, Appli
17	1139	42.4	459	4 US-09-548-367D-32	Sequence 32, Appli
18	1127	41.9	433	4 US-09-548-372D-26	Sequence 26, Appli
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21	1127	41.9	446	4 US-09-548-367D-22	Sequence 22, Appli
22	1127	41.9	459	4 US-09-548-372D-24	Sequence 24, Appli
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24	1123	41.8	425	4 US-09-548-372D-28	Sequence 28, Appli
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29	1068	39.7	476	4 US-09-548-367D-6	Sequence 6, Appli
30	1028.5	38.3	428	4 US-09-548-372D-51	Sequence 51, Appli
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33	1028.5	38.3	434	4 US-09-548-367D-53	Sequence 53, Appli
34	308.5	11.5	412	1 US-08-208-007A-12	Sequence 12, Appli
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44	287	10.7	396	1 US-08-208-007A-13	Sequence 13, Appli
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ALIGNMENTS

RESULT 1					
US-08-999-723-2					
Sequence 2, Application US/08999723A					
Patent No. 6025180					
GENERAL INFORMATION:					
APPLICANT: Powell, David G.					
APPLICANT: Southan, Christopher					
APPLICANT: Chapman, Conrad G.					
APPLICANT: Evans, Joanne R.					
TITLE OF INVENTION: ASPI					
FILE REFERENCE: GH70262					
CURRENT APPLICATION NUMBER: US/08/999,723A					
CURRENT FILING DATE: 1997-10-06					
NUMBER OF SEQ ID NOS: 2					
SOFTWARE: PatentIn Ver. 2.0					
SEQ ID NO 2					
LENGTH: 518					
TYPE: PRT					
ORGANISM: Homo sapiens					
US-08-999-723-2					
Query Match					
Best Local Similarity 100.0%; Pred. No. 1e-243;					
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
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DB	1	MGALARALLPLLAQWLRAPELAPAPFTPLRVAATNRVAPTPGPTPAERHADGL	60		
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DB	61	ALALEPALASPAGANFLAMVDNLQDGRGYLEMLIGTPPOKQILVDTGSSNFAVAG	120		
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DB	301	IYDGGTTLRLPOKVPFAVVAEVARASLIPFSGFTGSLACWTNSETPMWYFPKISI	360		
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RESULT 2

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US-09-434-427-2
; Sequence 2, Application US/09434427
; Patent No. 6162630
; GENERAL INFORMATION:
; APPLICANT: POWELL, DAVID J.
; APPLICANT: SOUTHAN, CHRISTOPHER
; APPLICANT: CHAPMAN, CONRAD G.
; APPLICANT: EVANS, JOANNE R.
; TITLE OF INVENTION: ASPI
; FILE REFERENCE: GH-70262-D1
; CURRENT APPLICATION NUMBER: US/09/434,427
; CURRENT FILING DATE: 1999-11-04
; EARLIER APPLICATION NUMBER: US 08/999,723
; EARLIER FILING DATE: 1997-10-06
; EARLIER APPLICATION NUMBER: UK 9626022.9
; EARLIER FILING DATE: 1996-12-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-434-427-2
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Query Match 100.0%; Score 2687; DB 4; Length 518;
Best Local Similarity 100.0%; Pred. No. 1e-243;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 61 ALALEPALASPAGANFLAMVDNLOGDSGRGYLEMLIGTPPOKQIILVDTGSSNFAVAG 120
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RESULT 3

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; Sequence 2, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GIBNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-548-372D-2
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Query Match 100.0%; Score 2687; DB 4; Length 518;
Best Local Similarity 100.0%; Pred. No. 1e-243;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 4
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; Sequence 2, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280H
; CURRENT FILING DATE: US/09/548,367D
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-2

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Query Match      100.0%; Score 2687; DB 4; Length 518;
Best Local Similarity 100.0%; Pred. No. 1e-243;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
US-09-717-432-2
; Sequence 2, Application US/09717432
; Patent No. 6291223
; GENERAL INFORMATION:

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; APPLICANT: ZHU, YUAN
; APPLICANT: LI, XIAOTONG
; APPLICANT: CHRISTIE, GARY
; APPLICANT: POWELL, DAVID J.
; TITLE OF INVENTION: Mouse Aspartic Secretase-1 (MASP1)
; FILE REFERENCE: GP-70663
; CURRENT APPLICATION NUMBER: US/09/717,432
; CURRENT FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/166,974
; PRIOR FILING DATE: 1999-11-23
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 514
; TYPE: PRT
; ORGANISM: MUS MUSCULUS
US-09-717-432-2

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Query Match      89.1%; Score 2395; DB 4; Length 514;
Best Local Similarity 88.6%; Pred. No. 2.6e-216;
Matches 459; Conservative 20; Mismatches 35; Indels 4; Gaps 1;

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QY 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLEMLIGTPPOKQIIVDTGSSNPAVAG 120
DB 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLEMLIGTPPOKQIIVDTGSSNPAVAG 116
QY 121 TPHSYIDTYFPTERSSTYRSKGFDTVVKYTOGSMTFVGEDLVITPKGFNTSFLVNIATI 180
DB 121 TPHSYIDTYFPTERSSTYRSKGFDTVVKYTOGSMTFVGEDLVITPKGFNTSFLVNIATI 176
QY 181 FESENFPLPGIKMNGIILGLAYATLAKPSSSLETFFDSLVTOANINVSQMCGAGLPVA 240
DB 181 FESENFPLPGIKMNGIILGLAYATLAKPSSSLETFFDSLVTOANINVSQMCGAGLPVA 236
QY 241 GSGTNGSLVVGIEPLSLYKGDWITTPKEWYQIEILKIEIGQSINLDCREYNADKA 300
DB 241 GSGTNGSLVVGIEPLSLYKGDWITTPKEWYQIEILKIEIGQSINLDCREYNADKA 296
QY 301 IVDSTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSOLACTNSETPMVSYPKXISI 360
DB 301 IVDSTTLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSOLACTNSETPMVSYPKXISI 356
QY 361 YLDENSSRSFRITILPOLYIQPMWAGLNECYRFGISPSSTNALVIGATWEGFYVIFD 420
DB 361 YLDENSSRSFRITILPOLYIQPMWAGLNECYRFGISPSSTNALVIGATWEGFYVIFD 416
QY 421 RAQRVGFRAAPCAEIAAAVSEISGPRSTEDVANSNCVPAOSLSFPIIMIVSYALMSVCG 480
DB 421 RAQRVGFRAAPCAEIAAAVSEISGPRSTEDVANSNCVPAOSLSFPIIMIVSYALMSVCG 476
QY 481 AILVLIVLILLLPFCORRPRDPEVNVDESSLVHRMK 518
DB 481 AILVLIVLILLLPFCORRPRDPEVNVDESSLVHRMK 514

```

```

RESULT 6
US-09-912-484-2
; Sequence 2, Application US/09912484
; Patent No. 6358725
; GENERAL INFORMATION:
; APPLICANT: Christie, Gary
; APPLICANT: Li, Xiaolong
; APPLICANT: Powell, David J.
; TITLE OF INVENTION: Mouse Aspartic Secretase-1 (MASP1)
; FILE REFERENCE: GP-70663-D1
; CURRENT APPLICATION NUMBER: US/09/912,484
; CURRENT FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/166,974

```



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0Y 9 LIPILQMLIRAPBELAPAF-----LPIRVAATNRVAFTPGPGTPARRADGLALA 63
Db 1 MAPALHMLLWVGSGMLPAQGTHGIRLPLRSGLA-----GPPGLRLPRETDEES----- 51
0Y 64 LEPALASPAGANFLMVDVLOGDSGRGYLLEMLIGTPPQLQIOLVDPGSSNFAVAGTPH 123
Db 52 -----BEPGRGSGFVEMVDMLRGSGGQYVEMVGSBPQTLNLLVDTGSSNFAVGAAPH 106
0Y 124 SYIDYFPTERSSTYRSKGFVTVKYTQGSWTFVGEDLVTIIPKGFNTSFLVNIATIFES 183
Db 107 PFLHRYYQRLQSTYRDLRKGVYVPTYQKWEKELGTDVLSIPHPNVTYRANIAITRES 166
0Y 184 ENFFLPGLIKWNGILGLATAYATLAKPSSSLETFPDSLVTOANIPNVFSMOMCGALPV---A 240
Db 167 DFFFIKGSWMEGLGLAAYAEIARPDLSLEPFPSLVKQTHLPNIFISLOLCAGAPLNQTE 226
0Y 241 GSGTNGSLVLGGIEBSLYGDIWYPIPKEMWYQIEIKIEIGOSLNLICREYNADKA 300
Db 227 ALASVGSMTIGGIDHSLSYGSIMYPIRREMYEVLIVREINGQDLKMKCKEYNDKS 286
0Y 301 IVDSGTTLRLPOKVFDAVEAVARASLIPFSDGFVTGSQLACMTNSETPMSYEPKISI 360
Db 287 IVDSGTTLRLPKVEEAAKSIKAASSTKPPGFMHGBLVCMQGTTPMNIFFVISTL 346
0Y 361 YRDENSSSFRITIIIPOLYIQPMGAGLNY-ECYRFGISPTNALVIGATVMEGFYIF 419
Db 347 YLMGEVTNOSFRITIIPOQYLREPVEDVATQODCKEFAVSQSSGTGWAGVIMEGFYVVF 406
0Y 420 DRAOKRVGAASCAELAGAAVEISGPFSTEDVANSVCVPQISLEPTLWVSVALMSVC 479
Db 407 DRAKRGIGAVSACHVDEFRTAABEFPVATJMEDCGYNIPTQDESTLMTIAYVMAIC 466
0Y 480 GAILLVILVLLPFCOR--RPRDPEVNDDESL 512
Db 467 -ALFMLPLCLMWQCMRCRLCRHQHDFADDISLL 500

RESULT 9
US-09-548-367D-8
; Sequence 8, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-548-367D-8

```

Query Match	44.1%	Score 1185;	DB 4;	Length 501;
Best Local Similarity	46.0%	Pred. No. 11e-102;		
Matches 237; Conservative	83;	Mismatches 169;	Indels 26;	Gaps 7;
Qy	9	ILPLIAQWILTRAPAEIAPAFPT	-----LPLRVAATNRVVAFTPGPGTPAERHADGLALA	63
5b	1	NAPALHFWILVWGSGMLPAQCTHGLGIRLPRRGLA	-----GPLLGRILRLREDEES	51

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QY 64 LEPALASAGANFLAMNDNIOGOSGGXYLEMIGRPPKLOILVDTGSSNFAVGTPH 123
Db 52 -----EEFGRRGSGFEMNDNLGRKSGGQSYVEMTVGSPPTLNLIVDTGSSNFAVGAAPH 106b
QY 124 SYIDTYPDTERSSSTYRSKGFVTVKTYTQGSWTGVSGLDVTLPKGFPTSLVNIATIFES 183b
Db 107 PFLHRYYQRLQSLSTFYRDLRKGVVYPYTGKKEGELGTDLVSLPHGPAVTVRANIATIFES 166b
QY 184 ENFFFLPGIKNNGGILGLAVATLAKSSSLFTFFPDSLVYQANIINVFNSOMOGAGLIPV--A 244b
Db 167 DKFFINGNSMWEIGLGLAAELIARPDSDLEPPFDSLVQTHPINFSLQICGAGPLNQTE 22c
QY 241 GSGTNGSGLVYAGLIEPRLYKGDIVWTPPIKEEYMQOIEILKLEIGOGSLNDCREYNADKA 300b
Db 227 ALASVSGSMITIGDISHSLYTGSLMYTTPHRRMYEYVAILVAEINGDGLKMDCKEYANDKS 286b
QY 301 IYDSGTTLLRLRPQKVPDAVVAEAVASLIIPESDGFMTQSOLACTWNSETPMSYFPIKSI 360b
Db 287 IYDSGTTMLRLPKVFEAAVKSILKAASTSEKFPDGFMLGDLVCMQAGTTPWNIFFVYISL 346b
QY 361 YLRDSSRSRRTIITLPOLYIQPMMGAGLNV-ECYRRGISPTNALYIGATVMEGFVIF 419b
Db 347 YLMGEVNTQSRITITLPPQYLRPVEDVATSDDDCYKRAVSSOSTGTYMGAVINEGFVVF 406b
QY 420 DRAQRGVFPAASPCAELIAGAASVEISGFFSTEDVNASNCVPAOSLSEPIILAIIVSALMSVC 479b
Db 407 DRARKRIGFPAVSACHVHDEFTFAVEGPFVJADMEDCGYNIPOQDESTLMTIAYVMAIC 466b
QY 480 GAILLIVLIVLILPPRCOR--RPDPDEVANDESL 512
Db 467 -ALFMLPLCLMVCQMRCLRCRHODHDFADISLL 500

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RESULT 10
US-09-548-372D-4
; Sequence 4, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/52801
; CURRENT APPLICATION NUMBER: US/09/548, 372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-4

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Query Match	Best Local Similarity	Score	IDB	Length
43.9%	46.2%	1178.5	4	501
Matches 240; Conservative	82; Mismatches 164; Indels 33; Gaps 9			
QY	7 ALLPLLAQWLLRAAPBELAPAFET-----LPLRVAATNTRVAPPPGGTPAERHADGLA	61		
DB	2 AQAALWLLIM---GAGVLPAGHTGHRLLPLRSLG-----GAPL-----GUR	42		
QY	62 LALE--PALASPAAGANFLAMTDNIQGDGSGRGVYLEMLIGTPQKQLLLVDGSSNFAVA	119		
DB	43 LPRETDDEEDEFGRGSGVEVMVDNLRGSGGQYIEMTVGSPQTLNILLVDGSSNFAVG	102		
QY	120 GPHSYIDITYPTERSSTYRSKGPDVTKYKTLQGSWTGVEGDLVTI PKGFNTSPLVNIAIT	179		

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Db 103 AAPHFLLRYQOROLSTYRDLRKGVYVPYTOGKMEGELGTDLVSI PRGPVNTVPANITAA 162
Qy 180 IFSEENFLLPGIKXNGILGLAVATLAKPSSLETFPDSLVTQANIPNFSMQMGAGLPV 239
Db 163 ITESDKFFINSNWEGLGLAEIARPDSDLEFPDSLVTQTHVFNLFSLQCGAGPPL 222
Qy 240 AGS---GTNGSLVVGIEPSLYKGDIMWYPIKEEMWYQIEILKLEIGOSLINDCREYN 296
Db 223 NQSEVLASVSGSMITGGIDHSLYTGSLWYTPIRREMYEVLIVREINGQDLKMDCKEYN 282
Qy 297 ADKAIVDSGTTLLRIPQKVPDAVAVARASLIPEFSDFWTGSQLACWNSLFTWSTFP 356
Db 283 YDKSIVDSGTTNLRIPKVFEEAAVKSIIKAASSTKFPDGFWMGEOQVCMQAGTTPMNIFF 342
Qy 357 KISITLDENSSRSFRITLLPOLYIOPMMGAGLNY-ECYRFGISPTNALVIGATVMEGF 415
Db 343 VISLYLMEVYNQSFRTITLLPOOYLRPVEDVATSODDCYKFAISQSGTGMGAVIMEGF 402
Qy 416 YVIFDRAQRVGFAPCAEIIAGAASEISGPFSTEDVASCVPQASISEPILMTVSVAL 475
Db 403 YVIFDRAKRIGFAPVACHVDEFTAAVEGPFVTLDMEDCGYNIPTQDESTLMTIAYVM 462
Qy 476 MSVCGAILLVILLPLFCRQ--RPRDPEVNDSSL 512
Db 463 AAI-C-ALFMLPLCLMVCMWRCLRCLRQCHDDFADDISLL 500

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RESULT 11
US-09-548-367D-4
; Sequence 4, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE OF INVENTION: THEROF
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548.367D
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-4

```

```

Query Match 43.9%; Score 1178.5; DB 4; Length 501;
Best Local Similarity 46.2%; Pred. No. 4.3e-102;
Matches 240; Conservative 82; Mismatches 164; Indels 33; Gaps 9;

Qy 7 ALLPLLAQWLIRAAPELAPAPT-----LPIRAAATNRVAVPFGPTPAERHADGLA 61
Db 2 AQAFLPMLLM---GAGVLPAGTQHGIRLPLRSGIG-----GAPL-----GLR 42
Qy 62 LALF--PALASPAGANFLAMVDNLODGGRGYLEMLGTTPROKQIILVDDGSSNFAVA 119
Db 43 LPREDEDEEPEGRRGSRFVEMVDNLKSGGQGYVEMTGSPPQTNILIVDGGSSNFAVG 102
Qy 120 GTPHSYIDYPTERSSTYRSKGFVDVTVYKQSGWTGFGEDLVTPKGFNTSFLVNIAT 179
Db 103 AAPHFLLRYQOROLSTYRDLRKGVYVPYTOGKMEGELGTDLVSI PRGPVNTVPANITAA 162
Qy 180 IFSEENFLLPGIKXNGILGLAVATLAKPSSLETFPDSLVTQANIPNFSMQMGAGLPV 239

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Db 163 ITESDKFFINSNWEGLGLAEIARPDSDLEFPDSLVTQTHVFNLFSLQCGAGPPL 222
Qy 240 AGS---GTNGSLVVGIEPSLYKGDIMWYPIKEEMWYQIEILKLEIGOSLINDCREYN 296
Db 223 NQSEVLASVSGSMITGGIDHSLYTGSLWYTPIRREMYEVLIVREINGQDLKMDCKEYN 282
Qy 297 ADKAIVDSGTTLLRIPQKVPDAVAVARASLIPEFSDFWTGSQLACWNSLFTWSTFP 356
Db 283 YDKSIVDSGTTNLRIPKVFEEAAVKSIIKAASSTKFPDGFWMGEOQVCMQAGTTPMNIFF 342
Qy 357 KISITLDENSSRSFRITLLPOLYIOPMMGAGLNY-ECYRFGISPTNALVIGATVMEGF 415
Db 343 VISLYLMEVYNQSFRTITLLPOOYLRPVEDVATSODDCYKFAISQSGTGMGAVIMEGF 402
Qy 416 YVIFDRAQRVGFAPCAEIIAGAASEISGPFSTEDVASCVPQASISEPILMTVSVAL 475
Db 403 YVIFDRAKRIGFAPVACHVDEFTAAVEGPFVTLDMEDCGYNIPTQDESTLMTIAYVM 462
Qy 476 MSVCGAILLVILLPLFCRQ--RPRDPEVNDSSL 512
Db 463 AAI-C-ALFMLPLCLMVCMWRCLRCLRQCHDDFADDISLL 500

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RESULT 12
US-09-009-191-2
; Sequence 2, Application US/09009191
; Patent No. 6319689
; GENERAL INFORMATION:
; APPLICANT: POWELL, DAVID
; APPLICANT: CHAPMAN, CONRAD
; APPLICANT: MURPHY, KAT
; APPLICANT: SMITH, TRUDI
; TITLE OF INVENTION: ASP2
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESS: RATTNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,191
; FILING DATE: 20-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 9701684.4
; FILING DATE: 28-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 123,031
; REFERENCE/DOCKET NUMBER: GH-70368
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 501 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-009-191-2

```

```

Query Match 43.6%; Score 1172.5; DB 4; Length 501;
Best Local Similarity 46.1%; Pred. No. 1.6e-101;
Matches 239; Conservative 82; Mismatches 165; Indels 33; Gaps 9;

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QY 7 ALLPPLAQLRAAPLAPLAPFT-----LPIRVAATAANRVVAPPPGCTPAERHADGIA 61
DB 2 AQAALPMLLLMM---GAGVLPAPHTQHGIRLPLRSGLG-----GAPL-----GLR 42
QY 62 LALE--PLALAPAGANLANLAWDNIGDSGRGYILEMLIGTPPKLOILVDTGSSNFAVA 119
DB 43 LPREDEEPEERGRGRSGEVEWVDNLGRKSGQGYVEMTVGSPPTLNLIVDTGSSNFAVG 102
QY 120 GTPHSYITDYEDTERSTYRSKGFVTVKYGTSWTFVGEEDLVITPKGFNTSFLVNIAT 179
DB 103 AAPHFLHRYRQRLSTYRDRKRGVYEPYTOGKMEGLDLDVSIPIHGPVTVRANITAA 162
QY 180 IFESENFPLPGIKMNGILGLAVATLAKPSSLETFPDSLVTOANIPNVFSMOMGAGLPV 239
DB 163 ITESKFFINSGNMEGILGLAVAEIARPDLSLEFPDLSVKTQHVPLFSLQCGAFPL 222
QY 240 AGS--GTNGSLVIGIEPLSYKGDIVYTPIKEWYIOIEILKLEIGGOSLNDCREYN 296
DB 223 NQSEVLASVSGSMITGGIDHSLYTGSLWYTPIRREWYEVILVVEINGQDLKMDCKEYN 282
QY 297 ADKAVDSGTLRLRPOKVPFAVVEAVARASLIPESDGFMTGSOLACMTNSETPMSYFP 356
DB 283 YKSLIVDSGTLNLRPKKVFELAVASLIPASSTKFPDGFMLGEOLVCMQAGTTMNLFP 342
QY 357 KISITLSDENSSRSFRITILPOLYIQPMGAGLNY-ECYRFGISPTNALVIGATVMEGF 415
DB 343 VISLIMEVLTNQSFRITILPOLYARPVEDVATSDDCYKFAISGSGTGVMAVIMGEF 402
QY 416 YVIFDRAOKRGVPAAPCAEITAGAAVSEISGPFSTEDVASCNCPAQSLSEPIILMIVSYAL 475
DB 403 YVIFDRAOKRGVPAAPCAEITAGAAVSEISGPFSTEDVASCNCPAQSLSEPIILMIVSYAL 462
QY 476 MSVCGAILLVILVILLPFCOR--RPRDPEVNDSSU 512
DB 463 ALIC-ALFMLPLCLMVCMQRCRLRQOHDPADDISLL 500

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RESULT 13
US-09-009-191-4
Sequence 4, Application US/09009191
Patent No. 6319689
GENERAL INFORMATION:
APPLICANT: POWELL, DAVID
APPLICANT: CHAPMAN, CONRAD
APPLICANT: MURPHY, KAY
APPLICANT: SMITH, TRUDI
TITLE OF INVENTION: ASP2
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATTNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,191
FILING DATE: 20-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 9701684.4
FILING DATE: 28-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-70368
TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-009-191-4

Query Match 43.2%; Score 1160.5; DB 4; Length 774;
Best Local Similarity 47.5%; Pred. No. 4.3e-100;
Matches 224; Conservative 80; Mismatches 137; Indels 31; Gaps 5;

QY 76 NPLAMVDNLQDSSGRGYILEMLIGTPPKLOILVDTGSSNFAVAGTPHSYIDYEDTERS 135
DB 2 SFVEWVDNLGRKSGQGYVEMTVGSPPTLNLIVDTGSSNFAVGAAPHPFLHRYRQRLS 61
QY 136 STYRSKGFVTVKYGTSWTFVGEEDLVITPKGFNTSFLVNIATIPESENFPLGKIKNG 195
DB 62 STYRDLRKGVYEPYTOGKMEGLDLDVSIPIHGPVTVRANITAAITESDKFFINGSMNEG 121
QY 196 ILGLAVATLAKPSSSLETFPDSLVTOANIPNVFSMOMGAGLPVAGS--GTNGSLVIG 252
DB 122 ILGLAVAEIARPDLSLEFPDLSVKTQHVPLFSLQCGAFPLNQSGLVLSVSGSMITIG 181
QY 253 GIEPSLYKGDIVYTPIKEWYIOIEILKLEIGGOSLNDCREYNADKAVIUSGTLRLP 312
DB 182 GIDHSLYTGSLWYTPIRREWYEVILVVEINGQDLKMDCKEYVNDKSIIVDSGTLNLRP 241
QY 313 QKVPFAVVEAVARASLIPESDGFMTGSOLACMTNSETPMSYFPKISITLSDENSSRSFR 372
DB 242 KKVFEAAVASKAASPREKFPDGFMLGEOLVCMQAGTTMNLFPVILSYLMEVLTNQSFR 301
QY 373 ITILPOLYIQPMGAGLNY-ECYRFGISPTNALVIGATVMEGFYVIFDRAOKRGVPAAS 431
DB 302 ITILPOLYARPVEDVATSDDCYKFAISGSGTGVMAVIMGEFYVIFDRAOKRGVPAAS 361
QY 432 PCAEITAGAAVSEISGPFSTEDVASCNCPAQSLSEPIILMIVSYALMSVCGAILLVILV 491
DB 362 ACHVHDEFRTAAVGEFPTLDMEDCGYNIPTDESTIMTIYVAAIC-ALFMLPLCLMV 420
QY 492 LPRCQRRRPP--EVNDESSLV-----RRRW 517
DB 421 CQWRCLRCLRQMDPFADDISLLKGPWEKXDRSPGTTTPWFTLVTSRRHRW 472

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RESULT 14
US-09-548-372D-30
Sequence 30, Application US/09548372D
Patent No. 6420534
GENERAL INFORMATION:
APPLICANT: GURNEY ET AL.
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 28915/62801
CURRENT APPLICATION NUMBER: US/09/548,372D
CURRENT FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 30
LENGTH: 453
TYPE: PRT

ORGANISM: Homo sapiens
US-09-548-372D-30

Query Match 42.4%; Score 1139; DB 4; Length 453;
Best Local Similarity 49.6%; Pred. No. 1.9e-98;
Matches 227; Conservative 67; Mismatches 134; Indels 30; Gaps 7;

QY 7 ALLPLLAQWLLRAAPLAPAPFT-----LPLRVAATNRVVAAPPGCTPAERHADGLA 61
DB 2 AQAIPWLLLMW---GAGVLPAGHTGHCIRLPLRSGLG-----GAPL-----GLR 42
QY 62 LALE--PALASPAGANFLAMVDNLQDSSGRGYYLEMLIGTPPOKQIIVDTGSSNFAVA 119
DB 43 LPRTEDEPEEPGRGRSFVEMVDNLRKSGQGYVEMTVGSPQTLNIIIVDTGSSNFAVG 102
QY 120 GTPHSYIDTYFDTERSSSTYRSKGFVDVTKYTOGSGWTFVGEDVLTIPKGNVTSFLVNIAT 179
DB 103 AAPHPFLHRYQROLSSSTYRDLRKGVVVPYTOGKMEGELGTDLVSIIPHGNVTVRANIIAA 162
QY 180 IFESSENFELPGIKWNGILGLAYATLAKPSSSETFPDSLVTQANIPNVFSMOMCGAGLPV 239
DB 163 ITESDKFFINGSNWEGILGLAYAIARPDSDLFPDLSLVKQTHVPLFSLQCGAGFPL 222
QY 240 AGS---GTNGGSLVLGIEPSLYKGDWYTPPIKEWYQIEILKLEIGGSLNIDCREYN 296
DB 223 NQSEVLASVGSMTIGIDHSLYGLTWYPIRREMYEVIIVRVEINGQDLKMDCKEYN 282
QY 297 ADKAIIVDSGTTLLRLPKQVDAVVAVARASLIPESDGFMTGSQLACWNTSETPMSYFP 356
DB 283 YDKSIVDSGTTNLRPKVFEAAVKSIIKAASSTKEFPDGFMLGEOVCWQAGTTPMNIIFP 342
QY 357 KISYLRDENSSRSFRITILLPOLYIOPMMGAGLNY-ECYRFGISPTNALVIGATVMEGF 415
DB 343 VISLYLMEVTVNOSFRITILLPOQYLRPEVDVATSODDCYKFAISQSSGTGMGAVIMEGF 402
QY 416 YVIFDRAQKRVGAFAASPCAETAGAAVSEISGPFSTEDV 453
DB 403 YVIFDRAKRIKGFVAVSACHVHDEFRTAAVEGPFVTLDM 440

RESULT 15
US-09-548-367D-30
Sequence 30, Application US/09548367D
Patent No. 6440698
GENERAL INFORMATION:
APPLICANT: CURNEX ET AL.
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
FILE OF INVENTION: THEREOF
FILE REFERENCE: 29915/6280H
CURRENT APPLICATION NUMBER: US/09/548,367D
PRIOR APPLICATION NUMBER: US 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 30
LENGTH: 453
TYPE: PRT
ORGANISM: Homo sapiens
US-09-548-367D-30

Query Match 42.4%; Score 1139; DB 4; Length 453;
Best Local Similarity 49.6%; Pred. No. 1.9e-98;
Matches 227; Conservative 67; Mismatches 134; Indels 30; Gaps 7;

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DB 43 LPRTEDEPEEPGRGRSFVEMVDNLRKSGQGYVEMTVGSPQTLNIIIVDTGSSNFAVG 102
QY 120 GTPHSYIDTYFDTERSSSTYRSKGFVDVTKYTOGSGWTFVGEDVLTIPKGNVTSFLVNIAT 179
DB 103 AAPHPFLHRYQROLSSSTYRDLRKGVVVPYTOGKMEGELGTDLVSIIPHGNVTVRANIIAA 162
QY 180 IFESSENFELPGIKWNGILGLAYATLAKPSSSETFPDSLVTQANIPNVFSMOMCGAGLPV 239
DB 163 ITESDKFFINGSNWEGILGLAYAIARPDSDLFPDLSLVKQTHVPLFSLQCGAGFPL 222
QY 240 AGS---GTNGGSLVLGIEPSLYKGDWYTPPIKEWYQIEILKLEIGGSLNIDCREYN 296
DB 223 NQSEVLASVGSMTIGIDHSLYGLTWYPIRREMYEVIIVRVEINGQDLKMDCKEYN 282
QY 297 ADKAIIVDSGTTLLRLPKQVDAVVAVARASLIPESDGFMTGSQLACWNTSETPMSYFP 356
DB 283 YDKSIVDSGTTNLRPKVFEAAVKSIIKAASSTKEFPDGFMLGEOVCWQAGTTPMNIIFP 342
QY 357 KISYLRDENSSRSFRITILLPOLYIOPMMGAGLNY-ECYRFGISPTNALVIGATVMEGF 415
DB 343 VISLYLMEVTVNOSFRITILLPOQYLRPEVDVATSODDCYKFAISQSSGTGMGAVIMEGF 402
QY 416 YVIFDRAQKRVGAFAASPCAETAGAAVSEISGPFSTEDV 453
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QY 297 ADKAIIVDSGTTLLRLPKQVDAVVAVARASLIPESDGFMTGSQLACWNTSETPMSYFP 356
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QY 357 KISYLRDENSSRSFRITILLPOLYIOPMMGAGLNY-ECYRFGISPTNALVIGATVMEGF 415
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Search completed: April 1, 2003, 11:35:13
Job time : 19 secs

GenCore version 5.1.4 p5.4578
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OM protein - protein search, using sw model

Run on: April 1, 2003, 11:34:29 ; Search time 37 Seconds

(without alignments)
855.905 Million cell updates/sec

Title: US-09-668-314C-2

Perfect score: 2687

Sequence: 1 MGALRALLLPLLAQMLIRA.....RPRDPEVNDSSLVRRHWK 518

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 248812 seqs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep:*

2: /cgn2_6/ptodata/1/pubpaa/PTC_NEW_PUB pep:*

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14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2687	100.0	518	US-09-978-295A-196	Sequence 196, App
2	2687	100.0	518	US-09-886-143-2	Sequence 2, Appl
3	2687	100.0	518	US-09-978-697-196	Sequence 196, App
4	2687	100.0	518	US-09-978-192A-196	Sequence 196, App
5	2687	100.0	518	US-09-999-832A-196	Sequence 196, App
6	2687	100.0	518	US-09-978-189-196	Sequence 196, App
7	2687	100.0	518	US-10-174-590-72	Sequence 72, Appl
8	2687	100.0	518	US-10-176-758-72	Sequence 72, Appl
9	2687	100.0	518	US-10-175-737-72	Sequence 72, Appl
10	2687	100.0	518	US-10-173-706-72	Sequence 72, Appl
11	2687	100.0	518	US-10-175-738-72	Sequence 72, Appl
12	2687	100.0	518	US-10-175-752-72	Sequence 72, Appl
13	2687	100.0	518	US-10-176-482-72	Sequence 72, Appl
14	2687	100.0	518	US-10-176-757-72	Sequence 72, Appl
15	2687	100.0	518	US-10-176-913-72	Sequence 72, Appl
16	2687	100.0	518	US-10-180-552-72	Sequence 72, Appl
17	2687	100.0	518	US-10-180-557-72	Sequence 72, Appl
18	2687	100.0	518	US-10-173-700-72	Sequence 72, Appl
19	2687	100.0	518	US-10-174-572-72	Sequence 72, Appl

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21	2687	100.0	518	US-10-174-582-72	Sequence 72, Appl
22	2687	100.0	518	US-10-174-588-72	Sequence 72, Appl
23	2687	100.0	518	US-10-175-739-72	Sequence 72, Appl
24	2687	100.0	518	US-10-175-740-72	Sequence 72, Appl
25	2687	100.0	518	US-10-175-743-72	Sequence 72, Appl
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36	2687	100.0	518	US-10-173-695-72	Sequence 72, Appl
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45	2687	100.0	518	US-10-176-487-72	Sequence 72, Appl

ALIGNMENTS

RESULT 1

US-09-978-295A-196

Sequence 196, Application US/09978295A

Patent No. US20020156006A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gertisen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J

APPLICANT: Kijavyn, Ivar J.

APPLICANT: Kuo, Sophia S.

APPLICANT: Napier, Mary A.

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2630P1C11

CURRENT APPLICATION NUMBER: US/09/978, 295A

CURRENT FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/064249


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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

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Query Match      100.0%; Score 2687; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 2,3e-217;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 TPHSYIDTYFPTERSSTYRSKGFVTVKYTGSGWTFVGEDLVTTIPKGFNTSFLVNIATI 180
D 121 TPHSYIDTYFPTERSSTYRSKGFVTVKYTGSGWTFVGEDLVTTIPKGFNTSFLVNIATI 180
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D 181 FESENFPLPGIKMNGIIGLAAYATLAKPSSSLETFFDSLVTQANIPIVFSMQMCGAGLPVA 240
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D 241 GSGNGGSLVIGGLEPSLYKGDWYTPIKEEYVQIETLKIEIGOSINLDCREYNADKA 300
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D 301 IVDGTTLLRLPQKVFDAVAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
QY 361 YLRDENSRSRRTITLLPOLYIQPMWAGLNYECYRFGISPTNALVIGATWEGFYIYFD 420
D 361 YLRDENSRSRRTITLLPOLYIQPMWAGLNYECYRFGISPTNALVIGATWEGFYIYFD 420
QY 421 RAOKRVGPAAPCAEIAAGAVSEISGPFSTEDVANSNCVPAQSLSEPIIMIVSYALMSVCG 480
D 421 RAOKRVGPAAPCAEIAAGAVSEISGPFSTEDVANSNCVPAQSLSEPIIMIVSYALMSVCG 480
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RESULT 2

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US-09-886-143-2
; Sequence 2, Application US/09886143
; Patent No. US2002015991A1
; GENERAL INFORMATION:
; APPLICANT: Cordell, Barbara
; APPLICANT: Schimmler, Frauke
; APPLICANT: Liu, Yu-Wang
; APPLICANT: Quon, Diana Hom
; TITLE OF INVENTION: Modulation of A Levels by
; FILE REFERENCE: SCIOS.022A
; CURRENT APPLICATION NUMBER: US/09/886,143
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/215,729
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 6

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-886-143-2

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Query Match      100.0%; Score 2687; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 2,3e-217;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 241 GSGNGGSLVIGGLEPSLYKGDWYTPIKEEYVQIETLKIEIGOSINLDCREYNADKA 300
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D 301 IVDGTTLLRLPQKVFDAVAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
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QY 421 RAOKRVGPAAPCAEIAAGAVSEISGPFSTEDVANSNCVPAQSLSEPIIMIVSYALMSVCG 480
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RESULT 3

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; Sequence 196, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;

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APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC27
CURRENT APPLICATION NUMBER: US/09/978,697
PRIOR FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR APPLICATION NUMBER: 60/085689
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PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 2687; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 2,3e-217;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLPLLAQWLRAPABELAPAPPTLEPLRVAATNRVVAATPGGPAPERHADGL 60
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DB 61 ALALEPALASPAGANFLAMVDNLQDSDRGYYLEMLIGTPPOKQIILVDTGSSNPAVAG 120
QY 121 TPHSYIDYPTTERSSYRSKGFDTVYKYTGSGMTGFVGEDLVTI PKGFNTSFLVNIATI 180
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QY 181 FESENFPLPGIKWNGIILGLAVATLAKPSSSLETFPDSLVTOANIPNFSMOWCGAGLPVA 240
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QY 241 GSGTNGSLVIGTERPSLYKODIWTTPKEEYVYQIEILKLEIGQSLNDQREYNADKA 300
DB 241 GSGTNGSLVIGTERPSLYKODIWTTPKEEYVYQIEILKLEIGQSLNDQREYNADKA 300
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DB 301 IVDSTTLRLPQKVFDAVEAVARASLIPEPSDFMTGSQLACTNSETPMSTPKXSI 360
QY 361 YLRDENSRSFRITTLPOLYIQPMWAGLNYECYRFGISPSITNALVIGATWEGFYVFD 420
DB 361 YLRDENSRSFRITTLPOLYIQPMWAGLNYECYRFGISPSITNALVIGATWEGFYVFD 420
QY 421 RAQKRVGAAPCAEIAAGAAVEISGPFSTEVANSCYPAQSLSPILMYSYALMSVCG 480
DB 421 RAQKRVGAAPCAEIAAGAAVEISGPFSTEVANSCYPAQSLSPILMYSYALMSVCG 480
QY 481 AILVLVILLLPFCQRRPRDPEVWNDESSLVRHRMK 518
DB 481 AILVLVILLLPFCQRRPRDPEVWNDESSLVRHRMK 518

RESULT 4
US-09-978-192A-196
Sequence 196, Application US/09978192A
Patent No. US2002017753A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertelsen, Mary E.
APPLICANT: Goddard, Audrey
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APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James J.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secured and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC9
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PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 2687; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No.2.3e-217; Indels 0; Gaps 0;
Matches 518; Conservative 0; Mismatches 0;

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DB 121 TP HSYIDTYFPTERSSTYRSKGFVDYTVK YTGSSWTFGVEGLVYTI PKGFNTSFLVNIATI 180

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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
Query Match 100.0%; Score 2687; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 2, 3e-217;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGALARALLPLLAQWILRAAPETLAPFTLPLVAAATNRVAVPTGPGTPAERHADGL 60
DB 1 MGALARALLPLLAQWILRAAPETLAPFTLPLVAAATNRVAVPTGPGTPAERHADGL 60
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QY 181 FESENFPLPGIKWNGILGLAVATLAKPSSSLETFPDSLVTQANI PNVSQMCGAGLPVA 240
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QY 241 GSGTNGGSLVUGGIEPISLYKDDIWTTPKEMWYQIEILKLEIGQSLNLDCCREYNADKA 300
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DB 301 IYDSGTTLLRLPOKVPDAVAVARASLIPEFSDGFTGSLACMTSETPMSYFPKISI 360
QY 361 YLRDENSRSFRITILPOLYIQPMGAGLNEYCYRFGISPTNALVTGATMEGFYVIFD 420
DB 361 YLRDENSRSFRITILPOLYIQPMGAGLNEYCYRFGISPTNALVTGATMEGFYVIFD 420
QY 421 RAQKRVGFAPCAEIAAASEISGPSTEDVASCNCPAOSLSEPLIMIVYALMSVCG 480
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DB 481 AILLVILVLLLPFCQRPDPPEVNDSSLVHRMK 518
RESULT 6
US-09-978-189-196
Sequence 196, Application US/09978189
Publication No. US20030004102A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gettitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Kuo, Sophia S.

APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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; PRIOR APPLICATION NUMBER: 60/085382
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
;
Query Match      100.0%; Score 2687; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.3e-217;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

OY 1 MGALRALLLPLLAQWLRAPELAPFTLPRLVAAATNRVVAAPGCGTPAERHADGL 60
DB 1 MGALRALLLPLLAQWLRAPELAPFTLPRLVAAATNRVVAAPGCGTPAERHADGL 60
OY 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLEMLIGTPPOKQIILVDTGSSNFAVAG 120
DB 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLEMLIGTPPOKQIILVDTGSSNFAVAG 120
OY 121 TPHSYIDTYFDPTERRSTYRSKGFDTVVKYTGSGWTGFVEEDLVTIIPKGFNTSFLVNIATI 180
DB 121 TPHSYIDTYFDPTERRSTYRSKGFDTVVKYTGSGWTGFVEEDLVTIIPKGFNTSFLVNIATI 180
OY 181 FESSENFPLPGIKMNGILGLAAYATLAKPSSSLETFPDSLVTQANI PNVSQMCGAGLPVA 240
DB 181 FESSENFPLPGIKMNGILGLAAYATLAKPSSSLETFPDSLVTQANI PNVSQMCGAGLPVA 240
OY 241 GSGTNGSGLVGLIEPSLYKGDIMWTPRIKEEMYYQIEILKLEIGQSINLDCREYNADKA 300
DB 241 GSGTNGSGLVGLIEPSLYKGDIMWTPRIKEEMYYQIEILKLEIGQSINLDCREYNADKA 300
OY 301 IYDSGTTLLRLPQKVFDAVAVARASLIPEFSDGFWTGSQACWNTSETPWSYFPKXISI 360
DB 301 IYDSGTTLLRLPQKVFDAVAVARASLIPEFSDGFWTGSQACWNTSETPWSYFPKXISI 360
OY 361 YIRDENSSRSFRITTLPOLYIQPMGAGLNEYECYRFGISPTNALVIGATMEGFIYVFD 420
DB 361 YIRDENSSRSFRITTLPOLYIQPMGAGLNEYECYRFGISPTNALVIGATMEGFIYVFD 420
OY 421 RAQKRVGAASPCAEIAGAASEISGPFSTEDVANSNCVPAQSLSEPTILMIVSYALMSVCG 480
DB 421 RAQKRVGAASPCAEIAGAASEISGPFSTEDVANSNCVPAQSLSEPTILMIVSYALMSVCG 480
OY 481 AILVLIVLILLPFCQRRPRDPEVYNDESSLVHRWK 518
DB 481 AILVLIVLILLPFCQRRPRDPEVYNDESSLVHRWK 518
```

```

RESULT 7
US-10-174-590-72
; Sequence 72. Application US/10174590
; Publication No. US20030008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C42
; CURRENT APPLICATION NUMBER: US/10/174,590
; PRIOR APPLICATION REMOVED - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PR1
; ORGANISM: Homo Sapien
US-10-174-590-72
```

```

Query Match      100.0%; Score 2687; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.3e-217;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

OY 1 MGALRALLLPLLAQWLRAPELAPFTLPRLVAAATNRVVAAPGCGTPAERHADGL 60
DB 1 MGALRALLLPLLAQWLRAPELAPFTLPRLVAAATNRVVAAPGCGTPAERHADGL 60
OY 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLEMLIGTPPOKQIILVDTGSSNFAVAG 120
DB 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLEMLIGTPPOKQIILVDTGSSNFAVAG 120
OY 121 TPHSYIDTYFDPTERRSTYRSKGFDTVVKYTGSGWTGFVEEDLVTIIPKGFNTSFLVNIATI 180
DB 121 TPHSYIDTYFDPTERRSTYRSKGFDTVVKYTGSGWTGFVEEDLVTIIPKGFNTSFLVNIATI 180
OY 181 FESSENFPLPGIKMNGILGLAAYATLAKPSSSLETFPDSLVTQANI PNVSQMCGAGLPVA 240
DB 181 FESSENFPLPGIKMNGILGLAAYATLAKPSSSLETFPDSLVTQANI PNVSQMCGAGLPVA 240
OY 241 GSGTNGSGLVGLIEPSLYKGDIMWTPRIKEEMYYQIEILKLEIGQSINLDCREYNADKA 300
DB 241 GSGTNGSGLVGLIEPSLYKGDIMWTPRIKEEMYYQIEILKLEIGQSINLDCREYNADKA 300
OY 301 IYDSGTTLLRLPQKVFDAVAVARASLIPEFSDGFWTGSQACWNTSETPWSYFPKXISI 360
DB 301 IYDSGTTLLRLPQKVFDAVAVARASLIPEFSDGFWTGSQACWNTSETPWSYFPKXISI 360
OY 361 YIRDENSSRSFRITTLPOLYIQPMGAGLNEYECYRFGISPTNALVIGATMEGFIYVFD 420
DB 361 YIRDENSSRSFRITTLPOLYIQPMGAGLNEYECYRFGISPTNALVIGATMEGFIYVFD 420
OY 421 RAQKRVGAASPCAEIAGAASEISGPFSTEDVANSNCVPAQSLSEPTILMIVSYALMSVCG 480
DB 421 RAQKRVGAASPCAEIAGAASEISGPFSTEDVANSNCVPAQSLSEPTILMIVSYALMSVCG 480
OY 481 AILVLIVLILLPFCQRRPRDPEVYNDESSLVHRWK 518
DB 481 AILVLIVLILLPFCQRRPRDPEVYNDESSLVHRWK 518
```

RESULT 8

```

US-10-176-758-72
; Sequence 72, Application US/10176758
; Publication No. US20030008353A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C104
; CURRENT APPLICATION NUMBER: US/10/176,758
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-758-72

Query Match          100.0%; Score 2687; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 2,3e-217;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLLPQLQWLRAAPBELAPAPFTLPLRVAAATNRVVAAPTPGPGTPAERHADGL 60
DB 1 MGALARALLLPQLQWLRAAPBELAPAPFTLPLRVAAATNRVVAAPTPGPGTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAWNDLQSGSGRYLEMLIGTPPOKQLIIVDTGSSNFAVAG 120
DB 61 ALALEPALASPAGANFLAWNDLQSGSGRYLEMLIGTPPOKQLIIVDTGSSNFAVAG 120
QY 121 TPHSYIDTYEPTTERRSSTYRSKGFDTVTKYTGSGWTGFVGEDLVITIPKGFNTSFLVNIATI 180
DB 121 TPHSYIDTYEPTTERRSSTYRSKGFDTVTKYTGSGWTGFVGEDLVITIPKGFNTSFLVNIATI 180
QY 181 FESENFPLPGIKMNGIIGLAVATLAKPSSSLETFPDSLVTQANIPNVFSMQCGAGLPVA 240
DB 181 FESENFPLPGIKMNGIIGLAVATLAKPSSSLETFPDSLVTQANIPNVFSMQCGAGLPVA 240
QY 241 GSGTNGGSLVIGIEPSLYKGDIMWTPIKEWYQIEILKLEIGGOSLNLDCREYNADKA 300
DB 241 GSGTNGGSLVIGIEPSLYKGDIMWTPIKEWYQIEILKLEIGGOSLNLDCREYNADKA 300
QY 301 IVDGTTLLRLPQKVFDAVAVARASLIPEFSDGFTGSQLACWTNSETPWSYFPKISI 360
DB 301 IVDGTTLLRLPQKVFDAVAVARASLIPEFSDGFTGSQLACWTNSETPWSYFPKISI 360
QY 361 YLRDENSRSFRITILPOLYIOPMMGAGLNYECYRFGISPTNALVIGATVMEGYIYFD 420
DB 361 YLRDENSRSFRITILPOLYIOPMMGAGLNYECYRFGISPTNALVIGATVMEGYIYFD 420
QY 421 RAQKRVGFAASPCAEIAAGAAVSEISGPFSTEDVANSNCVPAOSLSEPIIMIVSYALMSVCG 480
DB 421 RAQKRVGFAASPCAEIAAGAAVSEISGPFSTEDVANSNCVPAOSLSEPIIMIVSYALMSVCG 480
QY 481 AILVLIVLILLPRCQRRPRDPEVNDSSLVHRMK 518
DB 481 AILVLIVLILLPRCQRRPRDPEVNDSSLVHRMK 518

```

```

; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C50
; CURRENT APPLICATION NUMBER: US/10/175,737
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-737-72

Query Match          100.0%; Score 2687; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 2,3e-217;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGALARALLLPQLQWLRAAPBELAPAPFTLPLRVAAATNRVVAAPTPGPGTPAERHADGL 60
DB 1 MGALARALLLPQLQWLRAAPBELAPAPFTLPLRVAAATNRVVAAPTPGPGTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAWNDLQSGSGRYLEMLIGTPPOKQLIIVDTGSSNFAVAG 120
DB 61 ALALEPALASPAGANFLAWNDLQSGSGRYLEMLIGTPPOKQLIIVDTGSSNFAVAG 120
QY 121 TPHSYIDTYEPTTERRSSTYRSKGFDTVTKYTGSGWTGFVGEDLVITIPKGFNTSFLVNIATI 180
DB 121 TPHSYIDTYEPTTERRSSTYRSKGFDTVTKYTGSGWTGFVGEDLVITIPKGFNTSFLVNIATI 180
QY 181 FESENFPLPGIKMNGIIGLAVATLAKPSSSLETFPDSLVTQANIPNVFSMQCGAGLPVA 240
DB 181 FESENFPLPGIKMNGIIGLAVATLAKPSSSLETFPDSLVTQANIPNVFSMQCGAGLPVA 240
QY 241 GSGTNGGSLVIGIEPSLYKGDIMWTPIKEWYQIEILKLEIGGOSLNLDCREYNADKA 300
DB 241 GSGTNGGSLVIGIEPSLYKGDIMWTPIKEWYQIEILKLEIGGOSLNLDCREYNADKA 300
QY 301 IVDGTTLLRLPQKVFDAVAVARASLIPEFSDGFTGSQLACWTNSETPWSYFPKISI 360
DB 301 IVDGTTLLRLPQKVFDAVAVARASLIPEFSDGFTGSQLACWTNSETPWSYFPKISI 360
QY 361 YLRDENSRSFRITILPOLYIOPMMGAGLNYECYRFGISPTNALVIGATVMEGYIYFD 420
DB 361 YLRDENSRSFRITILPOLYIOPMMGAGLNYECYRFGISPTNALVIGATVMEGYIYFD 420
QY 421 RAQKRVGFAASPCAEIAAGAAVSEISGPFSTEDVANSNCVPAOSLSEPIIMIVSYALMSVCG 480
DB 421 RAQKRVGFAASPCAEIAAGAAVSEISGPFSTEDVANSNCVPAOSLSEPIIMIVSYALMSVCG 480
QY 481 AILVLIVLILLPRCQRRPRDPEVNDSSLVHRMK 518
DB 481 AILVLIVLILLPRCQRRPRDPEVNDSSLVHRMK 518

```

```

RESULT 9
US-10-175-737-72
; Sequence 72, Application US/10175737
; Publication No. US20030013153A1

```

```

RESULT 10
US-10-173-706-72
; Sequence 72, Application US/10173706
; Publication No. US20030022293A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian

```

```
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C7
CURRENT APPLICATION NUMBER: US/10/173, 706
CURRENT FILING DATE: 2002-06-17
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 72
LENGTH: 518
TYPE: PRT
ORGANISM: Homo Sapien
US-10-173-706-72
```

```
Query Match          100.0%; Score 2687; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.3e-217;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MGALARALLPLLAQWLIRAAPELAPPTLLPLRVAATNRVVAFTPGGTPARRHADGL 60
DB 1 MGALARALLPLLAQWLIRAAPELAPPTLLPLRVAATNRVVAFTPGGTPARRHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDGRGYYLEMLIGTPPOKLOILVDTGSSNFAVAG 120
DB 61 ALALEPALASPAGANFLAMVDNLQDGRGYYLEMLIGTPPOKLOILVDTGSSNFAVAG 120
QY 121 TPHSYIDYFPDTERSSYRSKGFDTVKYTGQSWTGFVEGDLVTIPKGFNTSFLVNIATI 180
DB 121 TPHSYIDYFPDTERSSYRSKGFDTVKYTGQSWTGFVEGDLVTIPKGFNTSFLVNIATI 180
QY 181 FESENFPLPGIKMNGIILGLAVATLAKPSSSLETFPDSLVTQANIPNVFSMQCAGLPVA 240
DB 181 FESENFPLPGIKMNGIILGLAVATLAKPSSSLETFPDSLVTQANIPNVFSMQCAGLPVA 240
QY 241 GSGTNGGSLVIGIIEPSLYKGDIMWTPIKEWYQIIEILKIEIGGOSINLDCREYNADKA 300
DB 241 GSGTNGGSLVIGIIEPSLYKGDIMWTPIKEWYQIIEILKIEIGGOSINLDCREYNADKA 300
QY 301 IVDGTTLLRLPQKYFDVAVEAVARASLIPEFSDGFWTGSQLAQWNTSETPWSYFPKISI 360
DB 301 IVDGTTLLRLPQKYFDVAVEAVARASLIPEFSDGFWTGSQLAQWNTSETPWSYFPKISI 360
QY 361 YLRDSSRSRFRITILLPOLYIQPMGAGLANECYRFGISPSSTNALVIGATVMEGFYIFD 420
DB 361 YLRDSSRSRFRITILLPOLYIQPMGAGLANECYRFGISPSSTNALVIGATVMEGFYIFD 420
QY 421 RAOKRVGFPAAPCAEIAAGAAVEISGPFSTEDVANCVPAOSLSEPIIMIVSYALMSVCG 480
DB 421 RAOKRVGFPAAPCAEIAAGAAVEISGPFSTEDVANCVPAOSLSEPIIMIVSYALMSVCG 480
QY 481 AILLVILVILLPLPRCQRRPRDPEVVDSSLVHRMK 518
DB 481 AILLVILVILLPLPRCQRRPRDPEVVDSSLVHRMK 518
```

RESULT 11
US-10-175-738-72
Sequence 72, Application US/10175738
Publication No. US20030022295A1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Chen, J'ian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.

```
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C45
CURRENT APPLICATION NUMBER: US/10/175, 738
CURRENT FILING DATE: 2002-06-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 72
LENGTH: 518
TYPE: PRT
ORGANISM: Homo Sapien
US-10-175-738-72
```

```
Query Match          100.0%; Score 2687; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.3e-217;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MGALARALLPLLAQWLIRAAPELAPPTLLPLRVAATNRVVAFTPGGTPARRHADGL 60
DB 1 MGALARALLPLLAQWLIRAAPELAPPTLLPLRVAATNRVVAFTPGGTPARRHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDGRGYYLEMLIGTPPOKLOILVDTGSSNFAVAG 120
DB 61 ALALEPALASPAGANFLAMVDNLQDGRGYYLEMLIGTPPOKLOILVDTGSSNFAVAG 120
QY 121 TPHSYIDYFPDTERSSYRSKGFDTVKYTGQSWTGFVEGDLVTIPKGFNTSFLVNIATI 180
DB 121 TPHSYIDYFPDTERSSYRSKGFDTVKYTGQSWTGFVEGDLVTIPKGFNTSFLVNIATI 180
QY 181 FESENFPLPGIKMNGIILGLAVATLAKPSSSLETFPDSLVTQANIPNVFSMQCAGLPVA 240
DB 181 FESENFPLPGIKMNGIILGLAVATLAKPSSSLETFPDSLVTQANIPNVFSMQCAGLPVA 240
QY 241 GSGTNGGSLVIGIIEPSLYKGDIMWTPIKEWYQIIEILKIEIGGOSINLDCREYNADKA 300
DB 241 GSGTNGGSLVIGIIEPSLYKGDIMWTPIKEWYQIIEILKIEIGGOSINLDCREYNADKA 300
QY 301 IVDGTTLLRLPQKYFDVAVEAVARASLIPEFSDGFWTGSQLAQWNTSETPWSYFPKISI 360
DB 301 IVDGTTLLRLPQKYFDVAVEAVARASLIPEFSDGFWTGSQLAQWNTSETPWSYFPKISI 360
QY 361 YLRDSSRSRFRITILLPOLYIQPMGAGLANECYRFGISPSSTNALVIGATVMEGFYIFD 420
DB 361 YLRDSSRSRFRITILLPOLYIQPMGAGLANECYRFGISPSSTNALVIGATVMEGFYIFD 420
QY 421 RAOKRVGFPAAPCAEIAAGAAVEISGPFSTEDVANCVPAOSLSEPIIMIVSYALMSVCG 480
DB 421 RAOKRVGFPAAPCAEIAAGAAVEISGPFSTEDVANCVPAOSLSEPIIMIVSYALMSVCG 480
QY 481 AILLVILVILLPLPRCQRRPRDPEVVDSSLVHRMK 518
DB 481 AILLVILVILLPLPRCQRRPRDPEVVDSSLVHRMK 518
```

RESULT 12
US-10-175-752-72
Sequence 72, Application US/10175752
Publication No. US20030022295A1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Chen, J'ian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria

```

; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C60
; CURRENT APPLICATION NUMBER: US/10/176,482
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-482-72

```

```

Query Match      100.0%; Score 2687; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.3e-217;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MGALARALLPLLAQWMLRAAPELAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
D 1 MGALARALLPLLAQWMLRAAPELAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSGSGRYLEMLIGTPPOKQILVDTGSSNFAVAG 120
D 61 ALALEPALASPAGANFLAMVDNLQDSGSGRYLEMLIGTPPOKQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTPPTERSSTYRSKGFDTVKYTOGSGMTGFVGEDLVITIPKGFNTSFLVNIATI 180
D 121 TPHSYIDTPPTERSSTYRSKGFDTVKYTOGSGMTGFVGEDLVITIPKGFNTSFLVNIATI 180
QY 181 FESNFPLPGIKMNGIIGLAVATLAKPSSLETFFDSLVTOANIPNVFSMQMCGAGLPVA 240
D 181 FESNFPLPGIKMNGIIGLAVATLAKPSSLETFFDSLVTOANIPNVFSMQMCGAGLPVA 240
QY 241 GSGTNGSLVIGIEPLSKGDIWYTPIKEWYQIILKLEIGGSLNDLCREYNADKA 300
D 241 GSGTNGSLVIGIEPLSKGDIWYTPIKEWYQIILKLEIGGSLNDLCREYNADKA 300
QY 301 IVDGTTLLRLPOKVPDAVVAVARASLIPEFSDGFWTGSOLACMTNSETPWSYFPKISI 360
D 301 IVDGTTLLRLPOKVPDAVVAVARASLIPEFSDGFWTGSOLACMTNSETPWSYFPKISI 360
QY 361 YLRDENSRSRRTITLIPOLYIQPMMGAGLNEYECYRFGISSTNALVIGATVMEGFYIFD 420
D 361 YLRDENSRSRRTITLIPOLYIQPMMGAGLNEYECYRFGISSTNALVIGATVMEGFYIFD 420
QY 421 RAQKRVGFPAASPCAEIAGAASEISGPFSTEDVASCNCPAQSISEPILMTIVSYALMSVCG 480
D 421 RAQKRVGFPAASPCAEIAGAASEISGPFSTEDVASCNCPAQSISEPILMTIVSYALMSVCG 480
QY 481 AILVLIVLILLLPRCQRRPRDPEVNDSESLVHRMK 518
D 481 AILVLIVLILLLPRCQRRPRDPEVNDSESLVHRMK 518

```

RESULT 13

```

US-10-176-482-72
; Sequence 72, Application US/10176482
; Publication No. US20030022296A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

```

```

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C70
; CURRENT APPLICATION NUMBER: US/10/176,482
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-482-72

```

```

Query Match      100.0%; Score 2687; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.3e-217;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MGALARALLPLLAQWMLRAAPELAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
D 1 MGALARALLPLLAQWMLRAAPELAPFTLPLRVAATNRVVAPTPGPTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSGSGRYLEMLIGTPPOKQILVDTGSSNFAVAG 120
D 61 ALALEPALASPAGANFLAMVDNLQDSGSGRYLEMLIGTPPOKQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTPPTERSSTYRSKGFDTVKYTOGSGMTGFVGEDLVITIPKGFNTSFLVNIATI 180
D 121 TPHSYIDTPPTERSSTYRSKGFDTVKYTOGSGMTGFVGEDLVITIPKGFNTSFLVNIATI 180
QY 181 FESNFPLPGIKMNGIIGLAVATLAKPSSLETFFDSLVTOANIPNVFSMQMCGAGLPVA 240
D 181 FESNFPLPGIKMNGIIGLAVATLAKPSSLETFFDSLVTOANIPNVFSMQMCGAGLPVA 240
QY 241 GSGTNGSLVIGIEPLSKGDIWYTPIKEWYQIILKLEIGGSLNDLCREYNADKA 300
D 241 GSGTNGSLVIGIEPLSKGDIWYTPIKEWYQIILKLEIGGSLNDLCREYNADKA 300
QY 301 IVDGTTLLRLPOKVPDAVVAVARASLIPEFSDGFWTGSOLACMTNSETPWSYFPKISI 360
D 301 IVDGTTLLRLPOKVPDAVVAVARASLIPEFSDGFWTGSOLACMTNSETPWSYFPKISI 360
QY 361 YLRDENSRSRRTITLIPOLYIQPMMGAGLNEYECYRFGISSTNALVIGATVMEGFYIFD 420
D 361 YLRDENSRSRRTITLIPOLYIQPMMGAGLNEYECYRFGISSTNALVIGATVMEGFYIFD 420
QY 421 RAQKRVGFPAASPCAEIAGAASEISGPFSTEDVASCNCPAQSISEPILMTIVSYALMSVCG 480
D 421 RAQKRVGFPAASPCAEIAGAASEISGPFSTEDVASCNCPAQSISEPILMTIVSYALMSVCG 480
QY 481 AILVLIVLILLLPRCQRRPRDPEVNDSESLVHRMK 518
D 481 AILVLIVLILLLPRCQRRPRDPEVNDSESLVHRMK 518

```

RESULT 14

```

US-10-176-757-72
; Sequence 72, Application US/10176757
; Publication No. US20030022297A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C86

```

```

; CURRENT APPLICATION NUMBER: US/10/176,757
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-757-72

```

```

Query Match      100.0%; Score 2687; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.3e-217;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MGALRALLLPLAOWMLRAABELAPAPFTLLPLRVAATNRVVAAPPGPTPAERHADGL 60
D 1 MGALRALLLPLAOWMLRAABELAPAPFTLLPLRVAATNRVVAAPPGPTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLEMLIGTPPOKLQILVDTGSSNFAVAG 120
D 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLEMLIGTPPOKLQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFDTERSSSTYRSKGFDTVKYTGSGWTGVEGDELVTIIPKGFNTSLVNIATI 180
D 121 TPHSYIDTYFDTERSSSTYRSKGFDTVKYTGSGWTGVEGDELVTIIPKGFNTSLVNIATI 180
QY 181 FESSENFPLPGIKMNGILGLAVATLAKPSSSLETFPDSLVTQANIENVFSMQMGAGLPVA 240
D 181 FESSENFPLPGIKMNGILGLAVATLAKPSSSLETFPDSLVTQANIENVFSMQMGAGLPVA 240
QY 241 GSGTNGGSLVIGGIEPSLYKGDWYTPIKEEWYQIEIKLEIGGOSLNDCREYNADKA 300
D 241 GSGTNGGSLVIGGIEPSLYKGDWYTPIKEEWYQIEIKLEIGGOSLNDCREYNADKA 300
QY 301 IVDGGTTLRLPQKVFDAVEAVARASLIPEFSDGFWTGSQLAQWNTSETPWSTPKISI 360
D 301 IVDGGTTLRLPQKVFDAVEAVARASLIPEFSDGFWTGSQLAQWNTSETPWSTPKISI 360
QY 361 YLRDSSRSFRITILLPOLYIQPMGAGLNEYCYRFGISPTNALVIGATWEGFYIFD 420
D 361 YLRDSSRSFRITILLPOLYIQPMGAGLNEYCYRFGISPTNALVIGATWEGFYIFD 420
QY 421 RAQKRVGFAASPACAEIAGAASEISGFSTEDVASCNCPAQSLEPILMIVSYALMSVCG 480
D 421 RAQKRVGFAASPACAEIAGAASEISGFSTEDVASCNCPAQSLEPILMIVSYALMSVCG 480
QY 481 ALLVLIVLILLPFCQRRPRDPEVNDSSLVRRHWK 518
D 481 ALLVLIVLILLPFCQRRPRDPEVNDSSLVRRHWK 518

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RESULT 15

```

US-10-176-913-72
; Sequence 72, Application US/10176913
; Publication No. US20030022298A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddard, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C66
; CURRENT APPLICATION NUMBER: US/10/176,913
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See file Wrapper or Palm

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; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 72
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-913-72

```

```

Query Match      100.0%; Score 2687; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.3e-217;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MGALRALLLPLAOWMLRAABELAPAPFTLLPLRVAATNRVVAAPPGPTPAERHADGL 60
D 1 MGALRALLLPLAOWMLRAABELAPAPFTLLPLRVAATNRVVAAPPGPTPAERHADGL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLEMLIGTPPOKLQILVDTGSSNFAVAG 120
D 61 ALALEPALASPAGANFLAMVDNLQDSGRGYLEMLIGTPPOKLQILVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFDTERSSSTYRSKGFDTVKYTGSGWTGVEGDELVTIIPKGFNTSLVNIATI 180
D 121 TPHSYIDTYFDTERSSSTYRSKGFDTVKYTGSGWTGVEGDELVTIIPKGFNTSLVNIATI 180
QY 181 FESSENFPLPGIKMNGILGLAVATLAKPSSSLETFPDSLVTQANIENVFSMQMGAGLPVA 240
D 181 FESSENFPLPGIKMNGILGLAVATLAKPSSSLETFPDSLVTQANIENVFSMQMGAGLPVA 240
QY 241 GSGTNGGSLVIGGIEPSLYKGDWYTPIKEEWYQIEIKLEIGGOSLNDCREYNADKA 300
D 241 GSGTNGGSLVIGGIEPSLYKGDWYTPIKEEWYQIEIKLEIGGOSLNDCREYNADKA 300
QY 301 IVDGGTTLRLPQKVFDAVEAVARASLIPEFSDGFWTGSQLAQWNTSETPWSTPKISI 360
D 301 IVDGGTTLRLPQKVFDAVEAVARASLIPEFSDGFWTGSQLAQWNTSETPWSTPKISI 360
QY 361 YLRDSSRSFRITILLPOLYIQPMGAGLNEYCYRFGISPTNALVIGATWEGFYIFD 420
D 361 YLRDSSRSFRITILLPOLYIQPMGAGLNEYCYRFGISPTNALVIGATWEGFYIFD 420
QY 421 RAQKRVGFAASPACAEIAGAASEISGFSTEDVASCNCPAQSLEPILMIVSYALMSVCG 480
D 421 RAQKRVGFAASPACAEIAGAASEISGFSTEDVASCNCPAQSLEPILMIVSYALMSVCG 480
QY 481 ALLVLIVLILLPFCQRRPRDPEVNDSSLVRRHWK 518
D 481 ALLVLIVLILLPFCQRRPRDPEVNDSSLVRRHWK 518

```

Search completed: April 1, 2003, 11:42:39
Job time : 40 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 1, 2003, 11:31:03 ; Search time 21 Seconds

(without alignments)
2371.316 Million cell updates/sec

Title: US-09-668-314c-2

Perfect score: 2687

Sequence: 1 MGALRALLLPLLAQWLRA.....RPDPEVNVNDESLVRRHRWK 518

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1178.5	43.9	501 2	AS9090
2	367.5	13.7	383 2	pepsinogen C - Afr
3	363.5	13.5	377 1	pepsinogen C - Afr
4	355.5	13.2	384 2	pepsinogen C - Afr
5	355	13.1	389 2	pepsinogen C - Afr
6	351.5	13.1	388 2	pepsinogen C - Afr
7	351.5	13.1	388 2	pepsinogen C - Afr
8	324.5	12.1	394 2	pepsinogen C - Afr
9	320	11.9	385 2	pepsinogen C - Afr
10	320	11.9	402 1	pepsinogen A - Afr
11	313.5	11.7	509 2	pepsinogen A - Afr
12	313	11.6	509 2	pepsinogen A - Afr
13	310	11.5	383 2	pepsinogen A - Afr
14	308.5	11.5	412 1	pepsinogen A - Afr
15	306.5	11.4	410 1	pepsinogen A - Afr
16	305.5	11.4	401 1	pepsinogen A - Afr
17	305	11.4	384 2	pepsinogen A - Afr
18	305	11.4	407 1	pepsinogen A - Afr
19	302	11.2	405 2	pepsinogen A - Afr
20	301.5	11.2	398 2	pepsinogen A - Afr
21	300.5	11.2	387 2	pepsinogen A - Afr
22	299	11.1	398 2	pepsinogen A - Afr
23	298.5	11.1	387 2	pepsinogen A - Afr
24	298.5	11.1	400 2	pepsinogen A - Afr
25	297	11.1	388 2	pepsinogen A - Afr
26	296	11.0	388 2	pepsinogen A - Afr
27	296	11.0	388 2	pepsinogen A - Afr
28	294.5	11.0	388 2	pepsinogen A - Afr
29	292	10.9	506 2	pepsinogen A - Afr

30	291	10.8	388 1	pepsin A (EC 3.4.2.1)
31	291	10.8	402 1	pepsin A (EC 3.4.2.1)
32	291	10.8	406 1	pepsin A (EC 3.4.2.1)
33	290.5	10.8	396 2	pepsin A (EC 3.4.2.1)
34	289	10.8	387 2	pepsin A (EC 3.4.2.1)
35	288	10.7	387 2	pepsin A (EC 3.4.2.1)
36	288	10.7	388 1	pepsin A (EC 3.4.2.1)
37	287.5	10.7	632 2	pepsin A (EC 3.4.2.1)
38	287	10.7	391 2	pepsin A (EC 3.4.2.1)
39	287	10.7	396 2	pepsin A (EC 3.4.2.1)
40	286.5	10.7	334 2	pepsin A (EC 3.4.2.1)
41	286	10.6	382 1	pepsin A (EC 3.4.2.1)
42	286	10.6	388 1	pepsin A (EC 3.4.2.1)
43	285.5	10.6	387 2	pepsin A (EC 3.4.2.1)
44	285	10.6	396 2	pepsin A (EC 3.4.2.1)
45	284.5	10.6	386 1	pepsin A (EC 3.4.2.1)

ALIGNMENTS

RESULT 1
AS9090
N:Alternate names: beta-secretase; beta-site APP cleaving enzyme
C:Species: Homo sapiens (man)
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 11-May-2000
R:Vaasat, R.; Bennett, B.D.; Babu-Khan, S.; Kahn, S.; Mendiaz, E.A.; Denis, P.; Teglou, M.A.; Biere, A.L.; Curran, E.; Burgess, T.; Louis, J.C.; Collins, F.; Treanor, J.; Roje Science 286, 735-741, 1999
A:Title: beta-Secretase cleavage of Alzheimer's amyloid precursor protein by the transmembrane aspartic protease BACE
A:Reference number: AS9090; MIM:2000297; PMID:10531052
A:Note: submitted to GenBank, September 1999
A:Accession: AS9090
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-501 <VAS>
A:Cross-references: GB:AF190725; NID:G6118538; PID:AA04142.1; PID:G6118539
C:Genetics:
A:Gene: BACE
C:Superfamily: beta-secretase
C:Keywords: Alzheimer's disease; aspartic protease; brain; glycoprotein; hydrolase; p
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-45/Domain: propeptide #status predicted <PRO>
F:46-501/Product: acid protease BACE #status predicted <MAT>
F:461-477/Domain: transmembrane #status predicted <TRN>
F:931-289/Active site: Asp #status predicted
F:153,172,223,354/Binding site: carbohydrate (asn) (covalent) #status predicted
F:330-380/Disulfide bonds: #status predicted

Query Match 43.9% Score 1178.5; DB 2; Length 501;
Best local Similarity 46.2% Pred. No. 3.3e-80;
Matches 240; Conservative 82; Mismatches 164; Indels 33; Gaps 9;

Qy 7 ALLPLLAQWLRAPELAPAFPT-----LPLRVAATNRVAVLPDGGCPAERHAGDIA 61
Db 2 AQLPLLLM---GAVLPKHGTGHRPLRSLG-----GAPL-----GLR 42

Qy 62 LALF-PALASPAGANFLAVNDLQDSDGRGYLEMLIGTPPKQILVDTGSSNPAVA 119
Db 43 LPREDEEPERGRGSRVENVDLRGSGGYVEMTVGSPPTLNLIVDTGSSNPAVG 102

Qy 120 GTPSYIDTYDTRSSSTYSKSGFDVYKQSGWTFGVGHDVLTIRKGMTSLVNIAI 179
Db 103 AAPHFHRYRYQRLSTYDLRKGVVVPYTGKMBEELGDLVSIHGPVATRAVIAA 162

Qy 180 IFSEENFPLPGIKWNGILGLAVATLAKSSSLTEFPDSLVTOANI PVVFSQMGAGAPV 239
Db 163 ITESDKFFINSGNEGLIGLAVATLAKPDDSLFFPSLVKQIHVPVLSIQLGAGAPL 222

Qy 240 AGS---GTNGSLVAGIEPSLYKGDIMYTPIKEMWYQIETLLETIGOSLNDCREYN 296
Db 240 AGS---GTNGSLVAGIEPSLYKGDIMYTPIKEMWYQIETLLETIGOSLNDCREYN 296

```

Db 223 NOSEVLAVSGVSMITIGIDHSLYTGSLWYTPIRREMYEVLIVRVEINGODLKMDCKEYN 282
Qy 297 ADKAVDSGTTLLRLPKQVFAVAVAVASALIPFSDGFMTGSLQACMTNSETPWSYFP 356
Db 283 YDKSLVDGTTNLRPKVFEAAVAKSIRKASSTKEFPDGFMLGEOLVCMQAGTTWNTLFP 342
Qy 357 KISILYRENSRSRFRITLLPOLYIQPMAGIANY-ECRFGISPTNALVIGATVMEGF 415
Db 343 VISLYLMEVITNOSFRITLLPOLYLRPEVDVATSDDDCKFALISSGTCGTWGAIVMEGF 402
Qy 416 YVIFDRAQKRVGFAASPCALAGAAVSEISGPFSTEDVANSVCVPAQSLEPIMLIVSYAL 475
Db 403 YVVFDRARRKRGFAVASACHVDEFRTAAVEGPFVLLDMEDCCYNIQDDESTLMTIAYVM 462
Qy 476 MSVCGAILLVILLPLPRQCR--RPRRDEVNNESSL 512
Db 463 AAIC-ALFMLPLCLMVCQRCRLCRLQCHDHPADIDISLL 500

RESULT 2
JC7573
pepsinogen C - African clawed frog
N/Alternate names: progastricsin
C/Species: Xenopus laevis (African clawed frog)
C/Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 03-Aug-2001
C/Accession: JC7573; PC7118
R/Ikuizawa, M.; Inokuchi, T.; Kobayashi, K.; Yasunasu, S.
J. Biochem. 129, 147-153, 2001
A/Title: Amphibian pepsinogens: Purification and characterization of Xenopus pepsinogens
A/Reference number: JC7573; MUID:21064922; PMID:11134969
A/Contents: Stomach
A/Accession: JC7573
A/Molecule type: mRNA
A/Residues: 1-383 <IKU>
A/Cross-references: DDBJ:AB045379
A/Accession: PC7118
A/Molecule type: protein
A/Residues: 17-68 <IK2>
C/Comment: This protein is a zymogen for gastric aspartic proteinase, with pepsin-like
C/Genetics:
A/Gene: PGC
C/Superfamily: pepsin
C/Keywords: stomach; zymogen

Query Match 13.7%; Score 367.5; DB 2; Length 383;
Best Local Similarity 28.9%; Pred. No. 8,7e-20;
Matches 132; Conservative 70; Mismatches 154; Indels 101; Gaps 25;

Qy 1 MGALRAALLPLLAQWILRAAPLAPFTLLPLRVAAATNRVVAAPTPGPTPAERHADGL 60
Db 1 MKFLIALVLCQLSGEILR-----VPLKKFKSMREVMRENGIKAPLVDPAT---KYNYCY 52

Qy 61 ALALEPALASPAGANFLAMVDNLQDSSRGYLEMLIGTPPOKQILVDTGSSNFAVAG 120
Db 53 ATAYEP-----LSNYMDM-----SYGEISIGTPPNFLVLPDTGSSNLMVAS 95

Qy 121 THSYLDT-----YEDERSSTYSKGFVTVKVTQSGMFGVEDLVITPKGNSTF 173
Db 96 T---YCQSQACTNHPILFNPSQSTYSNQQQFSLQYGTSLGILYDVTIIO----- 145

Qy 174 LVNIATIFESSEFFL---PG-----IKWNGILGLAVATLAKPSSILETFPDSLVTQANI 224
Db 146 --NVA--ISQGERGLSETEBGTNFVYAQFPDGLIGLAVPSIANGAR--TYMGQM--QQLL 198

Qy 225 PV--VFSMQMCGALPVAAGSGLVIGIEPSLYKDDIWTPIKEMYYOIEILKLE 282
Db 199 LNPQIFGFYLSQ-----SSQNGEVARFGVDQNYTQGIYWTPTSETWQIGIGFSS 252

Qy 283 TGGQSLNDCREYNADKALVDSGTTLLRLPKQVFAVAVAVASALIPFSDGFMTGSLQ 342
Db 253 INGAQTGW--CSQ--GCQALVDTGTSLTLTAQSVFSSLIQISG-----AQQDQNGQYV 301

Qy 343 ACWTNSETPWSYFPKISILYRENSRSRFRITLLPOLYI-QPMAGIANYECYRFGIS-- 399

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```

Db 302 VSCSNIQN-----LPTISFTI-----SGVSFPLP--PSAYVILQSSSG-----YC-TIGIMPT 345
Qy 400 --PSTNA---LVIGATVMEGFYVIEDRAQKRVGFAAS 431
Db 346 YLPSQNGQPLMILGDFLREYSYVDLGNNOVGFRATA 382

RESULT 3
PEMOCJ
gastricsin (EC 3.4.23.3) precursor - Japanese macaque (fragment)
N/Alternate names: pepsin C
C/Species: Macaca fuscata (Japanese macaque)
C/Date: 13-Aug-1986 #sequence_revision 19-Oct-1995 #text_change 18-Jun-1999
C/Accession: S19683; A00986; A22402; S16066
R/Kageyama, T.; Tanabe, K.; Koiwai, O.
Eur. J. Biochem. 202, 205-215, 1991
A/Title: Development-dependent expression of isozymogens of monkey pepsinogens and stru
A/Reference number: S19681; MUID:92037645; PMID:1935977
A/Accession: S19683
A/Molecule type: mRNA
A/Residues: 1-377 <KAG>
A/Cross-references: EMBL:X59754; NID:938072; PIDN:CAA42426.1; PID:938073
R/Kageyama, T.; Takahashi, K.
J. Biochem. 261, 4406-4419, 1986
A/Title: The complete amino acid sequence of monkey progastricsin.
A/Reference number: A00986; MUID:86168133; PMID:3514597
A/Accession: A00986
A/Molecule type: Protein
A/Residues: 6-330, 'V', 332-349, 'VY', 350-377 <KA2>
R/Kageyama, T.; Takahashi, K.
J. Biochem. 97, 1235-1246, 1985
A/Title: Monkey pepsinogens and pepsins. VII. Analysis of the activation process and de
pepsinogens.
A/Reference number: A22402; MUID:85289106; PMID:33928607
A/Accession: A22402
A/Molecule type: protein
A/Residues: 6-65 <KA3>
C/Comment: This enzyme has more restricted specificity than pepsin A.
C/Comment: The enzyme is activated in a two-step process that gives rise to two end pro
C/Superfamily: pepsin
C/Keywords: aspartic proteinase; gastric juice; hydrolase; protein digestion; stomach
F.1-5/Domain: signal sequence (fragment) #status experimental <2YM>
F.6-377/Product: progastricsin #status experimental <2YM>
F.6-45/Domain: activation peptide #status experimental <MIN>
F.46-377/Product: Gly-gastricsin #status experimental <APT>
F.49-377/Product: Ser-gastricsin #status experimental <MAT>
F.31-32/Cleavage site: Phe-Leu (pepsin) #status experimental
F.45-46/Cleavage site: Phe-Gly (pepsin) #status experimental
F.48-49/Cleavage site: Leu-Ser (pepsin) #status experimental
F.80,265/Active site: Asp #status predicted
F.93-98,256-260,299-332/Disulfide bonds: #status experimental

Query Match 13.5%; Score 363.5; DB 1; Length 377;
Best Local Similarity 28.9%; Pred. No. 1.7e-19;
Matches 118; Conservative 65; Mismatches 118; Indels 107; Gaps 19;

Qy 56 HADGLALALEPALASPAGANFLAMVDNLQDSSRGYLEMLIGTPPOKQILVDTGSSN 115
Db 44 HFGLDSVSTEP-----MAYMD-----AAVGEISIGTPPNFLVLPDTGSSN 85

Qy 116 FAV-----AGTPHSYIDTYFTDERSSTYSKGFVTVKVTQSGMFGVEDLVITPK 167
Db 86 LMVPSVYQSQACTSHS-----RFPNSBSTYSTNGQTSLSQYSGSLGFGFYDITLV-- 139

Qy 168 GNTSFLVNIATIFESSEFFLPD-----IKWNGILGLAVATLAKSSSLLETFPDSLVTQ 222
Db 140 ---QSIQVNPQGFGLSEN--EPGTNFVYAQFPDGLIGLAVPLTSVDGAR--TAMQMVQEG 192

Qy 223 NLPN-VFSMQMCGALPVAAGSGLVIGIEPSLYKDDIWTPIKEMYYOIEILKLE 281
Db 193 ALTSPISFVSYSIDQ-----QSSSGGAVVFGGVDSLSLTGQIYMAVQVLELYWQIGIEEF 246

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QY 282 EIGGSLNDGRENADKAIVDSGTTLLRLPKQVFDVAVEAVARASLIPEFSDGFWTGSQ 341
 DB 247 IIGGQASGM-CSE-GCQAIIVDTGSLTLVPOQYMSALLQA-----TGAQ 288
 QY 342 LACWTNSETPMGVF-----PKISITLSDENSRRFTILPOLYIOPMAGANLY 391
 DB 289 -----EDEYQFLVNCNSIONLPTLITII-----NGVEFPLPSSSTI-----LNN 328
 QY 392 ECV-REFISP-----STNALIVGATWMEGFYIFEDRAQKRVGFAAS 431
 DB 329 NGYCTGVVEPFTYLSAQNOSQPLWILGDVFLRSYYSYDLNNNRVGFATA 376

RESULT 4

A39314
 gastricsin (EC 3.4.23.3) precursor - bullfrog
 C/Species: Rana catesbeiana (bullfrog)
 C/Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 22-Jun-1999
 C/Accession: A39314
 R/Yakabe, E.; Tanji, M.; Ichinose, M.; Goto, S.; Miki, K.; Kurokawa, K.; Ito, H.; Kageya
 J. Biol. Chem. 266, 22436-22443, 1991
 A/Title: Purification, characterization, and amino acid sequences of pepsinogens and pep
 A/Reference number: A39314; MUID:92042186; PMID:1939266
 A/Accession: A39314
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-384 <YAK>
 A/Cross-references: GB:M73750; NID:G213687; PIDN:AAA9530.1; PID:G213688
 C/Superfamily: pepsin
 C/Keywords: aspartic proteinase; hydrolase; protein digestion

Query Match 13.2%; Score 355.5; DB 2; Length 384;
 Best Local Similarity 26.5%; Pred. No. 6.8e-19;
 Matches 120; Conservative 73; Mismatches 136; Indels 123; Gaps 21;

QY 23 ELARPFTLPLRVAAATRV-----APTPGCTPARHADGLALPEPALASAGAN 76
 DB 12 QLSGGITIVPLKFKSKMEVMDHGIKAPVDPAT--KYNNFTAFEP-----LAN 61
 QY 77 FLAWVDNLQDSDGRGYLEMLIGTPPOKLIQIVDTGSSNFAVAGPHSYIDT-----Y 129
 DB 62 YMDM-----SYGEISIGTPQNFVLVFDGSSNLWV--PSTYCSQAQTNHPQ 108
 QY 130 FDTERRSSTYRSKGFDTVTKYQGSWTFVGBDLVTIPKGFNTSFLVNIATIFESNFPL- 188
 DB 109 FNPSSSSSYSSNQOFSLOYGTSLTGILGYDTVQIQ-----NIA--ISQDEFGLS 157
 QY 189 ---PG-----IKMNGIILGLAATLAKPSSSLETFPDSLVTQANIPN--VFSMQMGAGLP 238
 DB 158 VTEPFTNFVAQFDGIIGLAYPSIAEGAT--TWQGM1-QQNLINQPLFAFYLSG---- 210
 QY 239 VAGSGTNGSLVLGIEPSLYKGDWYTPPIKEWYQIETLKEIGGSLNDGRENAD 298
 DB 211 -QONSQNGEAFAGVDQNYISGQYIWPVSEIYMQIGICGSVNGATGM-CSQ--GC 266
 QY 299 KAIVDSGTTLLRLPKQVFDVAVEAVARASLIPEFSDGFWTGSQ-----LACWTNSET 350
 DB 267 QGIYDTGSLTLTAPQSVSSLMQSI-----GAQDQNGQVAVSCNIOSL 311
 QY 351 PWSYFP-----KISITLSDENS--SRSPRITILPOLYIOPMAGANLYEYCFGIS 399
 DB 312 PTISFTISGVFPLPSPSYVYIQAQNSGYCTIGIMPTPLSPONGOPLM----- 357
 QY 400 PSTNALVIGATWMEGFYIFEDRAQKRVGFAAS 431
 DB 358 -----ILGDVFLRQYVSVYDLGNNOVGFATA 383

RESULT 5
 JE0371
 pepsin C (EC 3.4.23.-) precursor - chicken
 N/Alternate names: pepsinogen C
 C/Species: Gallus gallus (chicken)

C/Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000
 C/Accession: JE0371
 R/Sakamoto, N.; Saiga, H.; Yasugi, S.
 Biochem. Biophys. Res. Commun. 250, 420-424, 1998
 A/Title: Analysis of temporal expression pattern and cis-regulatory sequences of chicken
 A/Reference number: JE0370; MUID:98440813; PMID:9753645
 A/Accession: JE0371
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-389 <SAK>
 C/Superfamily: pepsin
 C/Keywords: aspartic proteinase; hydrolase

Query Match 13.2%; Score 355; DB 2; Length 389;
 Best Local Similarity 28.7%; Pred. No. 7.6e-19;
 Matches 114; Conservative 58; Mismatches 121; Indels 104; Gaps 16;

QY 75 ANFLAMDNLQDSDGRGYLEMLIGTPPOKLIQIVDTGSSNFAVAGT-----PHSYI 126
 DB 56 SNFATVAEPLANNMDMSYGEISIGTPQNFVLVFDGSSNLWVPSLTCOSQACANHN-- 113
 QY 127 DTVFDTERRSSTYRSKGFDTVTKYQGSWTFVGBDLVTIPKGFN-----TS 172
 DB 114 --EFDPNESSTFTQDEPFSLQSGSLTGIFGDTVTL-QGISITNOEFGLETPEGTS 170
 QY 173 FLVNIATIFESNFPLPGIKMNGIILGLAATLAKPSSSLETFPDSLVTQANIPN--VFSM 230
 DB 171 FLYS-----PDDGILGLAFPSI--SAGCATTVNQKMLQENLDFPVSF 212
 QY 231 QMCAGLPEVAGSGTNGSLVLGIEPSLYKGDWYTPPIKEWYQIETLKEIGGSLNL 290
 DB 213 YLSQ-----EGQGGELVFGVDVPMVLTQIWTPTVQTQYQIGIEDFAVAGQSGSW 266
 QY 291 DCREYNADKAIVDSGTTLLRLPKQVFDVAVEAVARASLIPEFSDGFWTGSQIACWTNSET 350
 DB 267 -CSQ--GCQGIYDTGSLTLVNPQVFTLMQYIG--AQADD--SGQYVASCNIE- 314
 QY 351 PWSYFPKI-----SITLSDENS--SRSPRITILPOLYIOPMAGANLYECY 394
 DB 315 ---YMFITTFVISTGSPPLPSPAYMLQNSNDYCVGIESIYLPSPQTQPLM----- 362
 QY 395 RFGISPESTNALVIGATWMEGFYIFEDRAQKRVGFAAS 431
 DB 363 -----ILGDVFLRVYYSIYDMNNOVGFATA 388

RESULT 6

A29937
 gastricsin (EC 3.4.23.3) precursor - human
 N/Alternate names: pepsin C; pepsinogen C
 C/Species: Homo sapiens (man)
 C/Date: 17-Oct-1988 #sequence_revision 17-Oct-1988 #text_change 31-Mar-2000
 C/Accession: A29937; A31811; PX0028; I54213; A31155; A23458
 R/Hayano, T.; Sogawa, K.; Ichihara, Y.; Fujii, Kuriyama, Y.; Takahashi, K.
 J. Biol. Chem. 263, 1382-1385, 1988
 A/Title: Primary structure of human pepsinogen C gene.
 A/Reference number: A29937; MUID:88087276; PMID:3335549

A/Accession: A29937
 A/Molecule type: DNA
 A/Residues: 1-388 <HAY>
 R/Taggart, R.T.; Caes, L.G.; Mohandas, T.K.; Derby, P.; Barr, P.J.; Pals, G.; Bell, G.I
 J. Biol. Chem. 264, 375-379, 1989
 A/Title: Human pepsinogen C (progastricsin). Isolation of cDNA clones, localization to
 A/Reference number: A31811; MUID:89079679; PMID:2809526
 A/Accession: A31811
 A/Molecule type: mRNA
 A/Residues: 1-388 <TAG>
 A/Cross-references: GB:J04443; NID:G551175; PIDN:AAA60074.1; PID:G551176
 R/Atchanda, S.B.P.; Tanji, M.; Kageyama, T.; Takahashi, K.
 J. Biochem. 106, 920-927, 1989
 A/Title: A comparative study on the NH2-terminal amino acid sequences and some other pr
 A/Reference number: PX0023; MUID:90130402; PMID:2515193
 A/Accession: PX0028

A:Molecule type: protein
A:Residues: 17-101 <ATH>
R:PaIs, G.; Azuma, T.; Mohandas, T.K.; Bell, G.I.; Bacon, J.; Samloff, I.M.; Walz, D.A.;
Genomics 4, 137-148, 1989
A:Title: Human pepsinogen C (progastricsin) polymorphism: evidence for a single locus
A:Reference number: 154213; PMID:89290840; PMID:2567697
A:Accession: 154213
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-388 <RES>
A:Cross-references: GB:M23077; NID:g189830; PID:AAA60063.1; PID:g387015; GB:J03063
A:Note: parts of this sequence, including the amino end and carboxyl ends of the mature
R:Foltmann, B.; Jensen, A.L.
Eur. J. Biochem. 128, 63-70, 1982
A:Title: Human progastricsin. Analysis of intermediates during activation into gastricsin
A:Reference number: A81125; MUID:83079318; PMID:6816595
A:Accession: A91125
A:Molecule type: protein
A:Residues: 17-39, 'ED', 42-51, 'S', 53-64 <FOL>
A:Note: pro-form: 29-Leu was also found
A:Note: activation at pH 2 is proposed to involve conformation change, cleavage after Pro
C:Genetics:
A:Gene: GDB:PGC
A:Cross-references: GDB:119485; OMTM:169740
A:Map position: 6p21.3-6p21.1
A:Introns: 20/2; 70/3; 110/1; 149/3; 216/2; 256/2; 305/3; 338/3
C:Superfamily: pepsin
C:Keywords: aspartic proteinase; hydrolase; protein digestion; stomach; zymogen
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-59/Domain: propeptide #status experimental <PRO>
F:60-388/Product: gastricsin #status experimental <NAT>

Query Match	13.1%	Score 353;	DB 2;	Length 388;
Best Local Similarity	29.1%;	Pred.No. 1.1e-18;		
Matches 120; Conservative	65;	Mismatches 120;	Indels 108;	Gaps 21;

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Oy 52 PAERHAGC-LALALEPALASAGAAFLAMVDNIQGSBGRGYIEMIGRPPQKQIYD 110
Db 50 PAMKRFEDLSVYER-----NAYD-----AAVFEISIGTPNQFLVLP 91
Oy 111 TGSSNFAV-----AGTPHSYIDTYEDTERSSSTYRSKGFVDVVKTKQGSMTGFVGEDL 162
Db 92 TOSSLUWMPYSVYCQSQACTSHS-----RNPBSSESTGTNGOTFSLQJGSSLSLGFQYD 147
Oy 163 VTIPIKGFNTSFLVNIATIFESENFPLPG-----IKMNGIIGLAYATILAKPSSSLETFPDS 217
Db 148 LTV-----QSIQVPQOEFGLSEN-EPGTNFVYAQFOGIMGLAPALSVBEAT--TAMQ 198
Oy 218 IYVTOANIR-VPSSMCMCAGLPVAGSGTNNGSLVIGIBSLYCGDIWYPIKEEMWYOI 276
Db 199 MWQEAULTSPVHSVYLSNQ-----QSSGGAVVGVGDSLSLYGQIYMPVQOELWQI 252
Oy 277 EILKLEIGOSLINDCREYNADKAIVDSGTTLLRLPKQVPFAVVEAVARASLIPFEDGF 336
Db 253 GIEEFLIGQAGM-CSE-GCQALVDYGTSLILVYPOQYMALQA-----235
Oy 337 WTGSQLACWTSSETPWSYF-----PKISILYRDENSSRSFRITILPOLYIOPMG 386
Db 296 -TGAQ-----EDEYQFLVNCNSIQMLPSITFI-----NGVEPPLPSSYI-----336
Oy 387 AALANECY-RGELSP-----STNA--LVIGATWEGFVIFDRAQKGVFAAS 431
Db 337 -LSNNGCTVGEVEPTLYSSQNGQPLWILGVFLRSYSYVADLNNNRYGATA 387

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RESULT 7
JC7246
pepsinogen C - common marmoset
C:Species: Callithrix jacchus (common marmoset)
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #next_change 21-Jul-2000
C:Accession: JC7246
R:Kageyama, T.
J. Biochem. 127, 761-770, 2000

```

A:Title: New world monkey pepsinogens A and C, and prochymosins. Purification, characterisation and properties of the enzymes.
A:Reference number: JC7245
A:Accession: UC7246
A:Molecule type: mRNA
A:Residues: 1-388 <KAG>
A:Cross-references: DDBJ:AB038385
A:Experimental source: strain NW791
C:Comment: This protein, a zymogen of pepsins, is the major proteolytic enzyme in vertebrate evolution of mammalian orders and families.
C:Superfamily: pepsin
C:Keywords: gastric juice; zymogen

Query Match	13.1%	Score 351.5;	DB 2;	Length 388;
Best Local Similarity	30.1%	Pred. No. 1.4e-18;		
Matches 112; Conservative	56;	Mismatches 115;	Indels 89;	Gaps 17;

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QY 92 YVEKMLITPQKQIILVDDGSSNFAY-----ACTPHSYLDYFEDTSSRSTYSKGF 143
Db 73 YPELSISTPQNPVLVFDJGSSMLWAPSYCOQACTSHS---RNPBSASTTYSNGO 128
QY 144 DVVAVYATGQSWTGFVEGDVLTVPKGFNTSPFLVNATIFESSENFLLP-----IKMGILG 198
Db 129 TFSIQYSGGSLTGFPGYDLTLV-----QSIQVNPQERFGJSEN--EPQTNVVAQPGQIMG 181
QY 199 LAYATLAKPSSSLETFPDSLVTQANTIN--VFSMOMCGAGLPVAGSGTNGSLVLGGIEBS 257
Db 182 LAYPALSMGCGAT--TAMQGMJQEGALTSPVFSEFLSNQ-----QGSOGGAVLFGGDSS 213
QY 258 LYKGBIWTLPKEBMYOYIELKLKIEGGSJLNDCREYNADKAIYBSGTLTLPLPOKVPD 317
Db 234 LYTGGIYVAPTOELIYMWIGIEBFLIGQASGM--CSF--CGQAIWDTGISLVLVPOQYMS 250
QY 318 AVEAVARASLIPERSDGFMTGSLACWNTSETPWSYF-----PKISITYLDENS 367
Db 291 AFLER-----TGAQ-----EDEYGFVNCDSIQMLPLTLFII----- 323
QY 368 SRSPFITLLPOLYIQPMMGAGLNECY-RGISP-----STNALYIGATWEGFVIYF 419
Db 324 -NGVEFPLPSPSYI-----LSNNGCTGVGBETTYLSONSQPLMIGVFLRSYSVF 375
QY 420 DRAOKRVGFAAS 431
Db 376 DLGNRRVGFAPA 387

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RESULT 8
B43356
gastricsin (EC 3.4.23.3) precursor - guinea pig

N.Alternate names: pepsin C
C.Species: Cavia porcellus (guinea pig)
C.Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 22-Jun-1999
C.Accession: B43356
R.Kagayama, T.; Ichinose, M.; Tsukada, S.; Miki, K.; Kurokawa, K.; Koizai, O.; Tanji, M
J. Biol. Chem. 267, 16450-16459, 1992
A.Title: Gastric procathepsin E and progastricsin from guinea pig. Purification, molecu
A.Reference number: A43356; MUID:92355614; PMID:1644829
A.Accession: B43356
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-394 <KAG>
A.Cross-references: GB:M88652; NID:G191296; PIDN:AAA37053.1; PID:G191297
A.Note: sequence extracted from NCBI backbone (NCBIN:110805, NCBIF:110806)
C.Keywords: aspartic proteinase, gastric juice, hydrolase, protein digestion, stomach
C:Superfamily: pepsin

Query Match	12.1%	Score 324.5	DB 2	Length 394
Best Local Similarity	29.0%	Pred. No. 1.5e-16		
Matches 107; Conservative	63;	Mismatches 116;	Indels 83;	Gaps 18;

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Qy 92 YLEMLIGTPQKQLQILVDTGSSNF-----AVAGTHPSYIDTFFDTERSSSTYRSKGF 143
      |:::|||||:::|||||:::|||||:::|||||:::
Db 79 YFGQISLGTIPQSQFQVLPDFTGSSNLWPPSVYCSSLACTTH---TRFNPRDSSSTYVATDQ 134

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OY 144 DVTAKYQSGMTGFVGEDVLT-----BK-GFNTSFLVNIAITFSENFPLG-----IK 192
DB 135 SFSLEGTGSLGVFGYDWTMTQIDVPPQEFGLS-----ETB-----EGSPFVVAE 181
OY 193 NNGIIGLAVALTAKPSSSLETFFDSLVTOANI--PNVFSQMCGAGLPVAGS--GTNGGSL 249
DB 182 FPGIIGLGPGLSEGAT--TAMQGLRREGALSQSLFSVYL-----GSGQGSSEGOL 231
OY 250 VLGIEPLSYKDDIWTYPIKEEMYYQIEILKLEIGQGSINLDCREYNADKAIVDSGTTLL 309
DB 232 ILGVDSESLYTGDYWTPTQELYNQIGLEGFLIDGSAGWCSR---GGQGLVDSTSL 268
OY 310 RLPQKVFDAVAVAVASASIPFESDGFMTGSQLACTWNTSETWSTFPKISTYLRDENSSR 369
DB 289 TVPSDYLSTLVQAIQABE--NEYGEYF-----VSCSSIDPLPLTFVLSGV----- 332
OY 370 SFRITILPOLYIQP-----MAGALNYECYRFGISPSTN--ALVIGATYMEGFYVFDRA 422
DB 333 --EFLSPBAYILSGENYCMVLESTY-----VDFGGEFVWITLGDVFLRSTYSVYDLA 384
OY 423 OKRVGFPAAS 431
DB 385 NNRVGFAPA 393

RESULT 9
UC7575
pepsinogen A - bullfrog
C.Species: Rana catesbeiana (bullfrog)
C.Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 03-Aug-2001
C.Accession: UC7575
R.Kuzawa, M.; Inokuchi, T.; Kobayashi, K.; Yasumasu, S.
J. Biochem. 129, 147-153, 2001
A.Title: Amphibian pepsinogens: Purification and characterization of Xenopus pepsinogens
A.Reference number: UC7573; MUID:21064922; PMID:11134969
A.Contents: Stomach
A.Accession: UC7575
A.Molecule type: mRNA
A.Residues: 1-385 <IKU>
A.Cross-references: DDBJ:AB045376
C.Comment: This protein is a zymogen for gastric aspartic proteinase, with pepsin-like
C.Genetics:
A.Gene: P9A
C.Superfamily: pepsin
C.Keywords: stomach; zymogen

Query Match 11.9%; Score 320; DB 2; Length 385;
Best Local Similarity 27.8%; Pred. No.3.1e-16;
Matches 111; Conservative 67; Mismatches 147; Indels 74; Gaps 15;

OY 50 GTPAERHADGLALALEPALASPAGANFLAMVDNLCQDSGRGYLEMLIGTPPKLQILV 109
DB 39 GDYLKHHYPRATKYFPLAQASG-----EPLQNTMDIEYFGTISIGTPPGSFYIIF 90
OY 110 DTGSSNFAVAGTPHSHYIDT-----YDTERSSYRSKGFVDYTVKYTGSGMTGFVGEDL 162
DB 91 DTGSSNMLNV---PSVYCCSPACTNHHMFNPQOSTFOANTPVSIOYGGWSGFLGDT 147
OY 163 VTIPKGFMTPLVNIAITFESE--NFFLPQIKMNGILGLAYATLAPSSSLETFPISLVQ 221
DB 148 VQVG---NIQTNTQIFGSSQSPGSLYSPDGILGLAFLPA--SSQATPVPFNNMNQ 202
OY 222 ANIP--NVFSQMCGAGLPVAGSGTNGGSLVLGIEPLSYKGIWVTPPIKEEMYYQIEILK 280
DB 203 GLIPDDLVSYL-----SSQGSQGSFVLPFGVDVTSYTGMLNVPLAETFWYQITVDS 255
OY 281 LEIGQGSINLDCREYNADKAIVDSGTTLLRLPQKVFDAVAVAVASASIPFESDGFMTGS 340
DB 256 ISIGQVIAACS---GSCSAIVDTGTSIAGSPPI--ANIQYIYIGAN---QDSNGQYV-- 305
OY 341 QLACTNSETPWSYFP-----KISTYLRDENSS--RSFRITILPOLYIQPMGAGLN 390
DB 306 -INCNNISNMPVFTVINGVQYLPASAYVRQSGQSGTSGFOAMNLP----- 351

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OY 391 YECYRFGISPSTNALVIGATYMEGFYVFDRAQKRVGA 429
DB 352 -----TSSGDLWILGDVFLREYVYVFDRAANNVAMA 382

RESULT 10
REMSK
renin (EC 3.4.23.15) precursor, renal - mouse
N.Alternate names: angiotensin-forming enzyme; angiotensinogenase; renin 1
C.Species: Mus musculus (house mouse)
C.Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 18-Jun-1999
C.Accession: A00989; S07636; A22058; 157576; A05137; JH0083
R.Holm, I.; Ollio, R.; Panthier, J.J.; Rougeon, F.
EMBO J. 3, 557-562, 1984
A.Title: Evolution of aspartyl proteases by gene duplication: the mouse renin gene is o
A.Reference number: A00989; MUID:84182525; PMID:6370666
A.Accession: A00989
A.Molecule type: DNA
A.Residues: 1-402 <HOL>
R.Kim, W.S.; Murakami, K.; Nakayama, K.
Nucleic Acids Res. 17, 9480, 1989
A.Title: Nucleotide sequence of a cDNA coding for mouse Ren1 preprorenin.
A.Reference number: S07636; MUID:90067953; PMID:2685761
A.Accession: S07636
A.Molecule type: mRNA
A.Residues: 1-402 <KIM>
A.Cross-references: EMBL:X16642; NID:953930; PIDN:CAA4636.1; PID:953931
R.Mullins, J.J.; Burt, D.W.; Windass, J.D.; McTurk, P.; George, H.; Brammar, W.J.
EMBO J. 1, 1461-1466, 1982
A.Title: Molecular cloning of two distinct renin genes from the DBA/2 mouse.
A.Reference number: A90968; MUID:84207899; PMID:6327270
A.Accession: A22766
A.Molecule type: mRNA
A.Residues: 269-314, D', 316 <MUL>
R.Panthier, J.J.; Dreyfus, M.; Roux, D.T.L.; Rougeon, F.
Proc. Natl. Acad. Sci. U.S.A. 81, 5489-5493, 1984
A.Title: Mouse kidney and submaxillary gland renin genes differ in their 5' putative re
A.Reference number: A22058; MUID:84298161; PMID:6089205
A.Accession: A22058
A.Molecule type: DNA
A.Residues: 1-30 <PAN>
R.Field, L.J.; Philbrick, W.M.; Howles, P.N.; Dickinson, D.P.; McGowan, R.A.; Gross, K.
Mol. Cell. Biol. 4, 2321-2331, 1984
A.Title: Expression of tissue-specific Ren-1 and Ren-2 genes of mice: Comparative analy
A.Reference number: 157576; MUID:85085936; PMID:6392850
A.Accession: 157576
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Residues: 1-31 <RES>
A.Cross-references: GB:K02800; NID:g200689; PIN:AAA4004.1; PID:g200690
C.Comment: The only known function of renal renin is to release angiotensin I from ang
C.Keyword: Renal renin is synthesized by the juxtaglomerular cells of the kidney in res
C.Genetics:
A.Gene: Ren-1
A.Introns: 31/2; 81/3; 123/1; 162/3; 228/2; 268/2; 316/3; 349/3
C.Superfamily: pepsin
C.Keywords: aspartic proteinase; blood pressure control; glycoprotein; hydrolase; kidne
F.1.1/Domain: signal sequence #status predicted <SIG>
F.12-64/Domain: propeptide #status predicted <PRO>
F.65-402/Product: renin #status predicted <WAT>
F.69-139/Binding site: carboxydrate (Asn) (covalent) #status predicted
F.102,287/Active site: Asp #status predicted

Query Match 11.9%; Score 320; DB 1; Length 402;
Best Local Similarity 28.6%; Pred. No.3.3e-16;
Matches 126; Conservative 66; Mismatches 181; Indels 68; Gaps 21;

OY 10 LPLAQLRAAPLAPPTLPKVAATNRVAVAPPG--PGTPAERHADGLALALE--- 65
DB 6 MPLWALLL-----WSPECTSLPRTATPERIPLKKPVSREILDERGVDMTRLSAEMGV 60

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Oy 66 -----PASPAGANFLAMVDNLQSGDSRGYILEMIGTPPOKLIQVDTGSSNFAV 118
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 FTKRSLNLTNSPVLTIVL-----NTQ-----YYGEIGIGTPPOKFKVIFPTGSANLW 110
Oy 119 AGPHSY-----IDYEDTERSSYRSKGFVTVKYGWTFGVGEDLVTPIGFNTS 172
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 111 PSTKCSRLYLACGHSLSYSSSSSSSSSSSSSSDFTIHYGSGRVKGLSODSVTV--GGIVT 169
Oy 173 FLVNATIFESNFPGLPKMGIIGLAVALTAKPSSLETFPDSLVTQANI--PVFMSQ 231
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 170 QTFGEVTEPLPIPEML--AKFDGVLGMFP--AQAVGVTPEVDHLSGVLEKEEVSFY 225
Oy 232 MCGAGLPVAGSGTNGSLVLCGIEPSLYKGDIMYPIKEWYQIETLLEIGOSLND 291
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 226 Y-----NRGSHLLGGEVVLGGSDPOHOGNFHYVSIKTDMSQITMKVSVG--SSTLL 277
Oy 292 CREYNADKAIIVDSGTTLLRLPKRVDAVEAV--APASLPEFSDFGWSQLACTNSET 350
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 278 CEEGCA--VVVDGSSPISAPTSKLIMQALGAKEREY-----VVC--SQV 324
Oy 351 PMSYPKISIVARDENSSSRFTITLLPOLYIQPMGAGL--NECYRFGISPTNAL--VIG 408
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 325 P--TLPDISFDL---GGAAVTLSTDVVLQYPNRRDKLCTIALHAMDIPPTGPVWVG 378
Oy 409 ATWEGFYVIFDPAQKRVGA 429
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 379 ATFIRKFTYEFRRHNRIGFA 399

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RESULT 11

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56516
oryzasin (EC 3.4.23.-) precursor - rice
N:Alternate names: aspartic proteinase 1
C:Species: Oryza sativa (rice)
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C/Accession: S66516; S66517
R:Asakura, T.; Matanabe, H.; Abe, K.; Arai, S.
Eur. J. Biochem. 232, 77-83, 1995
A:Title: Rice aspartic proteinase, oryzasin, expressed during seed ripening and germinat
A:Reference number: S66516; MUID:96048031; PMID:7556174
A:Accession: S66516
A:Molecule type: DNA
A:Residues: 1-509 <ASA>
A:Cross-references: EMBL:D32165; NID:g511665; PIDN:BAA06876.1; PID:g1030715
A:Accession: S66517
A:Molecule type: mRNA
A:Residues: 1-509 <ASZ>
A:Cross-references: EMBL:D32144; NID:g1255684; PIDN:BAA06875.1; PID:g1711289
C:Comment: The pair of saposin repeat homology domains tagged SAP1 and SAP2 represent a
C:Genetics:
A:Introns: 119/3; 140/1; 171/3; 209/2; 265/3; 279/1; 300/3; 338/3; 360/2; 412/3; 452/3;
C:Superfamily: oryzasin, saposin repeat homology
C:Keywords: aspartic proteinase, hydrolase
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-68/Domain: propeptide #status predicted <PRO>
F:68-509/Product: aspartic proteinase 1 #status predicted <MAT>
F:316-361/Domain: saposin repeat homology #status atypical <SAP1>
F:370-420/Domain: saposin repeat homology #status atypical <SAP2>
F:103,290/Active site: Asp #status predicted

```

Query Match 11.7%; Score 313.5; DB 2; Length 509;

Best Local Similarity 23.0%; Prec. No. 1,4e-15;

Matches 127; Conservative 75; Mismatches 179; Indels 171; Gaps 19;

```

Oy 3 ALARALLPLLAQWLRAAPELAPADFTLLPLRVAAATNRVAPTPGPGPAERHADGAL 62
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 5 SVALLVLAVALLQALLPASAEGLVRIALKRPIDENSRAALSG-----ERGARLGI 59
Oy 63 ALFPALASAGANFLAMVDNLQSGDSRGYILEMIGTPPOKLIQVDTGSSN----- 115
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 RGANSISGGGGGSDIVALKNYMAQ-----YFGSIGVGTPEPKQKTVIFDGSSNLWVPSAK 115

```

```

Oy 116 --FAVAGTPHSYIDYEDTERSSYRSKGFVTVKYGWTFGVGEDLVTPIGFNTS 173
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 116 CYFSIACFFHS-----RYKSGGSSTYQKXGKPAIOYGGSJAGFSSDSSTVGD----- 165
Oy 174 LVNATIFESNFP-----LPGI-----KMNGIIGLAVALTAKPSSLETFPDSLVTQANI 224
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 166 -----LVKODEFEIATKEPEGLTQVMAKFDGILGLGFOELISVGA-----V 206
Oy 225 PNVSQMCG-AGLPVAGSGTN-----GGSLVLCGIEPSLYKGDIMYPIKEWYQI 276
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 207 PWTXKMQGLVSEFPVPSFWMRNRHSDGEGEIVFGGMDPSHYGNHTYVVSQKQWQF 266
Oy 277 ELKLEIGOSLNDCEYNADKAIIVDSGTTLLRLPKRVDAVEAVARASLPE----- 331
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 267 EMGVLIGKTTGF--CA--SGCSAIDSGTSLAGPTAIIIEINEKIGATGVOECKTV 323
Oy 332 -----FSDGF----- 336
Db 324 VSQGGQILDLLLAETPDSKICSOVGLCTPDKKHGVSAGIKSVYDDDEAGSNGLOSGPMC 383
Oy 337 -----WTGSQLAQWTNSETPMSY-----FPKISYLRD 364
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 384 NACENAVVMQNGLAQNKTQDILINQLCDKLPSWGESSTVDCGLASPEISFTIGA 443
Oy 365 ENSRSRFTITLLPOLYIQPMGAGLNEYCY---RFGISPTNAL--VIGATWEGFYVIF 419
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 444 K-----KFAKPEEYIL-KVGEGLAAQICSGFTAMDIPPRGLMLIGDVFMAGYHTVF 496
Oy 420 DRQKRVGFAS 431
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 497 DYKMRVGFAS 508

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RESULT 12

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A24608
gastlicsin (EC 3.4.23.3) precursor - rat
N:Alternate names: pepsinogen C
N:Contains: pepsin A (EC 3.4.23.1) precursor
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Jun-1998 #sequence_revision 05-Aug-1994 #text_change 18-Jun-1999
C/Accession: A33510; A24608; C22434; A05145; A61298
R:Ichihara, T.; Ichihara, Y.; Hayano, T.; Katsura, I.; Sogawa, K.; Fujii-Kuriyama, Y.;
J. Biol. Chem. 264, 10193-10199, 1989
A:Title: Primary structure and transcriptional regulation of rat pepsinogen C gene.
A:Reference number: A33510; MUID:89255508; PMID:2722863
A:Accession: A33510
A:Molecule type: DNA
A:Residues: 1-392 <IGH>
A:Cross-references: GB:M25985
R:Ichihara, Y.; Sogawa, K.; Morohashi, K.; Fujii-Kuriyama, Y.; Takahashi, K.
Eur. J. Biochem. 161, 7-12, 1986
A:Title: Nucleotide sequence of a nearly full-length cDNA coding for pepsinogen of rat
A:Reference number: A24608; MUID:87054020; PMID:3780741
A:Accession: A24608
A:Molecule type: mRNA
A:Residues: 1-392 <ICH>
A:Cross-references: GB:X04644; NID:g56880; PIDN:CAA28305.1; PID:g56881
R:Ichihara, Y.; Sogawa, K.; Takahashi, K.
J. Biochem. 98, 483-492, 1985
A:Title: Isolation of human, swine, and rat prepepsinogens and calf preprochymosin, and
A:Reference number: A22434; MUID:86059312; PMID:2415509
A:Accession: C22434
A:Molecule type: protein
A:Residues: 1-19, 'X', 21-23, 'X', 25-29 <IC2>
R:Arai, K.M.; Muto, N.; Tani, S.; Akahane, K.
Biochim. Biophys. Acta 788, 256-261, 1984
A:Title: The N-terminal sequence of rat pepsinogen.
A:Reference number: A05145; MUID:84257697; PMID:6743670
A:Accession: A05145
A:Molecule type: protein
A:Residues: 17-30, 'Q', 32-102, 'A', 104-108, 'L', 110-112 <ARA>
A:Experimental source: Wistar strain
R:Ichihara, Y.; Sogawa, K.; Takahashi, K.

```

J. Biochem. 92, 603-606, 1992
A:Title: Rat gastric pepsinogen: in vitro synthesis and partial amino-terminal signal
A:Reference number: A61298; MUID:83030750; PMID:6182139
A:Accession: A61298
A:Molecule type: protein
A:Residues: 1; 'X', '4-6', 'X', '8-9', 'X', '11', 'X', '13-14', 'XXX', '18-19', 'X', '21', 'X', '23', 'XX', '26', 'X', '27'
C:Comment: This enzyme has more restricted specificity than pepsin A. It is the major pepsin in rat stomach.
C:Genetics:
A:introns: 20/2; 73/3; 113/1; 152/3; 219/2; 259/2; 309/3; 342/3
A>Note: there are at least two very similar genes for gastric pepsin in rat stomach.
C:Superfamily: pepsin
C:Keywords: aspartic proteinase; gastric juice; hydrolase; protein digestion; stomach
F:1-16/Domain: signal sequence #status experimental <SIG>
F:17-392/Product: pepsinogen #status experimental <MAT>
F:17-62/Domain: activation peptide #status experimental <ACT>
F:94-280/Active site: Asp #status predicted
F:107-112,270-275,314-347/Disulfide bonds: #status predicted

Query Match 11.6%; Score 313; DB 1; Length 392;
Best Local Similarity 29.5%; Pred. No. 1.1e-15;
Matches 105; Conservative 56; Mismatches 139; Indels 56; Gaps 16;

Oy 92 YLEMLIGTPPOKQIIVDTGSSNFAV-----AGPHSYIDYFDRERSTRSKGF 143
Db 76 YFGEISIGTPPONFLVLPDTGSSNLWSSVYCQSEACTTHA---RFPSSKSTYTTBGO 131
Oy 144 DTVKXYTQSGWTFEGEDLVTPKGFNTSFLVNIATIFESSENFPLPG-----IKNNGILG 198
Db 132 TFSLOYGSGSLTGFPGYDITLV-----QSIQVFNQBFGLSEN--BPGTNFVVAQGDGIMG 184
Oy 199 LAYATLAKPSSSLETFPDSLVLTQANI PNVSQMOCAGIPVAGS--GTNGSLVLGIEP 256
Db 185 LAYPLLS--SGGATFALQCMIGE---GALSQPLFGVYL---GSGQGSNGQIVFGVDK 235
Oy 257 SLXKDDIYTPKKEWYQIETLKIEIGQSLNDCRENADKAIVDSSTILLRPOKVF 316
Db 236 NLXYGEITWVPQTELYIQITTDPLIGQASGW--CSGQCG--QGIYDVTGTSILVMPAOYL 293
Oy 317 DAVEAVARASLIPEFSQGFMTGSOLACTNSETPMSYPRKISIVLRDENSRSFRITLL 376
Db 294 SELDTIGAQE--GEYGEYF-----VSCDSVSS-----LPTLSFVL-----NGYQFPLS 335
Oy 377 POLYIQPMGAGLVNVECYRFGISSTNALVIGATMEGFYVIFDPAQRVGFAPS 431
Db 336 PSSYIIQDNFCVMGLIESISLTSSESGQPLMIGDVFILRSYVAIFPMGNKVGILATS 391

RESULT 13
A41443
pepsin (EC 3.4.23.-) precursor, embryonic - chicken
C:Species: Gallus gallus (chicken)
C:Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 21-Jul-2000
A:Accession: A41443
R:Hayashi, K.; Agata, K.; Mochii, M.; Yasugi, S.; Eguchi, G.; Minuno, T.
J. Biochem. 103, 290-296, 1988
A:Title: Molecular cloning and the nucleotide sequence of cDNA for embryonic chicken pepsinogen.
A:Reference number: A41443; MUID:88227903; PMID:3131317
A:Accession: A41443
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-383 <HAV>
A:Cross-references: GB:D00215; NID:G2760810; PIDN:BA00153.1; PID:G222853
C:Superfamily: pepsin
C:Keywords: aspartic proteinase; hydrolase; protein digestion

Query Match 11.5%; Score 310; DB 2; Length 383;
Best Local Similarity 26.8%; Pred. No. 1.7e-15;
Matches 106; Conservative 63; Mismatches 136; Indels 90; Gaps 15;
Oy 56 HA--DGLALALEPALAPAGANFLAMVNDLQDSDGSGVYLEMLIGTPPOKQIIVDTGS 113
Db 55 HAFPDVLTVTTEPL-----NTLDM-----EYGTISIGTPPODFTVVDGTS 97

Oy 114 SNFVAG---TPHSYIDTYDTERSSYTRKSGEDVYKTYQSGWTFEGEDLVTPKGF 169
Db 98 SNLWVPSVSCSPACQSHQWNPSSSTYKSTGQNLHYETGMGEVGGCDTVVASIM 157
Oy 170 NTSPLVNIATIFESSENFPLGIKNNGILGLAVATLAKSSSLETFPDSLVQANI--PVVF 228
Db 158 DTNQFPGST--SEPGQFV--YKFDGILGLYPSLA--ADGTFVFDWVDSLEQNL 213
Oy 229 SMQMGAGLPVAGSGTNGSLVLGGIEPSLYKGDVWYPIKEWYQIETLKIEIGQSL 288
Db 214 SVYLSREM-----GSMVTFGIDESTYTGSIWNVPSYQGWQMSMSIIVNKEI 265
Oy 289 NLDCREYADKAIYDSGTTLLRPOKFDVAEVARASLIPEPSDGFWSQLACWTNS 348
Db 266 ACS-----SGCALIDTGTSLVAGPASPINDIOSAVG-----ANQ 300
Oy 349 ETPWGFPIKISIVLRDENSRSFRITLLPOLYIQPMGAGLVN-----ECY 394
Db 301 NTYGEY-----SVNCSHILAMPDVVF--VIG-GIQVPVPALEYQNGQGTGM 345
Oy 395 RFGISPTNALVIGATMEGFYVIFDPAQRVGFPA 429
Db 346 SSFQNSADLWILGDVFRVRYYSIFDRANNRVGLA 380

RESULT 14
KHHUD
cathepsin D (EC 3.4.23.5) precursor [validated] - human
N:Alternate names: preprocathepsin D
C:Species: Homo sapiens (man)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 15-Sep-2000
A:Accession: A25771; S30749; PC2066; I59236; I57716
R:Faust, P.L.; Kornfeld, S.; Chirgwin, J.M.
Proc. Natl. Acad. Sci. U.S.A. 82, 4910-4914, 1985
A:Title: Cloning and sequence analysis of cDNA for human cathepsin D.
A:Reference number: A25771; MUID:85270436; PMID:3927232
A:Accession: A25771
A:Molecule type: mRNA
A:Residues: 1-412 <FAU>
A:Cross-references: EMBL:M11233; NID:G181179; PIDN:AAS95929.1; PID:G181180
R:Westley, B.R.; May, F.E.B. 3773-3786, 1987
Nucleic Acids Res. 15, 3773-3786, 1987
A:Title: Oestrogen regulates cathepsin D mRNA levels in oestrogen responsive human breast cells.
A:Reference number: S30749; MUID:87231068; PMID:3588310
A:Accession: S30749
A:Molecule type: mRNA
A:Residues: 1-412 <MES>
A:Cross-references: EMBL:X05344; NID:G29677; PIDN:CAA28955.1; PID:G29678
R:May, F.E.B.; Smith, D.J.; Westley, B.R.
Gene 134, 277-282, 1993
A:Title: The human cathepsin D-encoding gene is transcribed from an estrogen-regulated promoter.
A:Reference number: PC2066; MUID:94085791; PMID:8262386
A:Accession: PC2066
A:Molecule type: DNA
A:Residues: 1-23 <MA>
A:Cross-references: GB:I12980; NID:G291930; PIDN:AAA1314.1; PID:G455429
A:Experimental source: MCF-7 cell
R:Cavallies, V.; Augereau, P.; Rochefort, H.
Proc. Natl. Acad. Sci. U.S.A. 90, 203-207, 1993
A:Title: Cathepsin D gene is controlled by a mixed promoter, and estrogens stimulate on its expression.
A:Reference number: I59236; MUID:93126342; PMID:8419924
A:Accession: I59236
A:Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-22 <CAV1>
A:Cross-references: GB:552557; NID:G263124; PIDN:AA013868.1; PID:G4261568
R:Augereau, P.; Miralles, F.; Cavallies, V.; Gaudelet, C.; Parker, M.; Rochefort, H.
Mol. Endocrinol. 8, 693-703, 1994
A:Title: Characterization of the proximal estrogen-responsive element of human cathepsin D promoter.
A:Reference number: I57716; MUID:95021301; PMID:7935465
A:Accession: I57716
A:Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA

A;Residues: 1-22 <CAV2>
 A;Cross-references: GB:574689; NID:9786350; PIDN:AA01456.1; PID:94261856
 R;Baldwin, E.T.; Bhat, T.N.; Gulnik, S.; Erickson, J.W.
 submitted to the Brookhaven Protein Data Bank, April 1993
 A;Reference number: A51839; PDB:1LXA
 A;Contents: annotation; X-ray crystallography, 2.5 angstroms, residues 65-161,1170-241
 R;Baldwin, E.T.; Bhat, T.N.; Gulnik, S.; Erickson, J.W.
 submitted to the Brookhaven Protein Data Bank, April 1993
 A;Reference number: A51840; PDB:1LYB
 A;Contents: annotation; X-ray crystallography, 2.5 angstroms, with inhibitor residues 65
 R;Baldwin, E.T.; Bhat, T.N.; Gulnik, S.; Hosur, M.V.; Sowder II, R.C.; Cachau, R.E.; Col
 Proc. Natl. Acad. Sci. U.S.A. 90, 6796-6800, 1993
 A;Title: Crystal structures of native and inhibited forms of human cathepsin D: implicat
 A;Reference number: A48229; MUID:93342076; PMID:8393577
 A;Contents: annotation; X-ray crystallography, 2.5 angstroms
 C;Comment: Cathepsin D is a ubiquitous lysosomal proteinase.
 C;Comment: In addition to the propeptide, residues 163-168 and 411-412 are proteolytical
 C;Comment: The carbohydrate bound to 134-Asn contains a mannose-6-phosphate that is bou
 C;Genetics:
 A;Gene: GDB:CTS0
 A;Cross-references: GDB:120512; OMIM:116840
 A;Map position: 11p15.5-11p15.5
 C;Function:
 A;Description: limited specificity endopeptidase
 A;Pathway: intracellular protein degradation
 C;Superfamily: peptin
 C;Keywords: aspartic proteinase; glycoprotein; hydrolase; lysosome; protein degradation
 F;1-20/Domain: signal sequence #status predicted <SIG>
 F;21-64/Domain: propeptide #status predicted <PRO>
 F;65-166,169-410/Product: cathepsin D #status experimental <MAT>
 F;267,339-356/Region: phosphotransferase recognition
 F;91-160,110-117,286-290,329-366/Disulfide bonds: #status experimental
 F;97,295/Active site: Asp #status experimental
 F;134,263/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 11.5%; Score 308.5; DB 1; Length 412;
 Best Local Similarity 27.1%; Pred. No. 2.5e-15;
 Matches 121; Conservative 75; Mismatches 180; Indels 71; Gaps 22;

9 LLPLAQLWLRAPLAPFTLPRLVAAATRVVAPRPG-----PGPARRHADGAL 62
 Db LPLPL--CLLAP--ASLVRIPLHKFTSTRRTSEVSGSLEDLAKPVKYGQAVPA 61
 63 ALPLASPAAGANFLAWVNLQSDSGRGVLEMLIGTPPKQLIIVDTGSSNFAVAGTP 122
 Db VTEGPI--PEVLKNTM-----DAQYGEIGIGTPQCFVTFVDTGSSNLWVPSIH 109
 123 HSYIT-----YFPTERSSTYRSKGFVDVTVYTGQSWTGFVGEDLVTP--KGFNTSL 174
 110 CKLDIACWIIHKYNSDKSTYVKNGTSPDIHYGSGSLSGYLSODTVSVPCQASASASAL 169
 175 --VNIAITFESNFPLPGI-----KWNGLGLAVATLAKPSSLETFPSLVTQANI--PN 226
 Db GGVKVERQVFGATKQPGITFTIAKFDGLGMAIYRIS--VNNVLPVFNLMQQLVDON 227
 227 VFSMQCGAGLPVAGSGTNGSGSLVLOGIEPSLYKGDIVYTPIKEMWYQIILKLEIGSQ 286
 228 IFSFY-----LSRDPDAQCGEIMLGTDSTKYKSLSYLANTRKAYWVHLDQVEV--AS 281
 287 SLNLDREYNADKALVDSGTTLLRLPQKVFDAVVEVAASLIPESDGFMTGSQACMT 346
 Db GLTL--CKE--GCEAIVDTGTSIMVGP--VDEVRELQAKAIGAVPLIQGEY-----MIPC-- 329
 347 NSETPMSVYPKISYLRDENSRSRFRITILPOLYIOPMAGALNVCYRF--GISPSIN 403
 Db ---EKVSTLPALITLKI-----GKGKYLK--PEDYTLKVSQAGKTLCLSGFMGMDIPPSG 380
 404 AL-VIGATVMEGFYVIFDRQKRVGFA 429
 Db PLMILGDVPIGRYTVFDRDNRVGA 407

KHMSD
 cathepsin D (EC 3.4.23.5) precursor - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text_change 18-Jun-1999
 C;Accession: I48278; S14704; S12587
 R;Herman, M.; Persch, A.; Saffig, P.; Von Figura, K.; Peters, C.
 DNA Cell Biol. 13, 419-427, 1994
 A;Title: Mouse cathepsin D gene: molecular organization, characterization of the promot
 A;Reference number: I48278; MUID:94280622; PMID:8011168
 A;Accession: I48278
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-410 <RES>
 A;Cross-references: EMBL:X68378; NID:950302; PIDN:CAA48453.1; PID:9817945
 R;Diedrich, J.F.; Staskus, K.A.; Retzel, E.F.; Haase, A.T.
 Nucleic Acids Res. 18, 7184, 1990
 A;Title: Nucleotide sequence of a cDNA encoding mouse cathepsin D.
 A;Reference number: S14704; MUID:91088345; PMID:2263503
 A;Accession: S14704
 A;Molecule type: mRNA
 A;Residues: 1-410 <DIE>
 A;Cross-references: EMBL:X53337; NID:950300; PIDN:CAA37423.1; PID:950301
 R;Grusby, M.J.; Mitchell, S.C.; Glimcher, L.H.
 Nucleic Acids Res. 18, 4008, 1990
 A;Title: Molecular cloning of mouse cathepsin D.
 A;Reference number: S12587; MUID:90326544; PMID:2374732
 A;Accession: S12587
 A;Molecule type: mRNA
 A;Residues: 1-410 <GRU>
 A;Cross-references: EMBL:X52886; NID:950298; PIDN:CAA37067.1; PID:950299
 C;Genetics:
 A;Introns: 23/2; 76/3; 118/1; 157/3; 233/2; 274/2; 322/3; 355/3
 C;Function:
 A;Description: limited specificity endopeptidase
 A;Pathway: intracellular protein degradation
 C;Superfamily: peptin
 C;Keywords: aspartic proteinase; glycoprotein; hydrolase; lysosome; protein degradation
 F;1-20/Domain: signal sequence #status predicted <SIG>
 F;21-64/Domain: propeptide #status predicted <PRO>
 F;65-410/Product: cathepsin D, single-chain form #status predicted <MAT>
 F;91-160,110-117,284-288,327-364/Disulfide bonds: #status predicted
 F;97,293/Active site: Asp #status predicted
 F;134,261/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 11.4%; Score 306.5; DB 1; Length 410;
 Best Local Similarity 27.5%; Pred. No. 3.4e-15;
 Matches 103; Conservative 64; Mismatches 123; Indels 85; Gaps 15;

92 YLEMLITPPKQLIIVDTGSSNFAVAGTPHSYITD-----YFPTERSSTYRSKGFVD 145
 Db YGDIIGTTPQCFVTFVDTGSSNLWVPSIHCKLDIACWIIHKYNSDKSTYVKNGTSP 138
 146 TVKYQGSWTFVGEDLVTPIKGFNTSEFLVNIAI-----IFESSENFPLPGI-----KWNGL 197
 Db DIHYSGSLSGYLSODTVSVPCQDQSKARIGIYKQIF--GEATKQPIIVVAAKFDL 197
 198 GLAVATLAKPSSLETFPSLVTQANI--PNVFSMQMGAGLPVAGSGTNGSLVIGIEP 256
 Db GMGYPHIS--VNNVLPVFDNLMQQLVDKNIFSFY-----LNRDEGPGGELMLGTD 250
 257 SLKGDIVYTPIKEMWYQIILKLEIGSGSLNLDREYNADKALVDSGTTLLRLPQKVF 316
 Db KYHGEISYLNWTRKAYVQVHMDQLEVNE--LTL--CK--GCEAIVDTGTSILVGPVEV 306
 317 DAVVEAARASLIPESDGFMTGSQALCMTNSETPMSYFPKISYLRDENSRSRFRITIL 376
 Db KELQRAIGAVPI-----GGEYMLPCKVSVSL 333
 377 POLYIOPMAGALNVCYRF--GISPSIN-----PSNNAIVGATVMEG 414
 Db PIVYIK--IG--GKYNELHPDKYILKVSQGGKTKCLSGFMGMDIPPSGPLMILGDVFIGS 390
 415 FYVIFDRQKRVGFA 429

Db 391 YTVFDRDNNRVGFA 405

Search completed: April 1, 2003, 11:34:51
Job time : 24 secs

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 1, 2003, 11:22:48 ; Search time 14 Seconds
(without alignments)
1534.624 Million cell updates/sec

Title: US-09-668-314C-2
Sequence: 1 MGALRALPLPLAQMILRA.....RPDPPEVNDSESLVRRHWK 518

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	2687	100.0	518 1	BAE2_HUMAN
2	1187	44.2	501 1	BACE_RAT
3	1185	44.1	501 1	BACE_MOUSE
4	1178.5	43.9	501 1	BACE_HUMAN
5	363.5	13.5	377 1	PEPC_MACFU
6	353	13.1	388 1	PEPC_HUMAN
7	351.5	13.1	388 1	PEPC_CALJA
8	324.5	12.1	394 1	PEPC_CAVPO
9	320	11.9	402 1	RENI_MOUSE
10	313.5	11.7	509 1	APRI_ORYSA
11	313	11.6	392 1	PEPC_RAT
12	310	11.5	483 1	PEPC_CHICK
13	308.5	11.5	412 1	CATD_HUMAN
14	306.5	11.4	410 1	CATD_MOUSE
15	305.5	11.4	401 1	RENS_MOUSE
16	305	11.4	407 1	CATD_RAT
17	302	11.2	324 1	PEP1_GADMO
18	302	11.2	405 1	PEP1_YEAST
19	301.5	11.2	398 1	CATE_RAT
20	300.5	11.2	387 1	PEP2_RABIT
21	300.5	11.2	397 1	CATE_MOUSE
22	299	11.1	398 1	CATD_CHICK
23	298.5	11.1	387 1	PEP4_RABIT
24	298.5	11.1	400 1	RENI_SHEEP
25	297	11.1	388 1	PEP4_HUMAN
26	294.5	11.0	388 1	PEP2_MACFU
27	291	10.8	388 1	PEP4_MACFU
28	291	10.8	402 1	RENI_RAT
29	291	10.8	406 1	RENI_HUMAN
30	290.5	10.8	396 1	CATE_RABIT
31	289	10.8	387 1	PEP3_RABIT
32	289	10.8	388 1	PAG_HORSE
33	288.5	10.7	390 1	CATD_BOVIN

34	288	10.7	387 1	PEP1_RABIT	P28712 oryctolagus
35	288	10.7	388 1	PEP1_MACFU	P03954 macaca fusc
36	287	10.7	367 1	PEP4_CHICK	P00793 gallus gall
37	287	10.7	391 1	CATE_CAVPO	P25796 cavia porce
38	287	10.7	396 1	CATE_HUMAN	P14091 homo sapien
39	286	10.6	388 1	PEP4_MACMU	P11489 macaca mula
40	285.5	10.6	387 1	PEP4_CALJA	Q9n2d4 callithrix
41	285	10.6	396 1	CARP_NEUCR	Q01294 neospora
42	284.5	10.6	386 1	PEP4_PIG	P00791 sus scrofa
43	284.5	10.5	388 1	PEP4_RABIT	P27823 oryctolagus
44	282.5	10.5	381 1	CHYM_SHEEP	P18276 ovis aries
45	282	10.5	398 1	ASP3_CABEL	P55956 caenorhabdi

ALIGNMENTS

RESULT 1	BAE2_HUMAN	STANDARD;	PRT;	518 AA.
ID	BAE2_HUMAN	Q9Y520; Q9YUT6;		
AC	Q9Y520; Q9YUT6;	30-MAY-2000 (Ref. 39, Created)		
DT	30-MAY-2000 (Ref. 39, Last sequence update)			
DT	15-JUN-2002 (Ref. 41, Last annotation update)			
DE	Beta secretase 2 precursor (EC 3.4.23.-) (Beta-site APP-cleaving enzyme 2) (Aspartyl protease 1) (Asp 1) (ASPI) (Membrane-associated aspartic protease 1) (Memapsin-1).			
DE	BACE2 OR ASP21.			
GN	BACE2 OR ASP21.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxId=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20051710; PubMed=10591213;			
RA	Yan R., Bienkowski M.U., Shuck M.E., Miao H., Tory M.C., Pauley A.M.,			
RA	Brashler J.R., Stratman N.C., Mathews W.R., Buhl A.E., Carter D.B.,			
RA	Tomasselli A.G., Parodi L.A., Heinrichson R.L., Gurney M.E.;			
RT	"Membrane-anchored aspartyl protease with Alzheimer's disease beta-secretase activity."			
RT	Nature 402:533-537(1999).			
RL	(2)			
RN	SEQUENCE FROM N.A.			
RP	TISSUE=Bone marrow;			
RA	Xin H., Stephens J.C., Duan X., Harrowe G., Kim E., Grieshammer U.,			
RA	Giese K.;			
RT	"Identification of a novel aspartic-C-like protease differentially expressed in human breast cancer cell lines."			
RT	Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.			
RN	(3)			
RP	SEQUENCE FROM N.A.			
RA	Accarino M.P., Fumagalli P., Ottolenghi S., Taramelli R.;			
RA	"Cloning of a gene from chromosome 21 Down region encoding a potential transmembrane aspartyl protease."			
RT	Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.			
RL	[4]			
RP	SEQUENCE FROM N.A.			
RA	Solans A., Estivill X., de la Luna S.;			
RA	"Cloning of a novel mammalian aspartyl protease."			
RT	Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.			
RL	[5]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=20120043; PubMed=10656250;			
RA	Hussein I., Powell D.J., Howlett D.R., Tew D.G., Meek T.D.,			
RA	Chapman C., Gloger I.S., Murphy K.E., Soutthan C.D., Ryan D.M.,			
RA	Smith T.S., Simmons D.L., Walsh F.S., Dingwall C., Christie G.;			
RT	"Identification of a novel aspartic proteinase (Asp 2) as beta-secretase."			
RT	Mol. Cell. Neurosci. 14:419-427(1999).			
RL	[6]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=20144060; PubMed=10677483;			
RA	Lin X., Koelsch G., Wu S., Downs D., Dashti A., Tang J.;			

RT "Human aspartic protease memapsin 2 cleaves the beta-secretase site of beta-amyloid precursor protein."
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1456-1460 (2000).
 RP [7]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=20289799; PubMed=10830953;
 RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
 RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Soeda E.,
 RA Ohki M., Takagi T., Sasaki Y., Taudien S., Blechschmidt K., Polley A.,
 RA Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
 RA Reichwald K., Rump A., Schillhaber M., Schudy A., Zimmermann W.,
 RA Roenthal A., Kudoh J., Shibuya K., Kawasaki S., Asakawa S.,
 RA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
 RA Minoshima S., Shimizu N., Nordstiek G., Hornischer K., Brandt P.,
 RA Schaefer M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecher H.,
 RA Ranner J., Beck A., Klages S., Hennig S., Rieselmann L., Dagand E.,
 RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
 RA Leinrich H., Reinhardt R., Yaspo M.-L.,
 RT "The DNA sequence of human chromosome 21."
 RL Nature 405:311-319 (2000).
 RN [8]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RA Straube R.;
 CC Submitted (Sep-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF200342; AAF17078.1; -
 DR EMBL; AF117892; AAD45240.1; -
 DR EMBL; AF050171; AAD45963.1; -
 DR EMBL; AF178532; AAF29494.1; -
 DR EMBL; AF204944; AAF26366.1; -
 DR EMBL; AF200192; AAF13714.1; -
 DR EMBL; AL163284; CAB90458.1; -
 DR EMBL; AL163285; CAB90458.1; -
 DR EMBL; BC014453; AAH14453.1; -
 DR HSSP; P00797; 2REN.
 DR MEROPS; A01.041; -
 DR Genew; HGNC:934; BACE2.
 DR MIM; 605668; -
 DR InterPro; IPR001461; Aspprotease1.
 DR InterPro; IPR001969; Aspprotease_site.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; P000792; PEPsin
 DR PROSITE; PS00141; ASP_PROTEASE; 2.
 KM Hydrolyase; Aspartyl protease; Glycoprotein; Zymogen; Transmembrane;
 Signal.
 FT SIGNAL. 1 20
 FT PROPEP 21 ?
 FT CHAIN 21 518
 FT DOMAIN 21 473
 FT TRANSMEM 474 494
 FT DOMAIN 495 518
 FT ACT_SITE 110 110
 FT ACT_SITE 303 303
 FT CARBOHD 170 170
 FT CARBOHD 366 366
 FT CONFLICT 36
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 Query Match 100.0%; Score 2687; DB 1; Length 518;
 Best Local Similarity 100.0%; Pred. No. 2,9e-187;
 Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGALRALLLPQLQWILLRAAPLPAPEFTPLRVAAATNRVAVPTGPGTPAERHADGL 60
 Db 1 MGALRALLLPQLQWILLRAAPLPAPEFTPLRVAAATNRVAVPTGPGTPAERHADGL 60
 Qy 61 ALALEPALASPAGANFLAMVDNIQSGSGRGVYLEMLIGTPPOKQLIVDGGSSNFAAG 120
 Db 61 ALALEPALASPAGANFLAMVDNIQSGSGRGVYLEMLIGTPPOKQLIVDGGSSNFAAG 120
 Qy 121 TPHSYIDTPPTTSSSTRSGKPDVTYKVGWTFVGEVDLVIIPKGFNTSFLVINATI 180
 Db 121 TPHSYIDTPPTTSSSTRSGKPDVTYKVGWTFVGEVDLVIIPKGFNTSFLVINATI 180
 Qy 181 FESENFPLPGIKMNGIIGLAYATLAKBSSLETPPDSLVTOANIINWFSSMCGAGLPVA 240
 Db 181 FESENFPLPGIKMNGIIGLAYATLAKBSSLETPPDSLVTOANIINWFSSMCGAGLPVA 240
 Qy 241 GSGTNGSLVUGGIEPSTLYKGDWYTPIKEMWYQIEILKLEIGQSINLDCREYNADKA 300
 Db 241 GSGTNGSLVUGGIEPSTLYKGDWYTPIKEMWYQIEILKLEIGQSINLDCREYNADKA 300
 Qy 301 IVDSGTTLRLPQKVFDAVAVARASLIPEFSGDFWTSQACWTNSETPMYFPKISI 360
 Db 301 IVDSGTTLRLPQKVFDAVAVARASLIPEFSGDFWTSQACWTNSETPMYFPKISI 360
 Qy 361 YLDNENSRSRFTITLPQLYIQPMGAGLNEYCYRFGISPTNALVIGATVMEGFYIFD 420
 Db 361 YLDNENSRSRFTITLPQLYIQPMGAGLNEYCYRFGISPTNALVIGATVMEGFYIFD 420
 Qy 421 RAQKRVGNAAPPCAEINAAVSEISGPESTDVASCNCPAOSLEPILMIVSYALMSVCG 480
 Db 421 RAQKRVGNAAPPCAEINAAVSEISGPESTDVASCNCPAOSLEPILMIVSYALMSVCG 480
 Qy 481 AILVLVILLPLPRCQRRPRDPEVNDSSLVHRMK 518
 Db 481 AILVLVILLPLPRCQRRPRDPEVNDSSLVHRMK 518
 RESULT 2
 BACE RAT STANDARD; PRT; 501 AA.
 AC P56819;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Beta-secretase precursor (EC 3.4.23.-) (Beta-site APP cleaving enzyme)
 DE (Beta-site amyloid precursor protein cleaving enzyme) (Aspartyl
 DE protease 2) (Asp 2) (ASP2) (Membrane-associated aspartic protease 2)
 DE BACE.
 GN BACE.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20002972; PubMed=10531052;
 RA Vassar R., Bennett B.D., Babu-Khan S., Kahn S., Mendiaz E.A.,
 RA Denis P., Teplow D.B., Ross S., Amarante P., Loebloff R., Luo Y.,
 RA Fisher S., Fuller J., Edenson S., Lile J., Jarosinski M.A.,
 RA Biere A.L., Curran E., Burgess T., Louis J.-C., Collins F.,
 RA Treanor J., Rogers G., Citron M.;
 RT "Beta-secretase cleavage of Alzheimer's amyloid precursor protein by
 RT the transmembrane aspartic protease BACE";
 RL Science 286:735-741 (1999).
 CC -1- FUNCTION: RESPONSIBLE FOR THE PROTEOLYTIC PROCESSING OF THE
 CC AMYLOID PRECURSOR PROTEIN (APP). CLEAVES AT THE AMINO TERMINUS OF
 CC THE A-BETA PEPTIDE SEQUENCE, BETWEEN RESIDUES 671 AND 672 OF APP,
 CC LEADS TO THE GENERATION AND EXTRACELLULAR RELEASE OF BETA-CLEAVED
 CC SOLUBLE APP. AND A CORRESPONDING CELL-ASSOCIATED CARBOXY-TERMINAL
 CC FRAGMENT WHICH IS LATER RELEASED BY GAMMA-SECRETASE (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.

```

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CC -----
DR EMBL; AF190727; AAF04144.1; -
DR HSSP; P32329; 1YPS.
DR MEROPS; A01.004; -.
DR InterPro; IPR001461; AsproteaseA1.
DR InterPro; IPR001969; Asprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPSIN.
DR PROSITE; PS00141; ASP_PROTEASE; 1.
KW Hydrolase; Aspartyl protease; Glycoprotein; Zymogen; Transmembrane;
KW Signal.
FT SIGNAL. 1 21 POTENTIAL.
FT PROPEP 22 45 POTENTIAL.
FT CHAIN 46 501 BETA-SECRETASE.
FT DOMAIN 22 457 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 458 478 POTENTIAL.
FT DOMAIN 479 501 CYTOPLASMIC (POTENTIAL).
FT ACT SITE 93 93 BY SIMILARITY.
FT ACT SITE 289 289 BY SIMILARITY.
FT DISULFID 216 423 BY SIMILARITY.
FT DISULFID 278 443 BY SIMILARITY.
FT DISULFID 330 380 BY SIMILARITY.
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 501 AA; 55806 MW; 24B445BCB87DE3 CMC64;

Query Match 44.2%; Score 1187; DB 1; Length 501;
Best Local Similarity 46.4%; Pred. No. 1.3e-78;
Matches 240; Conservative 82; Mismatches 165; Indels 30; Gaps 9;

QY 9 LPLLAQMLLAAPFLAAPT-----LPIRYAATNRVVAFTPP--GTPAERLADGLA 61
DB 1 WAPFLRWLLWVGSMPLPAQGHILRIPLRSGLA-----GPPVGLRLPRTDE-- 49

QY 62 LALPEALASPAGANFLAVNDLQDSRGVYLEMLIGTPOKLOILDVDTGSSNFAVAGT 121
DB 50 ---EE--EPPRRGSGFVEMVNLKRSKGGYVENTVSGPPTLILVDTGSSNFAVGA 104

QY 122 PHSYIDYFDTERSSSTYRSKGFVTVTKYQGSWTGFVGEDLVTLIPKGFNTSFLVNIATIF 181
DB 105 PHPFLHRYQQLASTYDRLKRSVVPYTOGKMGELGDLVSIPIHGNVTVRANIAIT 164

QY 182 ESENFLEGIKMGNGILGLAATLAPSSLETFPISLVTQANIPVNSMOCGAGLPV-- 239
DB 165 ESDKFFNGSWMGILGLAATLAPSSLETFPISLVTQANIPVNSMOCGAGLPV-- 224

QY 240 -AGSGTNGSLVGLGIEPISLYKGIWYTPIKEMYYOIEILKEIGGOSLMDCEYNAD 298
DB 225 TEALASVGSMTIGIDISLTYGSLMTYPIREMYEYIYRAVELNGDGLKMDCEIYND 284

QY 299 KAVDSGTTLLRLPOKVDVAVEAVARASLPEPSDGFMTGSQSLACWNTSETPMSYFPKI 358
DB 285 KSIYDSGTTNRLPKVFEAAVKAISKASSTKFPDGFMLGQLVCWQAGTTPMNIIPVI 344

QY 359 SIYLDENSSRSFRITIIIPOLYIQMGAGLVY--ECYRFGISPSINALVIGATWMEGYV 417
DB 345 SLVLMGEVYNGSFRITIIIPOLYLRVEDVAVTSQDCYKFAVNSSTGTVMGAVIMEGYV 404

QY 418 IFDRAQKVGFAASPCAEIAGAASEISGPFSTEDVANSVCVPAQSLSPILMIIVSYALMS 477
DB 405 VFDRAKRIIGFAVNSCHHDEFTAAVSGPYTADMECGNIIPOTDESTMTIAYVMAA 464

QY 478 VCGAILLVLLVLLLPFCQR--RPRDEVVNDESSL 512

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DB 465 IC-ALFEMLPICLVQWQWRCILRHQHDFFADISLL 500
RESULT 3
ID_BACE_MOUSE STANDARD; PRT; 501 AA.
AC P56818;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Beta-secretase precursor (EC 3.4.23.-) (Beta-site APP cleaving enzyme)
DE (Beta-site amyloid precursor protein cleaving enzyme) (Aspartyl
DE protease 2) (Asp 2) (ASP2) (Membrane-associated aspartic protease 2)
DE (Memapsin-2).
GN BACE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2002972; Pubmed=10531052;
RA Vassar R., Bennett B.D., Babu-Khan S., Kahn S., Mendiaz E.A.,
RA Denis P., Teplow D.B., Ross S., Amarante P., Loeloff R., Luo Y.,
RA Fisher S., Fuller J., Edenson S., Lile J., Jarosinski M.A.,
RA Biere A.L., Curran E., Burgess T., Louis J.-C., Collins F.,
RA Treanor J., Rogers G., Citron M.;
RT "Beta-secretase cleavage of Alzheimer's amyloid precursor protein by
RT the transmembrane aspartic protease BACE.";
RL Science 286:735-741(1999).
[2]
RP REVISIONS TO 6 AND 81-87.
RA Bennett B.D., Vassar R., Citron M.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=2005170; Pubmed=10591213;
RA Yan R., Bienkowski M.J., Shuck M.E., Miao H., Torry M.C., Pauley A.M.,
RA Brashers J.R., Stratman N.C., Mathews W.R., Buhl A.E., Carter D.B.,
RA Tomaseelli A.G., Parodi L.A., Heinrikson R.L., Garney M.E.;
RT "Membrane-anchored aspartyl protease with Alzheimer's disease
RT beta-secretase activity.";
RL Nature 402:533-537(1999).
-1- FUNCTION: RESPONSIBLE FOR THE PROTEOLYTIC PROCESSING OF THE
CC AMYLOID PRECURSOR PROTEIN (APP). CLEAVES AT THE AMINO TERMINUS OF
CC THE A-BETA PEPTIDE SEQUENCE, BETWEEN RESIDUES 671 AND 672 OF APP,
CC LEADS TO THE GENERATION AND EXTRACELLULAR RELEASE OF BETA-CLEAVED
CC SOLUBLE APP, AND A CORRESPONDING CELL-ASSOCIATED CARBOXY-TERMINAL
CC FRAGMENT WHICH IS LATER RELEASED BY GAMMA-SECRETASE (BY
CC SIMILARITY).
-1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- TISSUE SPECIFICITY: BRAIN.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
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DR EMBL; AF190726; AAF04143.2; -
DR EMBL; AF200346; AAF17082.1; -.
DR HSSP; P56272; 1AM5..
DR MEROPS; A01.004; -.
DR MGD; MGI:1346542; Bace.
DR InterPro; IPR001461; AsproteaseA1.
DR InterPro; IPR001969; Asprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPSIN.
DR PROSITE; PS00141; ASP_PROTEASE; 1.

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KM Hydrolyase; Aspartyl protease; Glycoprotein; Zymogen; Transmembrane;
 KM Signal. 1 21 POTENTIAL.
 FT SIGNAL. 22 45 POTENTIAL.
 FT PROPEP 46 501 BETA-SECRETASE.
 FT CHAIN 22 457 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 458 478 POTENTIAL.
 FT TRANSMEM 479 501 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 93 93 BY SIMILARITY.
 FT ACT_SITE 289 289 BY SIMILARITY.
 FT ACT_SITE 216 420 BY SIMILARITY.
 FT DISULFID 278 443 BY SIMILARITY.
 FT DISULFID 330 380 BY SIMILARITY.
 FT DISULFID 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 501 AA; 55747 MW; C085A013145E474E CRC64;
 Query Match 44.1%; Score 1185; DA 1; Length 501;
 Best Local Similarity 46.0%; Pred. No. 1,8e-78;
 Matches 237; Conservative 83; Mismatches 169; Indels 26; Gaps 7;
 QY 9 LIPLIAQWLRAPAPLAPFT-----LPLRVAAATNRVAPTPGGPTPAERHADGLALA 63
 D 1 MAPALHWLLWVSGWMLPAQGTGLRLPLRSGLA-----GPLGLRLPRETDEES----- 51
 QY 64 LEPALASPAGANFLAMVNDLOGDSRGVYLEMLGTSPKQIIVDSSNFAVAGTPH 123
 D 52 -----EPPRRGGSFVEMVNDNRKSGQGYVEMTVGSPQTNILVDGSSNFAVAGAPH 106
 QY 124 SYIDTYPTERSSTYRSKGFDTVYKQSGWGFVGEDLVITPKGFNTSFLVNATIFES 183
 D 107 PFLHYYQRQLSTYRDLARKGVYVPTQCKMGELGTDLVSLPHGPNVTVRANIALITTS 166
 QY 184 ENFELPGIKWNCILGLAYATLAKPSSSLFTFPDSLVTQANINNVSMQCGGLPV---A 240
 D 167 DKFFINGSMWEGILGLAYAEIARPDLSLEPFDSLVTQKHINITSLOLCGAGFPLNQT 226
 QY 241 GSGTNGSLVLDGIEPSLVKGDIMWTPIMEENYGOIEIKLIGGGSNLDREYNADA 300
 D 227 ALASVGSWITIGIDHSITSLGSLWTPIKREYEVITVIRVINGDLMCKETIYDSS 286
 QY 301 IYDSGTTLLRLPOKYEDAVAEVARSILPEFSDGFWTSQDCAWNTSETPMSYEPKISI 360
 D 287 IYDSGTTNRLKPKYFEAVVKSIIKASSTREKPPDGFMLGEQLVCQAGTTPNIPFVLSL 346
 QY 361 YIRDENSSRSFRITTLIPQIYIOPMAGLNY-ECYRFGISPTNALVIGATWEGFYVF 419
 D 347 YLMGEVTVNQSFRTITLIPQYLRPVEDVATSDQCYKFAVSQSGTVMGAVIMEGFYVF 406
 QY 420 DRACRKGVAASPCAEINAAVSEISGPSTEDVANSNCVPAQSLSPILMITSYALMSVC 479
 D 407 DARRKRIGFAVACHVDEFRTAAVEGPFVTADMEDCGYNIPQTBESTLMTIAYMAALC 466
 QY 480 GAILLVILVLLPFCOR--RPDEEVNDESSL 512
 D 467 -ALFVLPICLWCGWRKCLRLAHQHDDPADDISL 500
 RESULT 4
 BACE_HUMAN STANDARD: PRT: 501 AA.
 AC P56817; OSUTS: Q9BYC1; Q9BYC0; Q9BYB9;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Beta-secretase precursor (BC 3.4.23.-) (Beta-site APP cleaving enzyme)
 DE (Beta-site amyloid precursor protein cleaving enzyme) (Aspartyl
 protease 2) (Asp 2) (Asp2) (Membrane-associated aspartic protease 2)
 DE (Memapsin-2).
 GN BACE OR BACE1.
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM A).
 RC TISSUE=Brain.
 RX MEDLINE=20002972; PubMed=10531052;
 RA Vaasat R., Bennett B.D., Babu-Khan S., Kahn S., Mendiaz E.A.,
 RA Denis P., Teplow D.B., Ross S., Amarante P., Loeffler R., Luo Y.,
 RA Fisher S., Fuller J., Ederson S., Lile J., Jarosinski M.A.,
 RA Biere A.L., Curran E., Burgess T., Louis J.-C., Collins F.,
 RA Treanor J., Rogers G., Citron M.,
 RT "Beta-secretase cleavage of Alzheimer's amyloid precursor protein by
 the transmembrane aspartic protease BACE.";
 RL Science 286:735-741(1999).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM A), SEQUENCE OF 46-68, AND
 RP CHARACTERIZATION.
 RC TISSUE=Brain.
 RX MEDLINE=20057171; PubMed=10591214;
 RA Silva S., Anderson J.P., Barbour R., Basi G.S., Caccavello R.,
 RA Davis D., Doan M., Dovey H.F., Frigon N., Hong J., Jacobson-Croak K.,
 RA Jewett N., Keim P., Knops J., Lieberburg I., Power M., Tan H.,
 RA Tacsuno G., Tung J., Schenk D., Seubert P., Sotomasa S.M., Wang S.,
 RA Walker D., Zhao J., McConlogue L., Varghese J.;
 RT "Purification and cloning of amyloid precursor protein beta-secretase
 from human brain.";
 RL Nature 402:537-540(1999).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM A).
 RX MEDLINE=20057170; PubMed=10591213;
 RA Yan R., Bienkowski M.J., Shuck M.E., Miao H., Tory M.C., Paulay A.M.,
 RA Brashers J.R., Strattman N.C., Mathews W.R., Buhl A.E., Carter D.B.,
 RA Tomasselli A.G., Parodi L.A., Heinrichson R.L., Gunney M.E.;
 RT "Membrane-anchored aspartyl protease with Alzheimer's disease beta-
 secretase activity.";
 RL Nature 402:533-537(1999).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM A).
 RX MEDLINE=20120043; PubMed=10656250;
 RA Hussain I., Powell D.J., Howlett D.R., Tew D.G., Meek T.D.,
 RA Chapman C., Glover I.S., Murphy K.E., Southan C.D., Ryan D.M.,
 RA Smith T.S., Simmons D.L., Walsh F.S., Dingwall C., Christie G.;
 RT "Identification of a novel aspartic proteinase (Asp 2) as beta-
 secretase.";
 RL Mol. Cell. Neurosci. 14:419-427(1999).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM B).
 RC TISSUE=Brain, and Pancreas;
 RA Michel B., De Pietri Tonelli D., Zaccchetti D., Keller P.;
 RT "New beta-site APP cleaving enzyme isoform (BACE-1B) obtained from
 human brain and pancreas.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM C).
 RC TISSUE=Pancreas;
 RA Zaccchetti D., De Pietri Tonelli D., Schnurp R.;
 RT "New beta-site APP cleaving enzyme isoform (BACE-1C) obtained from
 human pancreas.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORMS B; C AND D).
 RC TISSUE=Brain;
 RX MEDLINE=21408467; PubMed=11516562;
 RA Tanahashi H., Tabira T.,
 RT "Three novel alternatively spliced isoforms of the human beta-site
 amyloid precursor protein cleaving enzyme (BACE) and their effect on
 amyloid beta-peptide production.";
 RL Neurosci. Lett. 307:9-12(2001).
 RN [8]
 RP SEQUENCE OF 14-501 FROM N.A. (ISOFORM A), AND CHARACTERIZATION.
 RX MEDLINE=20144060; PubMed=10677483;
 RL Lin X., Koelsch G., Wu S., Downs D., Dashti A., Tang J.;

RT "Human aspartic protease memapsin 2 cleaves the beta-secretase site of
 RT beta-amyloid precursor protein.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1456-1460(2000).
 RN (9)
 RP DISULFIDE BONDS.
 RX MEDLINE=21950860; PubMed=11953458;
 RA Fischer F., Molinari M., Bodendorf U., Paganetti P.;
 RT "The disulphide bonds in the catalytic domain of BACE are critical but
 RT not essential for amyloid precursor protein processing activity.";
 RL J. Neurochem. 80:1079-1088(2002).
 CC -1- FUNCTION: RESPONSIBLE FOR THE PROTEOLYTIC PROCESSING OF THE
 CC AMYLOID PRECURSOR PROTEIN (APP). CLEAVES AT THE AMINO TERMINUS OF
 CC THE A-BETA PEPTIDE SEQUENCE, BETWEEN RESIDUES 671 AND 672 OF APP,
 CC LEADS TO THE GENERATION AND EXTRACELLULAR RELEASE OF BETA-CLEAVED
 CC SOLUBLE APP, AND A CORRESPONDING CELL-ASSOCIATED CARBOXY-TERMINAL
 CC FRAGMENT WHICH IS LATER RELEASED BY GAMMA-SECRETASE.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 4 isoforms: A/BACE-1a/BAC-501 (shown here),
 CC B/BACE-1b/BACE-1-476; C/BACE-1c/BACE-1-457 and D/BACE-1d/BACE-1-
 CC 432; are produced by alternative splicing.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; AF190725; AAF04142.1; -
 DR EMBL; AF201468; AAF18982.1; -
 DR EMBL; AF200343; AAF17079.1; -
 DR EMBL; AF204943; AAF26367.1; -
 DR EMBL; AF318816; AAK38374.1; -
 DR EMBL; AF318817; AAK38375.1; -
 DR EMBL; AB050436; BAB40931.1; -
 DR EMBL; AB050437; BAB40932.1; -
 DR EMBL; AB050438; BAB40933.1; -
 DR EMBL; AF200193; AAF13715.1; -
 DR HSSP; P32329; 1YPS.
 DR MEROPS; A01.004; -
 DR GENE; HGNC:933; BACE.
 DR MIM; 604252; -
 DR InterPro: IPR001461; Aspprotease1.
 DR InterPro: IPR001969; Aspprotease_site.
 DR Pfam; PF00026; aep; 1.
 DR PRINTS; PR00792; PEPsin.
 DR PROSITE; PS00141; ASP_PROTEASE; 1.
 KW Hydrolase; Aspartyl protease; Glycoprotein; Zymogen; Transmembrane;
 KW Signal; Alternative splicing.
 FT SIGNAL 1 21
 FT PROPEP 22 45
 FT CHAIN 46 501
 FT DOMAIN 22 457
 FT TRANSMEM 458 478
 FT DOMAIN 479 501
 FT ACT_SITE 93 93
 FT ACT_SITE 289 289
 FT DISULFID 216 420
 FT DISULFID 278 443
 FT DISULFID 330 380
 FT CARBOHYD 153 153
 FT CARBOHYD 172 172
 FT CARBOHYD 223 223
 FT CARBOHYD 354 354
 FT VASPLC 146 189
 FT VASPLC 190 214
 SO SEQUENCE 501 AA; 55763 MW; 377CE4C824ACF05 CMC64;
 Query Match Score 1178.5; DB 1; Length 501;
 Best Local Similarity 46.2%; Pred. No. 5.2e-78;

Matches 240; Conservative 82; Mismatches 164; Indels 33; Gaps 9;
 QY 7 ALLPPLAQLWLLRAAPELAPFT----LPRLVAATAATNRVAPTPGCTPAERHADGLA 61
 DB 2 AQLPFWLLWM---GAGVLPAGHTQHGIRLPLRSGLG-----GAPL-----GLR 42
 QY 62 LALE--PALASPAGANFLAVNDNLQDSDGRCYILEMLIGTPQKLQLVUTGSSNFAVA 119
 DB 43 LPREIDEEPEEPGRGSGFVEAVNDMLRGSGGQYVEMVVGSPPTLNLVDTGSSNFAVG 102
 QY 120 GTPHSYIDTYEDTERRSYRSGFDVTKYQSGMTGSGVSDLTITPGFNTSFLVNAT 179
 DB 103 AAPHPFLHRYTQRQUSSTYRLRKGVVPTYQKMEGLDVLSPHENVYRANIAA 162
 QY 180 IPESNFPLPGIKNKGILGLAVATLAKSSSLTFPDSLVTQANI PVNFSMQMGAGLNV 239
 DB 163 ITESGKFFINSNMEGLIGLVAELIARDSDLEFPFSLVQHTVPMFLSLQCGAGPFL 222
 QY 240 AGS---GTNGSLVLGGIEPILYKGDLYWYTIKBEWYQIILKLEIGGSLNDCREYN 296
 DB 223 NQSEVLASVGSMTIGGIDHSLYGSIMYTPIRREWYEVYIVVEINGQDLKMDCKEYN 282
 QY 297 ADKAVDSCTLLLPQKVPDAVVAVARASLIEFSDGFMTGSOLACMTSETPWSYEP 356
 DB 283 YKSTIVDSGTTNLRPKVFAVAKSTIAASTKFPDGFMLGQLVCWQAGTTPMNLFP 342
 QY 357 KISITLIDENSSRSFRITILPOLYIOPMAGALNV-ECYRFGISPTNALVIGATVMEGF 415
 DB 343 VISLYLMEVINGSPRITILPQYLPRVEDVATQDDCYKALISQSGTGMGAVINMGF 402
 QY 416 YVDPRAQKRGVFAASPCAEITAGAAVSEISGPESTEDVASCVPASLSEPIILVSYAL 475
 DB 403 YVDFRARKRIGFVASACHVDEFTTAVBESPTLIMEDCGYNIPTDESTLMTIAYVM 462
 QY 476 MSVCGAILLVILVLLPFCQR--RPDPDVNVDESL 512
 DB 463 AATC-ALFMLPLCLMVCWRCRLRQOHDPADDISL 500
 RESULT 5
 PEP_C MACFU STANDARD; PRT; 377 AA.
 AC P03955;
 DT 23-OCT-1986 (Rel. 02, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Gastricisin precursor (EC 3.4.23.3) (Pepsinogen C) (Fragment).
 GN PGC.
 OS Macaca fuscata fuscata (Japanese macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9543;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Gastric mucosa;
 RX MEDLINE=92037645; PubMed=1935977;
 RA Kageyama T., Tanabe K., Koiwai O.;
 RT "Development-dependent expression of isozymogens of monkey
 RT pepsinogens and structural differences between them.";
 RL Eur. J. Biochem. 202:205-215(1991).
 RN [2]
 RP SEQUENCE OF 6-377.
 RX MEDLINE=86168133; PubMed=3514597;
 RA Kageyama T., Takahashi K.;
 RT "The complete amino acid sequence of monkey progastricsin.";
 RL J. Biol. Chem. 261:4406-4419(1986).
 RN [3]
 RP SEQUENCE OF 6-66.
 RX MEDLINE=85289106; PubMed=3928607;
 RA Kageyama T., Takahashi K.;
 RT "Monkey pepsinogens and pepsins. VII. Analysis of the activation
 RT process and determination of the NH2-terminal 60-residue sequence of

RT Japanese monkey progastricsin, and molecular evolution of
 RT pepsinogen.";
 RL J. Biochem. 97:1235-1246(1985).
 CC -1- CATALYTIC ACTIVITY: More restricted specificity than pepsin A, but
 CC shows preferential cleavage at Tyr-Xaa bonds; high activity
 CC towards hemoglobin as substrate.
 CC -1- PPM: EACH PEPSINOGEN IS CONVERTED TO CORRESPONDING PEPSIN AT PH
 CC 2.0 IN PART AS A RESULT OF THE RELEASE OF A 47 AA ACTIVATION
 CC SEGMENT AND IN PART AS A RESULT OF STEPWISE PROTEOLYTIC CLEAVAGE
 CC VIA AN INTERMEDIATE FORM(S).
 CC -1- MISCELLANEOUS: THE EXPRESSION OF PEPSINOGEN GENES IS REGULATED BY
 CC HORMONES AND RELATED SUBSTANCES.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
 CC -----
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 CC -----
 DR EMBL, X59754; CAA42426.1; -.
 DR PIR, A00986; PEMQCU.
 DR PIR, A22402; A22402.
 DR PIR, S19683; S19683.
 DR PIR, S16066; S16066.
 DR HSSP, P20142; 1AYF.
 DR MEROPS; A01.003; -.
 DR InterPro; IPR001461; Asproctaseal.
 DR InterPro; IPR001969; Asproctaseal_site.
 DR Pfam; PF00026; aep; 1.
 DR PROSITE; PS00141; ASP_PROTEASE; 2.
 KW Hydroxylase; Aspartyl protease; Zymogen; Digestion; Signal.
 FT SIGNAL 1 1
 FT PROPEP 6 31 ACTIVATION PEPTIDE.
 FT PROPEP 32 48 ACTIVATION PEPTIDE.
 FT CHAIN 49 377 GASTRISIN.
 FT DISULFID 93 98
 FT DISULFID 256 260
 FT DISULFID 299 332
 FT ACT SITE 80 80
 FT ACT SITE 265 265
 FT CONFLICT 331 331
 FT CONFLICT 349 349
 SEQUENCE 377 AA; 41148 MW; 2C8B8FB26D77CE CRC64;
 Query Match 13.5%; Score 363.5; DB 1; Length 377;
 Best Local Similarity 28.9%; Pred. No. 3.9e-19;
 Matches 118; Conservative 65; Mismatches 118; Indels 107; Gaps 19;
 Oy 56 HADGIALALEPLASPAAGANFLAWNDINQSGSGRYIEMLIGRPQQLIVDTGSSN 115
 Db 44 HFGDLSVSEY-----MAYMD-----AAVFEISIGTPQPFVLFDTGSSN 85
 Oy 116 FAV-----AGTPHSYIDYFDFERSSTYRSKGFVDVVKXTQSGWTFVGEDVLTIPK 167
 Db 86 LWPVSVCOSQACTSHS-----RNPESSTYSTNGQTSFLQSGSLTFPGYDITLV-- 139
 Oy 168 GFNTSFLVNIATIFESSEFLPG-----IKWGIIGLAVATLAKSSSLTFPDSLVTA 222
 Db 140 ---QSIQVNOSEFGLSEN--EPGTNVAQPFQINGLAFPTLSVDAAT--TMOGVGNG 192
 Oy 223 NIPN-VFSHQMGAGLVPVAGSGTNGSLVGLIEPSLYGDIWYPIKEEWYQIEILKL 281
 Db 193 ALTSPISFVYSLDQ-----QSSSGCAVVFQGVDSLSLYGOIYMAVPTOLYMOIGIEEF 246
 Oy 282 EIGGGSGLNDCEHYNADKAIYVSGTLLLPQKVPFAVVEAVARSLIEFSDGFMTGSG 341
 Db 247 LIGGQASGM-CSE--GCQAIYDTGTSLLVPOQYMSALQA-----TGAO 288
 Oy 342 IACWNSETPMSYF-----PKISYLRDENSESRFRITILPOLYIQPMWAGALNY 391

Db 289 -----EDEXGFLVNCNSIQMLPTLFTI-----NGVEFPLPSSYL-----LNN 328
 Oy 392 ECV-RFGISP-----STNALVIGATVMEGFYIFPDAQKRVFAAS 431
 Db 329 NGCTVGEVPEYLSAQNSQPLMITIGDVFSLYSYVLSLNNRVGFAPA 376
 RESULT 6
 PEPC_HUMAN
 ID PEPC_HUMAN STANDARD; PRT; 388 AA.
 AC P20142;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-JUN-2002 (Rel. 41, Last annotation update)
 DE Gastricsin precursor (EC 3.4.23.3) (Pepsinogen C).
 GN PGC.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NX NCBI_TaxID=9606;
 RX [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86087276; PubMed=3335549;
 RA Hayano T., Sogawa K., Ichihara Y., Fujii-Kuriyama Y., Takahashi K.;
 RT "Primary structure of human pepsinogen C gene.";
 RL J. Biol. Chem. 263:1382-1385(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89079679; PubMed=2909526;
 RA Taggart R.T., Cass L.G., Mohandas T.K., Derby P., Barr P.J., Pals G.,
 RT "Human pepsinogen C (progastricsin). Isolation of cDNA clones,
 RT localization to chromosome 6, and sequence homology with pepsinogen
 RT A.";
 RL J. Biol. Chem. 264:375-379(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Placenta;
 RX MEDLINE=89290840; PubMed=2567697;
 RA Pals G., Azuma T., Mohandas T.K., Bell G.I., Bacon J.,
 RA Samloff I.M., Walz D.A., Barr P.J., Taggart R.T.;
 RT "Human pepsinogen C (progastricsin) polymorphism: evidence for a
 RT single locus located at 6p21.1-pter.";
 RL Genomics 4:137-148(1989).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Wong R.N.S., Tang J.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 17-101.
 RX MEDLINE=90130402; PubMed=2515193;
 RA Athauda S.B.P., Tanji M., Kageyama T., Takahashi K.;
 RT "A comparative study on the NH2-terminal amino acid sequences and
 RT some other properties of six isozytic forms of human pepsinogens and
 RT pepsins.";
 RL J. Biochem. 106:920-927(1989).
 RN [6]
 RP SEQUENCE OF 17-64.
 RX MEDLINE=83079318; PubMed=6816595;
 RA Foltmann B., Jensen A.L.;
 RT "Human progastricsin. Analysis of intermediates during activation
 RT into gastricsin and determination of the amino acid sequence of the
 RT propept.";
 RL Eur. J. Biochem. 128:63-70(1982).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (1.62 ANGSTROMS).
 RX MEDLINE=95230687; PubMed=7714902;
 RA Moore S.A., Sielecki A.R., Chernia M.M., Tarasova N.I., James M.N.G.;
 RT "Crystal and molecular structures of human progastricsin at 1.62-A
 RT resolution.";
 RL J. Mol. Biol. 247:466-485(1995).
 RN [8]

RP X-RAY CRYSTALLOGRAPHY (2.36 ANGSTROMS).
 RX MEDLINE=98069649; PubMed=9406551;
 RA Khan A.R., Cherney M.M., Tarasova N.I., James M.N.;
 RT "Structural characterization of activation 'intermediate 2' on the
 RT pathway to human gastricsin.";
 RL Nat. Struct. Biol. 4:1010-1015(1997).
 CC -1- CATALYTIC ACTIVITY: More restricted specificity than pepsin A, but
 CC shows preferential cleavage at Tyr-Xaa bonds; high activity
 CC towards hemoglobin as substrate.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
 CC -----
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 CC -----
 DR EMBL; M18667; AAA60062.1; ALT_INIT.
 DR EMBL; M18659; AAA60062.1; JOINED.
 DR EMBL; M18660; AAA60062.1; JOINED.
 DR EMBL; M18661; AAA60062.1; JOINED.
 DR EMBL; M18662; AAA60062.1; JOINED.
 DR EMBL; M18663; AAA60062.1; JOINED.
 DR EMBL; M18664; AAA60062.1; JOINED.
 DR EMBL; M18665; AAA60062.1; JOINED.
 DR EMBL; M18666; AAA60062.1; JOINED.
 DR EMBL; M23077; AAA60063.1; -
 DR EMBL; M23069; AAA60063.1; JOINED.
 DR EMBL; M23070; AAA60063.1; JOINED.
 DR EMBL; M23071; AAA60063.1; JOINED.
 DR EMBL; M23072; AAA60063.1; JOINED.
 DR EMBL; M23073; AAA60063.1; JOINED.
 DR EMBL; M23074; AAA60063.1; JOINED.
 DR EMBL; M23075; AAA60063.1; JOINED.
 DR EMBL; J04443; AAA60074.1; -
 DR EMBL; U75272; AAB18273.1; -
 DR PIR; A23458; A23458.
 DR PIR; A29937; A29937.
 DR PIR; A31811; A31811.
 DR PIR; PX0028; PX0028.
 DR PDB; 1HTR; 26-JAN-95.
 DR PDB; 1AVF; 25-FEB-98.
 DR MEROPS; A01.003; -
 DR Genew; HGNC:8890; PGC.
 DR MIM; 169740; -
 DR InterPro; IPR001461; AsproteaseA1.
 DR InterPro; IPR001969; Asprotease_site.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPsin.
 DR PROSITE; PS00141; ASP_PROTEASE; 2.
 KW Hydrolyase; Aspartyl protease; Zymogen; Digestion; Signal;
 KW 3D-structure.
 FT SIGNAL 1 16
 FT PROPEP 17 59 ACTIVATION PEPTIDE.
 FT CHAIN 60 388 GASTRISIN.
 FT ACT_SITE 91 91
 FT DISULFID 276 276
 FT DISULFID 104 109
 FT DISULFID 267 271
 FT DISULFID 310 343
 FT CONFLICT 40 41 GE -> ED (IN REF. 6).
 FT CONFLICT 52 52 W -> S (IN REF. 6).
 SQ SEQUENCE 388 AA; 42426 MW; F862DDC1438BB92 CRC64;

Query Match 19.1%; Score 353; DB 1; Length 388;
 Best local similarity 12.1%; Pred. No. 2.3e-18;
 Matches 120; Conservative 65; Mismatches 120; Indels 108; Gaps 21;

QY 52 PAHRADG-LALALEPALASPGANFLAMVDNLOGDSGRGYLEMLGTTPQKILVLD 110
 DB 50 PAMKIRFDLSVTEP-----MAYMD-----AAFGESIGTTPQNFVLVLD 91

QY 111 TGSSNFAV-----ACTPHSYIDTYEDTERSSSTYRSKGFVYKTYQGSMTGFVGEDL 162
 DB 92 TGSSNLWAPSVYCSOACTSHS-----RNPSSSTYSTNGQTFSLQYSGSLTGFPGYDT 147
 QY 163 VTIPGFTSTFLVNATIFESSENFPLPG-----IKMNIILGLAVNTLAKPSSSLETFPDS 217
 DB 148 LTV-----QSIVPNOEFGISEN--EPGTNFVAVQFDDIMGLAVALSVDBAT--TAMQG 198
 QY 218 LVTOANIPN-VFSMQMOCAGLPVAGSGTNGSLVIGIEPLSYGGDIYVTPIKEEMVYQI 276
 DB 199 MVQEGALNSPVPYSVLSNQ-----QSSSGAVPFGVDSLLYGLQIYMAVYQELVQI 252
 QY 277 EILKLEIGGSLNDCREYNADKAIVDSGTLRLPQKVPFAVVAVARASLIEFSDGF 336
 DB 253 GIEFLIGGQASGW-CSE--GCAIVDTGTSLLVPOQYMALIQA----- 295
 QY 337 WTGSLACWTNSEPTMWSF-----PKISYLRDENSESRFRITILPOLYIQPMMG 386
 DB 296 TGAQ-----EDEYGOFLVNCNSIQMLPSLTFRI-----NGVEPFLPPSSYI----- 336
 QY 387 AGLVNECY-RFGISP-----STNA--LVIGATWEGFVIFDRAQKRGFPAAS 431
 DB 337 --LSNNGICTVGEPTYLSQNGPLWLGDFLRSYVYDLGNRRVGFATA 387

RESULT 7
 ID PEP_CALJA STANDARD; PRT; 388 AA.
 AC Q9N2D3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Gastricsin precursor (EC 3.4.23.3) (Pepsinogen C).
 GN PGC.
 OS Callithrix jacchus (Common marmoset).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
 OC Callithrix.
 OX NCBI_TaxID=9483;
 RN [1]
 RP SEQUENCE FROM N.A., SEQUENCE OF 17-26, FUNCTION, AND ENZYME
 RP REGULATION.
 RC TISSUE=Gastric mucosa;
 RX MEDLINE=20250834; PubMed=10788784;
 RA Kageyama T.;
 RT "New world monkey pepsinogens A and C, and prochymosins. Purification,
 RT characterization of enzymatic properties, cDNA cloning, and molecular
 RT evolution.";
 RL J. Biochem. 127:761-770(2000).
 CC -1- FUNCTION: Hydrolyses a variety of proteins.
 CC -1- CATALYTIC ACTIVITY: More restricted specificity than pepsin A, but
 CC shows preferential cleavage at Tyr-Xaa bonds; high activity
 CC towards hemoglobin as substrate.
 CC -1- ENZYME REGULATION: Inhibited by pepstatin.
 CC -1- MISCELLANEOUS: The optimal pH is around 2.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
 CC -----
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 CC -----
 DR EMBL; AB038385; BAA90872.1; -
 DR HSSP; P20142; 1AVF.
 DR MEROPS; A01.003; -
 DR InterPro; IPR001461; AsproteaseA1.
 DR InterPro; IPR001969; Asprotease_site.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPsin.

DR PROSITE; PS00141; ASP_PROTEASE; 2.
 KW Hydrolyase; Aspartyl protease; Zymogen; Digestion; Signal.
 FT SIGNAL 1 16
 FT PROPEP 17 59 ACTIVATION PEPTIDE (BY SIMILARITY).
 FT CHAIN 60 388
 FT ACT_SITE 91 91 BY SIMILARITY.
 FT ACT_SITE 276 276 BY SIMILARITY.
 FT DISULFID 104 109 BY SIMILARITY.
 FT DISULFID 267 271 BY SIMILARITY.
 FT DISULFID 310 343 BY SIMILARITY.
 SQ SEQUENCE 388 AA; 42503 MW; 08C48BD1F7DD8C CRC64;

Query Match 13.1%; Score 351.5; DB 1; Length 388;
 Best Local Similarity 30.1%; Pred. No. 3e-18;
 Matches 112; Conservative 56; Mismatches 115; Indels 89; Gaps 17;

QY 92 YLEMLITPPKQIIVDTGSSNFV-----AGTSHYIDTYFPTERSSTYRSKGF 143
 DB 73 YFGEISIGTPQNPLVLFPTGSSNLWPSVYCQSQAQTSHS---RFPNSASTYSSNQ 128
 QY 144 DVTYKYTGSMWTFVGEDELVTIPKGFNTSFLVNIATIFESSENFPLPG-----IKNNGILG 198
 DB 129 TFSLOYGSGSLTGFPGYDILTV-----QSIQVPNOGFGLSEN--EKGTFVVAQFDGIMG 181
 QY 199 LAYATLAKRSSLETFFPSLVTQANIPI-VFSMOCGAGLPVAGSGTGSGSLVLCGIEPS 257
 DB 182 LAYPALSMWGAT--TAMQGMLEGALTSVPFSFVLSNQ-----QSSSGAVIFGVSDS 233
 QY 258 LYKGIVWTPRIKEWYQIILKEIGGOSLMDREYNADKAIYDSCTTLRLQKVD 317
 DB 234 LTGQIVAMPVQELWQIGIEFLIGQASGM-CSE--GCQALVDTGTSLLTVPOQYMS 290
 QY 318 AVEAVARASLIPEFSDGFMTGSQALCMTNSETPMSYF-----PKISYLDENS 367
 DB 291 AFLER-----TGAQ-----EDRYGQFLVNCDSIQNPLTLFIIT----- 323
 QY 368 SRSFPIITLPOLIYOPMAGLNEYCY-RFGISP-----STNALVIGATMEGFYVIF 419
 DB 324 -NGVEFFPLPSSYI-----LSNNGYCTVGVEPFLYSSQNPMLILDVFLRSYSVF 375
 QY 420 DRQKRVGFPAAS 431
 DB 376 DIGNRVGFATA 387

RESULT 8
 PERC_CAVPO STANDARD; PRT; 394 AA.
 ID PERC_CAVPO
 AC Q64411;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Gastric precursor (EC 3.4.23.3) (pepsinogen C).
 GN PGC.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92355614; PubMed=1644829;
 RA Kageyama T., Ichinose M., Tsukada S., Miki K., Kurokawa K., Koiwai O.,
 RA Tanji M., Yakabe E., Athauda S.B., Takahashi K.;
 RT "Gastric procathepsin E and procathepsin from guinea pig.
 RT Purification, molecular cloning of cDNAs, and characterization of
 RT enzymatic properties, with special reference to procathepsin E.";
 RL J. Biol. Chem. 267:16450-16459(1992).
 CC -i CATALYTIC ACTIVITY: More restricted specificity than pepsin A, but
 CC shows preferential cleavage at Tyr-Xaa bonds, high activity
 CC towards hemoglobin as substrate.
 CC -i SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
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 CC or send an email to license@isb-sib.ch).

DR EMBL; M88652; AAA37053.1; -
 DR HSSP; P20142; IAVF.
 DR MEROPS; A01.003; -.
 DR InterPro; IPR001451; AsproteaseA1.
 DR InterPro; IPR001963; Asprotease_site.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPSPIN.
 DR PROSITE; PS00141; ASP_PROTEASE; 2.
 KW Hydrolyase; Aspartyl protease; Zymogen; Digestion; Signal.
 FT SIGNAL 1 16
 FT PROPEP 17 65
 FT CHAIN 66 394
 FT ACT_SITE 97 97 BY SIMILARITY.
 FT ACT_SITE 283 283 BY SIMILARITY.
 FT DISULFID 110 115 BY SIMILARITY.
 FT DISULFID 273 277 BY SIMILARITY.
 FT DISULFID 316 349 BY SIMILARITY.
 SQ SEQUENCE 394 AA; 42995 MW; 114F08E105D49865 CRC64;

Query Match 12.1%; Score 324.5; DB 1; Length 394;
 Best Local Similarity 29.0%; Pred. No. 2.8e-16;
 Matches 107; Conservative 63; Mismatches 116; Indels 83; Gaps 18;

QY 92 YLEMLITPPKQIIVDTGSSNF-----AVAGTSHYIDTYFPTERSSTYRSKGF 143
 DB 79 YFGQISLGTGPQSFQVLVLDTGSSNLWPSVYCSSLACTTH---TRFNPRDSSTVARDQ 134
 QY 144 DVTYKYTGSMWTFVGEDELVTI--PK-GENTSFLVNIATIFESSENFPLPG-----IK 192
 DB 135 SFSLEIGTSLGVFGVYMTITQDIQVPEKQFGLS-----ETP---PGSDFVYAE 181
 QY 193 WNGILGLAYATLAKRSSLETFFPSLVTQANI-PNVFSMOCGAGLPVAGS--GTNGGSL 249
 DB 182 FDGILGLGYPLGSESGAR--TAMQGLAREGALSQSLFVYL-----GSQGSDEBQQL 231
 QY 250 VLGGIEPSLYKQDIWYTPRIKEWYQIILKEIGGOSLMDREYNADKAIYDSCTTL 309
 DB 232 ILGVDSESLYTDIYWTPTVQELWQIGIEGFLIDGSASGWCSSR---CQCGIVDTGTSLL 288
 QY 310 RLPOKVPFAVBAVARASLIPEFSDGFMTGSQALCMTNSETPMSYFPKISYLDENS 369
 DB 289 TVPSDYLTSTLVOAIGAE--NEYGEYF-----VSCSSIQDPLTLFVISGV----- 332
 QY 370 SFRITILPOLYIOP-----MMGAGLNEYCYRFGISPTN--ALVIGATMEGFYVIFPRA 422
 DB 333 --EFLPSAAILISGENCMVGLESTY-----VSPGGGEVWILGDVFLNYSYVDLA 384
 QY 423 QKRVGFPAAS 431
 DB 385 NNRVGFATA 393

RESULT 9
 RENI_MOUSE STANDARD; PRT; 402 AA.
 ID RENI_MOUSE
 AC P06281; O62153; P97911; O62154;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Renin precursor, renal (EC 3.4.23.15) (Angiotensinogenase).
 GN RENI OR REN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=84182525; PubMed=6370686;
RA Holm I., Olio R., Pantier J.-J., Rougeon F.;
RT "Evolution of aspartyl proteases by gene duplication: the mouse renin gene is organized in two homologous clusters of four exons.";
RL EMBL J. 3:357-362(1984).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=Kidney;
RX MEDLINE=90067953; PubMed=2685761;
RA Kim W.S., Murakami K., Nakayama K.;
RT "Nucleotide sequence of a cDNA coding for mouse Ren1 preprorenin.";
RL Nucleic Acids Res. 17:9480-9480(1989).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=DRA/2; and C57BL/10;
RX MEDLINE=90108722; PubMed=2691339;
RA Burt D.W., Mullins L.D., George H., Smith G., Brooks J., Ploil D.,
RA Brammar W.J.;
RT "The nucleotide sequence of a mouse renin-encoding gene, Ren-1d, and its upstream region.";
RL Gene 84:91-104(1989).
[4]
RP SEQUENCE OF 1-30 FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=84298161; PubMed=6089205;
RA Pantier J.-J., Dreyfus M., Roux D.T.L., Rougeon F.;
RT "Mouse kidney and submaxillary gland renin genes differ in their 5' putative regulatory sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5489-5493(1984).
[5]
RP SEQUENCE OF 1-31 FROM N.A.
RX MEDLINE=85085936; PubMed=6392850;
RA Field L.J., Philbrick W.M., Howles P.N., Dickinson D.P.,
RA McGowan R.A., Gross K.W.;
RT "Expression of tissue-specific Ren-1 and Ren-2 genes of mice: comparative analysis of 5'-proximal flanking regions.";
RL Mol. Cell. Biol. 4:2321-2331(1984).
[6]
RP SEQUENCE OF 22-37 AND 72-80.
RC STRAIN=C57BL/10ROS X C3H/HEROS; TISSUE=Kidney;
RX MEDLINE=97182599; PubMed=9030738;
RA Jones C.A., Petrovic N., Novak E.K., Swank R.T., Sigmund C.D.,
RA Gross K.W.;
RT "Bioynthesis of renin in mouse kidney tumor A64.1 cells.";
RL Eur. J. Biochem. 243:181-190(1997).
CC -1- FUNCTION: Renin is a highly specific endopeptidase, whose only known function is to generate angiotensin I from angiotensinogen in the plasma, initiating a cascade of reactions that produce an elevation of blood pressure and increased sodium retention by the kidney.
CC -1- CATALYTIC ACTIVITY: Cleaves Leu-|- bond in angiotensinogen to generate angiotensin I.
CC -1- TISSUE SPECIFICITY: KIDNEY.
CC -1- INDUCTION: RENAL RENIN IS SYNTHESIZED BY THE JUXTAGLOMERULAR CELLS OF THE KIDNEY IN RESPONSE TO DECREASED BLOOD PRESSURE AND SODIUM CONCENTRATION.
CC -1- POLYMORPHISM: In inbred mouse strains, there are at least two alleles which can occur at the Ren1 locus: Ren-1d and Ren-1c.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
CC -----
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CC -----
DR EMBL; X00810; CAA25391.1; -
DR EMBL; X00811; CAA25391.1; JOINED.

DR EMBL; X00812; CAA25391.1; JOINED.
DR EMBL; X00813; CAA25391.1; JOINED.
DR EMBL; X00814; CAA25391.1; JOINED.
DR EMBL; X00815; CAA25391.1; JOINED.
DR EMBL; X00816; CAA25391.1; JOINED.
DR EMBL; X00850; CAA25391.1; JOINED.
DR EMBL; X00851; CAA25391.1; JOINED.
DR EMBL; X16642; CAA34636.1; -
DR EMBL; K02596; AAA40045.1; -
DR EMBL; M32352; AAA40043.1; -
DR EMBL; K02800; AAA40044.1; -
DR EMBL; M34190; AAA40042.1; -
DR PIR; A00989; REMSK.
DR PIR; S07636; S07636.
DR PIR; A22058; A22058.
DR HSSP; P00796; 1SMR.
DR MEROPS; A01.007; -
DR MGD; MGI:97898; Ren1.
DR InterPro; IPR001461; AsparticaseA1.
DR InterPro; IPR001969; Asparticase_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; 2.
KW Hydrolase; Aspartyl protease; Plasma; Glycoprotein; Zymogen;
KW Signal.
FT SIGNAL 1 21
FT PROPEP 22 71
FT CHAIN 72 402
FT ACT_SITE 102 102
FT ACT_SITE 287 287
FT DISULFID 115 122
FT DISULFID 278 282
FT CARBOHYD 69 69
FT CARBOHYD 139 139
FT CARBOHYD 320 320
FT VARIANT 58 58
FT VARIANT 68 68
FT VARIANT 160 160
FT VARIANT 315 315
FT VARIANT 352 352
FT CONFLICT 6 23
FT CONFLICT 24 24
FT CONFLICT 163 163
SQ SEQUENCE 402 AA; 44342 MW; D42920B55597A38 CRC64;

Query Match 11.9%; Score 320; DB 1; Length 402;
Best Local Similarity 28.6%; Pred. No. 6.1e-16;
Matches 126; Conservative 66; Mismatches 181; Indels 68; Gaps 21;

10 LPLLAQWLRLRAPELADAPFTLPLRVAATNRVVAFTPG-
6 MFLWALLL-----WSPCTSLPRTNTRFERIPKAMPSTREILEHGVDMTRLSAMGV 60
66 ----PA--LASPAGANFLAMVDNLGDSGRGYLEMLIGTPPOKQILVDTGSSNPAV 118
61 FTKPSSTNLNLSPVVLNLYL-----NTQ-----YGGIGIGTPQTPKVIFFDTGSANLWV 110
119 AGTFHSY-----IDYFEDERSSTYRSKGPDYVVKXTQGSWMGVFVEDLVITPKGNTS 172
111 PSTCSRLYLACGHSHYESDSSSYMENGSDFTIHGSGVKFSLQSDSTV-
173 FLVNIATFESSENFPLGIKWNGLGLAVATLAKPSSSLETFEDSLVTOANI-
170 QTFEVELPLRPLPML--AKFDGVLGNGFP--AQAVGVAPVDFHILISQGLAKEVSVY 225
232 MCGAGLPVAGSGTNGSLVIGIEPSLYKDDIWTYPIKEWYQIETLKEIGQSINLD 291
226 Y-----NRGSHLLGEGVHVAGSDPOHYQGNFHVYSISKTDSDWQITMKGVSVG--SSTLL 277
292 CREYNADKAIYDSTTLRLPKQVFDAVVEAV-ARABLIEFSGFVTSQGLACWNTSET 350
278 CEEGCA--VVVDGSSFLISAPTSSLKLIQALAKKERIRIEY-----VVNC---SQV 324

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QY 351 FWSYFPIKISIVLRDENSRSFRITLLPOLYIQPMWAGL-NYECYRFGISPTNAL-VIG 408
Db 325 P--TLPDISFDL---GGRAVTLSTSDVLYQYPNRDKLTALHAMDIPPTGVWVILG 378
QY 409 ATWMEGFYVTPDRACKYGA 429
Db 379 ATIRKFTYEDFRHNRIGFA 399

RESULT 10
APR1_ORYSA STANDARD; PRT; 509 AA.
AC Q42456;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Aspartic proteinase oryzaasin 1 precursor (EC 3.4.23.-).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare / Japonica; TISSUE=Seed;
RX MEDLINE=96048031; PubMed=7556174;
RA Asakura T., Watanabe H., Abe K., Arai S.;
RT "Rice aspartic proteinase, oryzaasin, expressed during seed ripening
RT and germination, has a gene organization distinct from those of
RT animal and microbial aspartic proteinases."
RL Eur. J. Biochem. 232:77-83(1995).
CC -1- DEVELOPMENTAL STAGE: SEED RIPENING AND GERMINATION.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D32165; BAA06876.1; -.
DR EMBL; D32144; BAA06875.1; -.
DR HSSP; P42210; IQDM.
DR MEROPS; A01.020; -.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001369; Aspprotease_site.
DR InterPro; IPR000004; SappB.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR ProDom; PD001732; SappB; 1.
DR SMART; SM00118; SAPPB; 2.
DR PROSITE; PS00141; ASP_PROTEASE; 2.
KW Hydroxylase; Aspartyl protease; Zymogen; Glycoprotein; Signal.
FT SIGNAL 1
FT PROPEP 21
FT CHAIN 68
FT DOMAIN 318
FT ACT SITE 103
FT ACT SITE 290
FT DISULFID 116
FT DISULFID 122
FT DISULFID 281
FT DISULFID 285
FT DISULFID 428
FT CARBOHYD 252
FT CARBOHYD 252
FT CARBOHYD 400
FT SEQUENCE 509 AA; 54145 MW; 182F5DADA4CB358 CRC64;

Query Match 11.7%; Score 313.5; DB 1; Length 509;
Best Local Similarity 23.0%; Pred. No. 2.5e-15;
Matches 127; Conservative 75; Mismatches 179; Indels 171; Gaps 19;

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QY 3 ALAPALLPLLAQMLLAAPDELAPFTLPLRVAAATNRVAPRPGCTPAERHADGLAL 62
Db 5 SVALVLLAAVLLQALLPLPASAEGLVRIALKRPIDENSRYAARLSG-----EGCARLGL 59
QY 63 ALBPALASPAGAAFLAMVNLQDSSGRGYYLEMLIGTPQKQLIVDTGSSN----- 115
Db 60 RGANSLGGGGEGEDIVALKYMNQ-----YFGEIGVGTTPQKFLVITDTSSNLMVPSAK 115
QY 116 --FAVAGTPHSYIDTYEDTERSSYTRSKGFDVYKTYOGSWTGVGDELVTIPKFNSTF 173
Db 116 CYFSIACFHS-----RYKSGGSTYQKNGKPAIOYGTGSIAGFPSSDSVTVGD----- 165
QY 174 LVNIATTFESENFP-----LRGI-----KMGILGLAATLAKPSSSLETFFSLVQTANI 224
Db 166 ----LVKODEFLEATKEPEGLTPMAKFGIILGLGFEQISVGD-----V 206
QY 225 PNVSMMQCG-AGL/PVAGSTN-----GGSLVGGIGEPSELKYGDIMYPIKEWYQI 276
Db 207 PWTIKMVEQGLVSEPVFSFWRNRHSDGEGEIVFGMDPSHYGNHTYVPSQKGYWQF 266
QY 277 EILKLEIGGOSLNDCREYNADKAIVDGTTLLRLPKQVPDAVVEAVARASLIPE----- 331
Db 267 EMGDVLIGKTTGF-CA--SGCSAIDSGTSLAGPTAITIEINEXIKATGVSQECKTV 323
QY 332 -----PSDGF----- 336
Db 324 VSQYGOQILDLLLAETOPSKICSGVGLCTPDGKHGVSAGIKSVVDDEAGESNGQSGPMC 383
QY 337 -----WTGSQLACMTNSETPMSY-----FPKISIVLRD 364
Db 384 NACEMAVVMQNLAKONKTODLLINYINOLCDKLPSPMGESSVDCGSIASPEISFTIGA 443
QY 365 ENSRSFRITLLPOLYIQPMWAGLNYECY---RFGISPTNAL-VIGATWMEGFYVIF 419
Db 444 K-----KFAKPEEYIL-KYGEGAAACIGSTFAMDIPPRGRLMLIGDVFMAGYHTVF 496
QY 420 DRAQKRVGFPAAS 431
Db 497 DYGRKRVGFPAAS 508

RESULT 11
PEPC_RAT STANDARD; PRT; 392 AA.
AC P04073;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Gastricisin precursor (EC 3.4.23.3) (Pepsinogen C).
GN PGC.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar;
RX MEDLINE=8925508; PubMed=2722863;
RA Ishihara T., Ichihara Y., Hayano T., Katsura I., Sogawa K.,
RA Fujii-Kuriyama Y., Takahashi K.;
RT "Primary structure and transcriptional regulation of rat pepsinogen C
RT gene."
RL J. Biol. Chem. 264:10193-10199(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar;
RX MEDLINE=87054020; PubMed=3780741;
RA Ichihara Y., Sogawa K., Morohashi K., Fujii-Kuriyama Y., Takahashi K.;
RT "Nucleotide sequence of a nearly full-length cDNA coding for
RT pepsinogen of rat gastric mucosa."
RL Eur. J. Biochem. 161:7-12(1986).
RN [3]
RP SEQUENCE OF 16-112.

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RC STRAIN=Miscar;
RX MEDLINE=84257697; PubMed=6743670;
RA Arai K.M., Muto N., Tani S., Akahane K.;
RT "The N-terminal sequence of rat pepsinogen.";
RL Biochim. Biophys. Acta 788:256-261(1984)
CC -1- CATALYTIC ACTIVITY: More restricted specificity than pepsin A, but
CC shows preferential cleavage at Tyr-I-Xaa bonds; high activity
CC towards hemoglobin as substrate.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M25993; AAA41827.1; JOINED.
DR EMBL; M25985; AAA41827.1; JOINED.
DR EMBL; M25986; AAA41827.1; JOINED.
DR EMBL; M25987; AAA41827.1; JOINED.
DR EMBL; M25988; AAA41827.1; JOINED.
DR EMBL; M25989; AAA41827.1; JOINED.
DR EMBL; M25990; AAA41827.1; JOINED.
DR EMBL; M25991; AAA41827.1; JOINED.
DR EMBL; M25992; AAA41827.1; JOINED.
DR EMBL; X04644; CAA28305.1; JOINED.
DR PIR; A24608; A24608.
DR PIR; A05145; A05145.
DR PIR; A3510; A3510.
DR HSSP; P20142; IAVF.
DR MEROPS; A01.003; -.
DR InterPro: IPR001461; AsproteaseA1.
DR InterPro: IPR001969; Asprotease_site.
DR Pfam; PF00026; asp.1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; 2.
KW Hydrolyase; Aspartyl protease; Zymogen; Digestion; Signal.
FT SIGNAL 1 16
FT PROPEP 17 62 ACTIVATION PEPTIDE.
FT CHAIN 63 392 GASTRININ.
FT ACT_SITE 94 94
FT ACT_SITE 280 280
FT DISULFID 107 112 BY SIMILARITY.
FT DISULFID 270 275 BY SIMILARITY.
FT DISULFID 314 347 BY SIMILARITY.
FT CONFLICT 31 31 E -> Q (IN REF. 3).
FT CONFLICT 103 103 S -> A (IN REF. 3).
FT CONFLICT 109 109 S -> L (IN REF. 3).
SQ SEQUENCE 392 AA; 42833 MW; 092A5EAF2783EDD1 CRC64;
Query Match 11.6%; Score 313; DB 1; Length 392;
Best Local Similarity 29.5%; Pred. No. 1.9e-15;
Matches 105; Conservative 56; Mismatches 139; Indels 56; Gaps 16;
QY 92 YLLEWLGTPPOKQIIVDTGSSNFAV-----AGTPHSIDITVPFERSSTYRSKGF 143
DB 76 YFGEISITPPQNPVLVLDTGSSNLMWSSVYCQSEACTTHA---RFPSSKSTIYTBGQ 131
QY 144 DVYKTYGTGSGTGFVGEDLVTTIPKGFNTSFLVNIATIFESSENFLLPG-----IKWNGILG 198
DB 132 TFSIQYGTGSLTGFGYDTLTV-----QSIQVNPGEFGLSEN--EPGTFVYAQFDGLMG 184
QY 199 LAYATLAPSSSLTFPFSLVQANIPVFSWQMGAGLPVAGS--GNGSGLVIGIEP 256
DB 185 LAYPLPS--SGATTLAQMLGE---GALSQPLFGVYL---GSQOQSGNGQIVFVGVDK 235
QY 257 SLVKGDIVYTIKPEWYQIETLKLEIGGOSLNLDCREYNADKAVDSGTTLLRPOKVF 316
DB 236 NLTYGEITWVETQGLYQITIDPLIDGQASGM--CSSQGC--QGLVDTGTSILVWPAQYL 293
QY 317 DAVEAVARASLIPEFSDGFWTGSQACWNSSETPWSYFPKISIVLRDENSRSFRITIL 376

DB 294 SELQITIAQD--GEYGEYF-----VSCDSVSS-----LPTLSFVL-----NGVQPLS 335
QY 377 POLY-IOPMGAGINVECYRGISPTNALIGATVMEGFVIFDRAQRYGPAAS 431
DB 336 PSSYIIQEDNFCWGLEISITLSGSGQPLWILGDVFLASVYALFDMGNKKVGLATS 391
RESULT 12
PEPE CHICK STANDARD; PRT; 363 AA.
AC P16476;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Embryonic pepsinogen precursor (EC 3.4.23.-).
OS Gallus gallus (chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_Taxid=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88227903; PubMed=3131317;
RA Hayashi K., Agata K., Mochii M., Yaeguchi S., Eguchi G., Mizuno T.;
RT "Molecular cloning and the nucleotide sequence of cDNA for embryonic
RT chicken pepsinogen: phylogenetic relationship with prochymosin.";
RL J. Biochem. 103:290-296(1988).
CC -1- DEVELOPMENTAL STAGE: SPECIFICALLY SECRETED DURING THE EMBRYONIC
CC PERIOD IN THE CHICKEN PROVENTRICULUS (GLANDULAR STOMACH).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D00215; BAA00153.1; -.
DR PIR; A41443; A41443.
DR HSSP; P00794; 4CMS.
DR MEROPS; A01.028; -.
DR InterPro: IPR001461; AsproteaseA1.
DR InterPro: IPR001969; Asprotease_site.
DR Pfam; PF00026; asp.1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; 2.
KW Hydrolyase; Aspartyl protease; Digestion; Signal; Glycoprotein.
FT SIGNAL 1 16
FT CHAIN 17 383
FT ACT_SITE 94 94 EMBRYONIC PEPSINOGEN.
FT ACT_SITE 276 276 BY SIMILARITY.
FT DISULFID 107 112 BY SIMILARITY.
FT DISULFID 267 271 BY SIMILARITY.
FT DISULFID 310 344 BY SIMILARITY.
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 204 204 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 309 309 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 51 51 T -> S.
SQ SEQUENCE 383 AA; 41719 MW; 1642796671611554 CRC64;
Query Match 11.5%; Score 310; DB 1; Length 383;
Best Local Similarity 26.8%; Pred. No. 3e-15;
Matches 106; Conservative 63; Mismatches 136; Indels 90; Gaps 15;
QY 56 HA--DGLALNLEPPLAPAGANFLAVWDNLQDSGSGYVLEMIIGTPPOKQIIVDTGS 113
DB 55 HAPPDVLTIVTEPL-----NTLDW-----EYGTGTSIGTPPODFVTFVPTGS 97
QY 114 SNFAVAG---TPHSYIDTVFERSSTYRSKGFDTVTKYTGSGWTFVGEDLVITPKGF 169

Db 98 SNLWPSVSTSPACQSHQMFNPSSSTFKSTGQNLISHYTGDMEGTVCDTVTVASIM 157
 Qy 170 NTSFLVNTATIFESENFLPGIKXNGIIGLAATATLAKPSSSLETFPDSLVYQANI-PNVE 228
 Db 158 DTNQLFGJST-SEPGQFFV-YKFFQDILGLGPSLA--ADGTFPVDDNNVNSLSLEQNL 213
 Qy 229 SMOWCAGLPVAGSGTNGSLVIGIEPSLYKGDWYTPPIKEWYQYQIETLLEIGQSL 288
 Db 214 SVYLSREEM-----GSMVYFGGIDBSYFLTGSINMIIPVSYQGWQJMSDSIYNKQEI 265
 Qy 289 NLDCEYVADKAIYDSGTTLLRLPKQVDPDAVEAVARASLIPEFSDGFWTSGQLACWTNS 348
 Db 266 ACS-----SGCQAIIDTGTSLVAGPASPDIINDIOSAVG-----ANQ 300
 Qy 349 EFPNMFYFKRISTYLADENSSRFRTIILPOLYIQPMGAGLNY-----ECY 394
 Db 301 NYGGEY-----SVNCSHILAMPDVVF--VTG-GIQYPPVAPALATYRONGQGTCTM 345
 Qy 395 RFGISPTALVIGATVMEGFYVIFDPAQKRVGFA 429
 Db 346 SSFQNSSADWLITGDVFIKVYYSIFDRANNRVGLA 380

RESULT 13

CATD_HUMAN STANDARD; PRT; 412 AA.
 AC P07339;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cathepsin D precursor (EC 3.4.23.5).
 GN CTSD.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85270436; PubMed=3927292;
 RA Faust P.L., Kornfeld S., Chirgwin J.M.;
 RT "Cloning and sequence analysis of cDNA for human cathepsin D";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:4910-4914(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87231068; PubMed=3588310;
 RA Westley B.R., May F.E.B.;
 RT "Oestrogen regulates cathepsin D mRNA levels in oestrogen responsive
 human breast cancer cells";
 RL Nucleic Acids Res. 15:3773-3786(1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91299158; PubMed=2069717;
 RA Redeker B., Heckendorf B., Grosch H.W., Wersmann G., Hasilik A.;
 RT "Molecular organization of the human cathepsin D gene";
 RL DNA Cell Biol. 10:423-431(1991).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Straube B.R.;
 RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 1-22 FROM N.A.
 RX MEDLINE=94085791; PubMed=8262386;
 RA May F.E., Smith D.J., Westley B.R.;
 RT "The human cathepsin D-encoding gene is transcribed from an estrogen-
 regulated and a constitutive start point";
 RL Gene 134:277-282(1993).
 RN [6]
 RP SEQUENCE OF 1-22 FROM N.A.
 RX MEDLINE=95021301; PubMed=7935485;
 RA Augereau P., Miralles F., Cavailles V., Gaudelot C., Parker M.,
 RA Rochefort H.;

RT "Characterization of the proximal estrogen-responsive element of
 human cathepsin D gene";
 RL Mol. Endocrinol. 8:693-703(1994).
 RN [7]
 RP SEQUENCE OF 170-180.
 RC TISSUE=Liver;
 RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,
 RA Paqualli C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R.,
 RA Appel R.D., Hughes G.J.;
 RL Submitted (JUN-1992) to the SWISS-PROT data bank.
 RN [8]
 RP VARIANT VAL-58.
 RX MEDLINE=20179010; PubMed=10716266;
 RA Passasotriopoulos A., Bagli M., Kurz A., Kornhuber J., Forestl H.,
 RA Maier W., Pauls J., Lautenschlager N., Heun R.;
 RT "A genetic variation of cathepsin D is a major risk factor for
 Alzheimer's disease";
 RL Ann. Neurol. 47:399-403(2000).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
 RC TISSUE=Spleen;
 RX MEDLINE=93223670; PubMed=8467789;
 RA Metcalf P., Fusek M.;
 RT "Two crystal structures for cathepsin D: the lysosomal targeting
 signal and active site";
 RL EMBO J. 12:1293-1302(1993).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RC TISSUE=Liver;
 RX MEDLINE=93342076; PubMed=8393577;
 RA Baldwin E.T., Bhat T.N., Gulnik S., Hoeser M.V., Sowder R.C. II,
 RA Cachau R.E., Collins J., Silva A.M., Erickson J.W.;
 RT "Crystal structures of native and inhibited forms of human cathepsin
 D: implications for lysosomal targeting and drug design";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:6796-6800(1993).
 CC -1- FUNCTION: Acid protease active in intracellular protein breakdown.
 CC Involved in the pathogenesis of several diseases such as breast
 CC cancer and possibly Alzheimer's disease.
 CC -1- CATALYTIC ACTIVITY: Specificity similar to, but narrower than,
 CC that of pepsin A. Does not cleave the 4-Gln-His-5 bond in B
 CC chain of insulin.
 CC -1- SUBUNIT: CONSISTS OF A LIGHT CHAIN AND A HEAVY CHAIN.
 CC -1- SUBCELLULAR LOCATION: Lysosomal.
 CC -1- POLYMORPHISM: The Val-58 allele is significantly overrepresented
 CC in demented patients (11.8%) compared with nondemented controls
 CC (4.9%). Carriers of the Val-58 allele have a 3.1-fold increased
 CC risk for developing AD than noncarriers.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
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 CC -----
 DR EMBL; M1233; AAB59529.1; -;
 DR EMBL; X05344; CAA28955.1; -;
 DR EMBL; M63138; AAB51922.1; -;
 DR EMBL; M63134; AAB51922.1; JOINED.
 DR EMBL; M63135; AAB51922.1; JOINED.
 DR EMBL; M63136; AAB51922.1; JOINED.
 DR EMBL; M63137; AAB51922.1; JOINED.
 DR EMBL; BC016320; AAB16320.1; -;
 DR EMBL; L12980; AAB16314.1; -;
 DR EMBL; S74689; AAD14156.1; -;
 DR EMBL; S52557; AAD13868.1; -;
 DR PIR; A25771; KHHUD.
 DR PDB; 1LYA; 31-JAN-94.
 DR PDB; 1LYB; 31-JAN-94.
 DR MEROPS; A01.009; -;
 DR SWISS-2DPAGE; P07339; HUMAN.

DR Siena-2DPAGE: P07339; -
 DR Genew; HGNC:2529; CTSD.
 DR MIM; 116840; -
 DR InterPro; IPR001461; Asprotease1.
 DR InterPro; IPR001969; Asprotease_site.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PERSIN.
 DR PROSITE; PS00141; ASP_PROTEASE; 2.
 KW Hydrolyase; Aspartyl protease; Glycoprotein; Lysosome; Signal; Zymogen;
 KW Polymorphism; Alzheimer's disease; 3D-structure.
 FT SIGNAL 1 18
 FT PROPEP 1 64
 FT CHAIN 65 412
 FT CHAIN 65 412
 FT CHAIN 161 412
 FT CHAIN 169 412
 FT ACT_SITE 97 97
 FT ACT_SITE 295 295
 FT DISULFID 91 160
 FT DISULFID 110 117
 FT DISULFID 286 290
 FT DISULFID 329 366
 FT CARBOHYD 134 134
 FT CARBOHYD 263 263
 FT VARIANT 58 58
 N-LINKED (GLCNAC. . .).
 N-LINKED (GLCNAC. . .).
 A -> V (ASSOCIATED WITH INCREASED RISK IN
 AD, POSSIBLY INFLUENCES SECRETION AND
 INTRACELLULAR MATURATION; IN
 DBSNP:17571).
 /FTID=VAR_011621.

FT STRAND 67 74
 FT TURN 75 77
 FT STRAND 78 85
 FT TURN 86 89
 FT STRAND 90 97
 FT TURN 98 99
 FT STRAND 103 107
 FT TURN 108 109
 FT TURN 112 113
 FT HELIX 115 118
 FT TURN 119 119
 FT STRAND 123 123
 FT HELIX 125 127
 FT TURN 129 130
 FT STRAND 132 141
 FT STRAND 146 158
 FT STRAND 172 184
 FT HELIX 188 192
 FT STRAND 197 200
 FT HELIX 204 206
 FT HELIX 208 210
 FT HELIX 214 220
 FT TURN 221 222
 FT STRAND 228 233
 FT STRAND 243 247
 FT TURN 248 248
 FT HELIX 252 254
 FT STRAND 255 263
 FT STRAND 267 267
 FT TURN 268 269
 FT STRAND 270 279
 FT TURN 280 281
 FT STRAND 284 285
 FT TURN 287 288
 FT STRAND 290 294
 FT TURN 296 297
 FT STRAND 298 298
 FT STRAND 301 303
 FT HELIX 305 315
 FT TURN 316 316
 FT STRAND 318 319
 FT TURN 322 323
 FT STRAND 325 328
 FT HELIX 329 334
 FT STRAND 338 342

FT TURN 343 344
 FT STRAND 345 349
 FT HELIX 351 354
 FT STRAND 355 357
 FT TURN 359 362
 FT STRAND 365 368
 FT STRAND 370 372

Query Match 11.5%; Score 308.5; DB 1; Length 412;
 Best Local Similarity 27.1%; Pred. No. 4.3e-15;
 Matches 121; Conservative 75; Mismatches 180; Indels 71; Gaps 22;

9 LPLPLAQLPLAPELLAPPTLLPLVAAATNRVVAFTPG-----PCTPAERHADGIAL 62
 6 LPLPLAL--CLLAAP--ASALVRIPLHKFTSIRRTMSEVGSVEDLIAKPVSKYSQAVPA 61
 63 ALERPLASPAQANFLAVNDLQGDSSGRGYLEWLGTPPQKQLQIYDVTGSSNFRVACTP 122
 62 VTEGPT--PEVLKNYM-----DAQYGEIGIGTPPOCFVFPDGTSSNLMVPSIH 109
 123 HSYIDT-----YEDTERSTYRSKGFDPVTKYTGQSWTGFVGEDLVITP--KGFNTSFL 174
 110 CKLDIACWIIHKXNSDSSTVYKNGTSFDIHGSGSLSGYLSQDTVSVPCQSASSAGAL 169
 175 --VNIATTFESENFPLPGI-----KMGIGLAAYATLAKPSSSLETFFDSIVTQANI--PN 226
 170 GGVKVERGVPEEATFQGPITFLIAKFDGILGMAYPRIS--VNNVLPVVDNLMQQLVDQN 227
 227 VFSMCMGAGLPVAGSGTNGSLVLCGIEPSLYKGDIMYTIKEMVQYIILKLEIGQ 286
 228 IFSEY----LSRDPDAPGGEMLGTDSTKYKGSLSYLVNTRKAWQVHLDQEV--AS 281
 287 SLNLDCREYNADKAIIVDSGTTILRLPKVFDAVVEAVARASLIPEFSDGFWTGSOLACMT 346
 282 GLTL-CKR--GCEALVDGTSLMWGP---VDEVELQKALGAVLLQGEY----MIPC-- 329
 347 NSETPWSYFPKISLYLRDENSRSRFRITLPOLYIQPMGAGLVECYR--GISPESTN 403
 330 --EKVSTLPATLKL-----CGKGYKLS--PEDYTLKVSQAKTLCLSGFMGMIDIPPPSG 380
 404 AL-VIGATMEGFYIIPDRAKRYGFA 429
 381 PLWILGDVFIGRYTYVFDNRNVRGFA 407

RESULT 14
 CATD_MOUSE STANDARD; PRT; 410 AA.
 ID CATD_MOUSE
 AC P18242;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cathepsin D precursor (EC 3.4.23.5).
 GN CTSD.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=91088345; PubMed=2263503;
 RA Diederich J.F., Staakus K.A., Retzel E.F., Haase A.T.;
 RT "Nucleotide sequence of a cDNA encoding mouse cathepsin D.";
 RL Nucleic Acids Res. 18:7184-7184(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=90326544; PubMed=2374732;
 RA Grusby M.J., Mitchell S.C., Glimcher L.H.;
 RT "Molecular cloning of mouse cathepsin D.";
 RL Nucleic Acids Res. 18:4008-4008(1990).
 RN [3]
 RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J;
 RX MEDLINE=94280622; PubMed=8011168;
 RA Herman M., Perschl A., Saftig P., von Figura K., Peters C.;
 RT "Mouse cathepsin D gene: molecular organization, characterization of
 the promoter, and chromosomal localization.";
 RL DNA Cell Biol. 13:419-427(1994).
 CC -1- FUNCTION: Acid protease active in intracellular protein breakdown.
 CC -1- CATALYTIC ACTIVITY: Specifically similar to, but narrower than,
 that of pepsin A. Does not cleave the 4-Gln-His-5 bond in B
 chain of insulin.
 CC -1- SUBUNIT: CONSISTS OF A LIGHT CHAIN AND A HEAVY CHAIN.
 CC -1- SUBCELLULAR LOCATION: Lysosomal.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.

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 DR EMBL; X53337; CAA37423.1; -;
 DR EMBL; X52886; CAA37067.1; -;
 DR EMBL; X68378; CAA48453.1; -;
 DR EMBL; X68379; CAA48453.1; JOINED.
 DR EMBL; X68380; CAA48453.1; JOINED.
 DR EMBL; X68381; CAA48453.1; JOINED.
 DR EMBL; X68382; CAA48453.1; JOINED.
 DR EMBL; X68383; CAA48453.1; JOINED.
 DR PIR; S14704; KHMED.
 DR HSSP; P07339; ILVB.
 DR MEROPS; A01.009; -;
 DR MGD; MGI:88562; Ctcd.
 DR InterPro; IPR001461; Aspproteasea1.
 DR InterPro; IPR001969; Aspprotease_site.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPsin.
 DR PROSITE; PS00141; ASP_PROTEASE; 2.
 KW Hydrolyase; Aspartyl protease; Glycoprotein; Lysosome; Zymogen; Signal.
 FT SIGNAL 1 20
 FT PROPEP 21 64
 FT CHAIN 65 410
 FT ACT SITE 97 97
 FT ACT SITE 293 293
 FT DISULFID 91 160
 FT DISULFID 110 117
 FT DISULFID 284 288
 FT DISULFID 327 364
 FT CARBOHYD 134 134
 FT CARBOHYD 261 261
 SEQUENCE 410 AA; 44954 MW; DC4928BC4692BBF0 CRC64;
 Query Match 11.4%; Score 306.5; DB 1; Length 410;
 Best Local Similarity 27.5%; Pred. No. 5, 9e-15;
 Matches 103; Conservative 64; Mismatches 123; Indels 85; Gaps 15;
 QY 92 YLEMIIGTPQQLQILVTGSSNFAVAGTPHSHYDT-----YPTESSTYRSKGFV 145
 DB 79 YGDDIGITPPQCFVTFVFTGSSNFWPSTHCKILDIACVHKKNSDKSTYVKKGTSP 138
 QY 146 TVKYTGSGTWGFEVDLVTIIPKGFNTSFLVNIAT---IFESENFPLPGI-----KNGNGL 197
 DB 139 DIHYGSGISGYSIDQTVSPCKSDSKARGIVYKQIF-GEATKPGIYFAVAKDGL 197
 QY 198 GLAVATLAPSSSLETFPSLVTQANI-PNVFSMQMGAGLPVAGSGTNGSLVIGIIEP 256
 DB 198 GNGYPIHS--VNVVLVPFQNLMOQKLVKNIFSFY-----LNNDPFGQGGELMLGCTDS 250
 QY 257 SLXGDIWTPPIKEWYIYQILEIKELIGGOSLMDREYNADAIYDSGTLILRLQKVF 316
 DB 251 KYHGBLSYLANVTKAYVQVHMDQLEVGNL-LTL-CK--GGCEAIYDTGSLVGVHEEV 306

QY 317 DAVEAVARASLIPEFSDGFTGSQLACWTNSETPMSIFPKISLYLDENSRSFRITIL 376
 DB 307 KELQKAIQAVPLI-----OGEWIPICEKXSSL 333
 QY 377 POLYIQPMWGMGLVYEC---YRGIS-----PSNNAVIGATWEG 414
 DB 334 FTVYK--LG-GKQVELHPDKYILIKVSGGKTTCLSGFMCMDIPPSGPLWIDGVIFGS 390
 QY 415 FYVIFDRAQKRVGFA 429
 DB 391 YTVFEDRNRRNVGFA 405
 RESULT 15
 RENS_MOUSE STANDARD; PRT; 401 AA.
 ID RENS_MOUSE
 AC P00796; P97955; Q62155; P70229;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUN-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Renin precursor, submandibular gland (EC 3.4.23.15)
 DE (Angiotensinogenase).
 GN RENS2.
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE OF 64-351 AND 354-401.
 RX MEDLINE=85014991; PubMed=6812055;
 RA Misono K.S., Chang J.-D., Inagami T.;
 RT "Amino acid sequence of mouse submaxillary gland renin.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:4858-4862(1982).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82220074; PubMed=6283373;
 RA Panthier J.-D., Foote S., Chambrind B., Strosberg A.D., Corvol P.,
 RA Rougeon F.;
 RT "Complete amino acid sequence and maturation of the mouse
 submaxillary gland renin precursor.";
 RL Nature 298:90-92(1982).
 RN [3]
 RP SEQUENCE OF 1-29 FROM N.A.
 RX MEDLINE=84298161; PubMed=6089205;
 RA Panthier J.-D., Dreyfus M., Roux D.T.L., Rougeon F.;
 RT "Mouse kidney and submaxillary gland renin genes differ in their 5'
 putative regulatory sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5489-5493(1984).
 RN [4]
 RP SEQUENCE OF 1-10 FROM N.A.
 RX MEDLINE=90108722; PubMed=2691339;
 RA But D.W., Mullins L.J., George H., Smith G., Brooks J., Pioli D.,
 RA Brammar W.J.;
 RT "The nucleotide sequence of a mouse renin-encoding gene, Ren-1d, and
 its upstream region.";
 RL Gene 84:91-104(1989).
 RN [5]
 RP SEQUENCE OF 1-30 FROM N.A.
 RX MEDLINE=85085936; PubMed=6392850;
 RA Field L.J., Philbrick W.M., Howles P.N., Dickinson D.P.,
 RA McGowan R.A., Gross K.W.;
 RT "Expression of tissue-specific Ren-1 and Ren-2 genes of mice:
 comparative analysis of 5'-proximal flanking regions.";
 RL Mol. Cell. Biol. 4:2321-2331(1984).
 RN [6]
 RP SEQUENCE OF 267-292 FROM N.A.
 RX MEDLINE=84057744; PubMed=6357783;
 RA Panthier J.-D., Rougeon F.;
 RT "Kidney and submaxillary gland renins are encoded by two non-allelic
 genes in Swiss mice.";
 RL EMBO J. 2:675-678(1983).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).

MEDLINE=92301530; PubMed=1608447;
 RA Dhanraj V., Dealwis C.G., Frazee C., Badasso M., Sibanda B.L.,
 RA Tickle I.J., Cooper J.B., Driessen H.P.C., Newman M., Aguilar C.,
 RA Wood S.P., Blundell T.L., Hobart P.M., Geoghegan K.F., Ammirati M.J.,
 RA Danley D.B., O'Connor B.A., Hoover D.J.;
 RT "X-ray analyses of peptide-inhibitor complexes define the structural
 RT basis of specificity for human and mouse renins.";
 RL Nature 357:466-472(1992).
 CC -I- FUNCTION: RENIN IS A HIGHLY SPECIFIC ENDOPEPTIDASE, RELATED TO
 CC PEPsin, WHOSE ONLY KNOWN FUNCTION IS TO GENERATE ANGIOTENSIN I
 CC FROM ANGIOTENSINOGEN IN THE PLASMA, INITIATING A CASCADE OF
 CC REACTIONS THAT PRODUCE AN ELEVATION OF BLOOD PRESSURE & INCREASED
 CC SODIUM RETENTION BY THE KIDNEY. ITS FUNCTION IN THE SALIVARY GLAND
 CC IS NOT UNDERSTOOD.
 CC -I- CATALYTIC ACTIVITY: Cleaves leu|- bond in angiotensinogen to
 CC generate angiotensin I.
 CC -I- SUBUNIT: DIMER OF A HEAVY CHAIN AND A LIGHT CHAIN JOINED BY A
 CC DISULFIDE BOND.
 CC -I- TISSUE SPECIFICITY: SUBMANDIBULAR GLAND.
 CC -I- MISCELLANEOUS: THE ACTIVE ENZYME ISOLATED FROM THE SUBMANDIBULAR
 CC GLAND HAS CATALYTIC AND ANTIGENIC ACTIVITIES SIMILAR TO RENAL
 CC RENIN.
 CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
 CC -I- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN IN HAVING 195-198
 CC LEU-SER-ARG-SER, WHICH IS DUE TO A SHIFT IN THE TRANSLATION
 CC READING FRAME, AND 395-VAL. THE AUTHORS' TRANSLATION FOR 99 AGREES
 CC WITH THAT SHOWN BUT DOES NOT AGREE WITH THE NUCLEIC ACID SEQUENCE.
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 DR EMBL; J06621; AAA40050.1; ALT_FRAME.
 DR EMBL; K02597; AAA40048.1; -.
 DR EMBL; M34191; AAA40046.1; -.
 DR EMBL; AF237860; AAA40047.1; -.
 DR PIR; A00988; REMS.
 DR PIR; B22058; B22058.
 DR PDB; 1SMR; 3I-JAN-94.
 DR MEROPS; A01.008; -.
 DR MGD; MGI:97899; Ren2.
 DR InterPro; IPR001461; Aspproteaseal.
 DR InterPro; IPR001969; Aspprotease_site.
 DR Pfam; PF00026; asp.1.
 DR PRINTS; PR00792; PEPsin.
 DR PROSITE; PS00141; ASP_PROTEASE; 2.
 DR Hydroclase; Aspartyl protease; Plasma; Signal; Zymogen;
 KM Submandibular gland; 3D-structure.
 FT SIGNAL 1 25 PROBABLE.
 FT PROPEP 26 63 ACTIVATION PEPTIDE.
 FT CHAIN 64 351 HEAVY CHAIN.
 FT CHAIN 354 401 LIGHT CHAIN.
 FT ACT_SITE 101 101
 FT ACT_SITE 286 286
 FT DISULFID 114 121
 FT DISULFID 277 281
 FT DISULFID 320 357
 FT CONFLICT 13 13 L -> W (IN REF. 4).
 FT STRAND 69 69
 FT STRAND 71 78
 FT TURN 79 81
 FT STRAND 82 89
 FT TURN 90 93
 FT STRAND 94 101
 FT TURN 102 103
 FT STRAND 107 111
 FT TURN 112 113
 FT TURN 116 117
 FT HELIX 119 123

FT STRAND 127 127
 FT HELIX 129 131
 FT TURN 133 134
 FT STRAND 136 146
 FT TURN 147 148
 FT STRAND 149 162
 FT TURN 163 164
 FT STRAND 165 176
 FT HELIX 179 182
 FT TURN 183 184
 FT STRAND 189 192
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 FT TURN 200 202
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 FT STRAND 216 216
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 FT HELIX 243 245
 FT STRAND 246 254
 FT STRAND 257 257
 FT TURN 258 261
 FT STRAND 262 270
 FT TURN 271 272
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 FT TURN 278 279
 FT STRAND 281 285
 FT TURN 287 288
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 FT HELIX 296 306
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 FT HELIX 320 325
 FT STRAND 329 333
 FT TURN 334 335
 FT STRAND 336 340
 FT HELIX 342 345
 FT STRAND 346 346
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 FT STRAND 356 359
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 FT STRAND 368 370
 FT STRAND 374 376
 FT HELIX 378 381
 FT TURN 382 383
 FT STRAND 384 389
 FT TURN 390 393
 FT STRAND 394 400
 SO SEQUENCE 401 AA; 44282 MW; D936931F91F82980 CRC64;
 Query Match 11.4%; Score 305.5; DB 1; Length 401;
 Best local Similarity 27.1%; Pred. No. 6.8e-15;
 Matches 121; Conservative 69; Mismatches 177; Indels 79; Gaps 21;
 Db 10 LPLAQLLRAPRLAPRLPLRVAATNRVAVPFGCTP-----ERADGLALA 63
 Db 6 MFLWALLLL-----WSPCTFSLP-----TGTTFERIPLRKMSVREILBERGDMTRL 54
 Qy 64 LE-----PALASPAGANFLAMVDNLQSGDSRGYLEMIGRPPOKLOLVDTGS 113
 Db 55 AEMDVFTKRSLDLPLISPVLTNYL-----NSQ-----YGEIGTGPOTFKVIFPTGS 104
 Qy 114 SNFAVAGTPHSY-----IDTYFDTERSSTYRSKGPDTVKYTOGSGTGVGEDLVTPK 167
 Db 105 ANLWVPSTKCSRLYLACGHSLSVSSSDSSYMEGDDFTIHYSGRVKGFLSGDSVTV-G 163
 Qy 168 GFNTSFLVNATIFESBNFLPLGKMGILGLAVATLAKSSSLSETFPDSLVTOANI-PN 226
 Db 164 GIVTQTFGEVTELLPLIPFML--AQPDGVLGMGP--AAQVGVGPVFDHILSGVLKER 219

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QY 227 VFSMOMCGAGLPVAGSGTNGSLVLGIEPSLYKGDWYTPYIKEMYQOIEILKLEIGQ 286
    |||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 220 VFSVYY-----NRGPHLLGGEVVLGSDPBEHYGDFFHYVLSKTDSDWQITMKGVSVG-- 271
    |||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 287 SLNDCREYNADKAIVDGTTLLRLPQKVFDVAVEAV-ARASLIPESDGFWTGSLACW 345
    |||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 272 SSTLLCEE--GCEVVVDTGSSPFIAPTSCLKLIMQALGAKERLHEY-----VWSC- 320
    |||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 346 TNSETPMWYFPKISLYLDENSSRSFRITILPQLYIQPMGAGL-NYECYRFGISPTNA 404
    |||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 321 --SQVP--TLPDISFNL---GGRAYTLLSSTDYVLOYPNRKPKLCTVALHAMDIPPTGP 372
    |||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 405 L-VIGATWMEGFYVIFDRRAQKRVGFA 429
    |||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 373 VMVLGATFIRKYTEFDRHNNRIGFA 398
    |||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

Search completed: April 1, 2003, 11:32:44
 Job time : 17 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 1, 2003, 11:29:48 ; Search time 92 Seconds
(without alignments)
1160.135 Million cell updates/sec

Title: US-09-668-314C-2
Perfect score: 2687
Sequence: 1 MGALRALLLPLLAQWLLRA.....RPRDPEVNDSSIVRHMK 518

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SPTREMBL_21:.*
2: sp_archaea:.*
3: sp_bacteria:.*
4: sp_fungi:.*
5: sp_human:.*
6: sp_invertebrate:.*
7: sp_mammal:.*
8: sp_mhc:.*
9: sp_organelle:.*
10: sp_phase:.*
11: sp_plant:.*
12: sp_ricent:.*
13: sp_virus:.*
14: sp_vertebrate:.*
15: sp_unclassified:.*
16: sp_rvirus:.*
17: sp_bacteriaph:.*
17: sp_archaeap:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2395	89.1	514	11	Q9JL18
2	2375	88.4	468	4	Q2N2L2
3	2293	85.3	439	4	Q9H2V8
4	1966	73.2	396	4	Q9N2L1
5	1246	46.4	255	11	Q9R1P7
6	1183.5	44.0	532	4	Q9ULS1
7	1068	39.7	476	4	Q9BYC1
8	1025.5	38.2	457	4	Q9BYC0
9	925	34.4	432	4	Q9BYB9
10	651	24.2	266	11	Q9CUD5
11	461	17.2	213	4	Q9P0D2
12	386	14.4	244	5	Q8W0Y9
13	367.5	13.7	383	13	Q9DEC3
14	361.5	13.5	389	6	Q9GMV4
15	355.5	13.2	384	13	Q91322
16	355	13.2	389	13	Q9PWK1

17	355	13.2	389	13	Q9W643	Q9W643 gallus gall
18	351.5	13.1	389	6	Q9GMV5	Q9GMV5 sinicus muri
19	351.5	13.1	389	6	Q9GMV3	Q9GMV3 rhinolophus
20	335.5	12.5	388	6	Q9GMV2	Q9GMV2 oryctolagus
21	334.5	12.4	391	5	Q9VKP6	Q9VKP6 drosophila
22	326	12.1	399	13	Q93458	Q93458 podarcis si
23	324.5	12.1	372	5	Q9VLK3	Q9VLK3 drosophila
24	324.5	12.1	383	13	Q9DE45	Q9DE45 salvelinus
25	322.5	12.0	390	6	Q8SQ41	Q8SQ41 canis famli
26	322.5	12.0	397	13	Q9W6D4	Q9W6D4 hyobius lae
27	320	11.9	387	13	Q9DEC4	Q9DEC4 rana catesb
28	319.5	11.9	387	13	Q9DDV5	Q9DDV5 salvelinus
29	319	11.9	419	5	Q9SVA2	Q9SVA2 cionorchis
30	318.5	11.9	396	13	Q93428	Q93428 chionodraco
31	316	11.8	378	13	Q9PUP9	Q9PUP9 pseudopleur
32	316	11.8	392	11	Q9D7R7	Q9D7R7 mus musculu
33	315.5	11.7	366	13	Q9D6X3	Q9D6X3 clupea hare
34	313	11.6	383	5	Q76856	Q76856 dictyosteli
35	312.5	11.6	354	5	Q9G1X7	Q9G1X7 boophilus m
36	305	11.4	384	13	Q9DEC2	Q9DEC2 xenopus lae
37	302	11.2	398	13	P87370	P87370 oncorhynch
38	301.5	11.2	401	11	Q91X66	Q91X66 mus musculu
39	300.5	11.2	366	6	Q9BCU5	Q9BCU5 bos taurus
40	295.5	11.0	390	6	Q9GK10	Q9GK10 camelus dro
41	295	11.0	376	13	Q9PUP8	Q9PUP8 pseudopleur
42	295	11.0	387	6	Q9GMV8	Q9GMV8 sorex ungu
43	294	10.9	413	3	Q14413	Q14413 pichia angu
44	293.5	10.9	386	6	Q9GMV7	Q9GMV7 rhinolophus
45	292	10.9	386	6	Q9GMV6	Q9GMV6 canis famli

ALIGNMENTS

RESULT 1	Q9JL18	PRELIMINARY;	PRT;	514 AA.
ID	Q9JL18			
AC	Q9JL18;			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DS	Aspartyl protease 1.			
GN	BACE2.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Choi D.K., Sugano S., Sakaki Y.;			
RT	"Molecular characterization of the mouse Aspl gene, a homolog of the			
RT	human Aspl (Down Syndrome Region aspartyl protease).";			
RL	Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF216310; AAF36599.1; -.			
DR	HSSP; P33329; IYPS.			
DR	MEROPS; A01.041; -.			
DR	MGI; MGI:1860440; Bace2.			
DR	InterPro; IPR001461; AsparticaseA1.			
DR	InterPro; IPR001969; AsparticaseA1.			
DR	Pfam; PF00026; asp. 1.			
DR	PRINTS; PR00792; PEPsin.			
DR	PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_2.			
KW	PROTEASE.			
SO	SEQUENCE 514 AA; 55799 MW; A70725F2C1DF5B47 CRC64;			
Query Match	89.1%; Score 2395; DB 11; Length 514;			
Best Local Similarity	88.6%; Pred. No. 1,4e-173;			
Matches	459; Conservative 20; Mismatches 35; Indels 4; Gaps 1;			

QY 1 MGALRALLLPLLAQWLLRAPEFTLPLEVAATNRVVAPTGCPARRHNDGL 60
DB 1 MGALRALLLPLLAQWLLSAVPAAPFTLPLOVAGATNRASAVPGLTPELRADGL 60

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QY 61 ALALEPALASPAGANFLAMVDNLQDSSGRGYLLEMLIGTPQKQLIVDTGSSNFAVAG 120
D 61 ALALEPVAAT-----ANFLAMVDNLQDSSGRGYLLEMLIGTPQKQLIVDTGSSNFAVAG 116
QY 121 TPHSYIDTYFPTERRSSTYRSKGFVDVTKYTGSGWTGFGVEDLVITIPKGFNTSFLVNIATI 180
D 121 TPHSYIDTYFPTERRSSTYRSKGFVDVTKYTGSGWTGFGVEDLVITIPKGFNTSFLVNIATI 180
QY 117 APHSYIDTYFDSSESSSTYRSKGFVDVTKYTGSGWTGFGVEDLVITIPKGFNTSFLVNIATI 176
D 117 APHSYIDTYFDSSESSSTYRSKGFVDVTKYTGSGWTGFGVEDLVITIPKGFNTSFLVNIATI 176
QY 181 FESENFPLPGIKMNGILGLAVATLAKPSSSLETFPDSLVTOANI PNVSQMCGAGLPVA 240
D 177 FESENFPLPGIKMNGILGLAVATLAKPSSSLETFPDSLVTOANI PNVSQMCGAGLPVA 236
QY 241 GSGTNGGSLVUGIEPISLYKGDVITWTPPIKEWYQIETLKEIGGOSLNLDCREYNADKA 300
D 237 GSGTNGGSLVUGIEPISLYKGDVITWTPPIKEWYQIETLKEIGGOSLNLDCREYNADKA 296
QY 301 IVDGTTLLRLPQKVPDAVAVARASLIPFSDGFWTGSQACMTNSTETPWSYFPKISI 360
D 297 IVDGTTLLRLPQKVPDAVAVARASLIPFSDGFWTGSQACMTNSTETPWSYFPKISI 356
QY 361 YLRDENSRSRFRITILPOLYIOPMMGAGLANECYRFGISPTNALVIGATVMEGFYVIFD 420
D 357 YLRDENSRSRFRITILPOLYIOPMMGAGLANECYRFGISPTNALVIGATVMEGFYVIFD 416
QY 421 RAQKRVGFPAAPCAEIAAGAAVSEISGPFSTEDVASCNCPAQSISEPILMIVSYALMSVCG 480
D 417 RAQKRVGFPAAPCAEIAAGAAVSEISGPFSTEDVASCNCPAQSISEPILMIVSYALMSVCG 476
QY 481 ALLVLYLVLLLPFCQRRPRDPDEVNDSSLVHRMK 518
D 477 ALLVLYLVLLLPFCQRRPRDPDEVNDSSLVHRMK 514

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RESULT 2

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Q9NZL2 PRELIMINARY; PRT; 468 AA.
ID Q9NZL2
AC Q9NZL2
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Aspartyl protease.
GN BACE2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20422477; PubMed=10965118;
RA Solans A., Estivill X., de la Luna S.;
RT "A new aspartyl protease on 21q22.3, BACE2, is highly similar to
RT Alzheimer's amyloid precursor protein beta-secretase.";
RL Cytochrome c Cell Gene. 89:177-184(2000).
DR EMBL; AF188276; AAF35835.1; -.
DR HSSP; P00797; 2REN.
DR MEROPS; A01.041; -.
DR InterPro; IPR001461; AsproteaseA1.
DR InterPro; IPR001969; Asprotease_site.
DR Pfam; PF00026; asp.1.
DR PRINTS; PR00792; PEPIN.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_2.
KW Protease.
SQ SEQUENCE 468 AA; 50324 MW; 717E0920126A0142 CRC64;

```

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Query Match 88.4%; Score 2375; DB 4; Length 468;
Best Local Similarity 90.3%; Pred. No. 4e-172;
Matches 468; Conservative 0; Mismatches 0; Indels 50; Gaps 1;

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```

QY 1 MGALRALILPLLAQWLRAAPELAPAPFTLPLRVAAATNRVAPRPGGTPAERHADDL 60
D 1 MGALRALILPLLAQWLRAAPELAPAPFTLPLRVAAATNRVAPRPGGTPAERHADDL 60
QY 61 ALALEPALASPAGANFLAMVDNLQDSSGRGYLLEMLIGTPQKQLIVDTGSSNFAVAG 120

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D 61 ALALEPALASPAGANFLAMVDNLQDSSGRGYLLEMLIGTPQKQLIVDTGSSNFAVAG 120
QY 121 TPHSYIDTYFPTERRSSTYRSKGFVDVTKYTGSGWTGFGVEDLVITIPKGFNTSFLVNIATI 180
D 121 TPHSYIDTYFPTERRSSTYRSKGFVDVTKYTGSGWTGFGVEDLVITIPKGFNTSFLVNIATI 180
QY 181 FESENFPLPGIKMNGILGLAVATLAKPSSSLETFPDSLVTOANI PNVSQMCGAGLPVA 240
D 181 FESENFPLPGIKMNGILGLAVATLAKPSSSLETFPDSLVTOANI PNVSQMCGAGLPVA 240
QY 241 GSGTNGGSLVUGIEPISLYKGDVITWTPPIKEWYQIETLKEIGGOSLNLDCREYNADKA 300
D 241 GSGTNGGSLVUGIEPISLYKGDVITWTPPIKEWYQIETLKEIGGOSLNLDCREYNADKA 300
QY 301 IVDGTTLLRLPQKVPDAVAVARASLIPFSDGFWTGSQACMTNSTETPWSYFPKISI 360
D 301 IVDGTTLLRLPQKVPDAVAVARASLIPFSDGFWTGSQACMTNSTETPWSYFPKISI 358
QY 361 YLRDENSRSRFRITILPOLYIOPMMGAGLANECYRFGISPTNALVIGATVMEGFYVIFD 420
D 359 YLRDENSRSRFRITILPOLYIOPMMGAGLANECYRFGISPTNALVIGATVMEGFYVIFD 370
QY 421 RAQKRVGFPAAPCAEIAAGAAVSEISGPFSTEDVASCNCPAQSISEPILMIVSYALMSVCG 480
D 417 RAQKRVGFPAAPCAEIAAGAAVSEISGPFSTEDVASCNCPAQSISEPILMIVSYALMSVCG 430
QY 481 ALLVLYLVLLLPFCQRRPRDPDEVNDSSLVHRMK 518
D 477 ALLVLYLVLLLPFCQRRPRDPDEVNDSSLVHRMK 468

```

RESULT 3

```

Q9H2V8 PRELIMINARY; PRT; 439 AA.
ID Q9H2V8
AC Q9H2V8
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE CDAL3.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PHOCHROMOCYTOMA;
RA Han Z.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF212252; AAC41783.1; -.
DR HSSP; P00797; 2REN.
DR InterPro; IPR001461; AsproteaseA1.
DR InterPro; IPR001969; Asprotease_site.
DR Pfam; PF00026; asp.1.
DR PRINTS; PR00792; PEPIN.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 439 AA; 48275 MW; 02EC0B050F11602 CRC64;

```

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Query Match 85.3%; Score 2293; DB 4; Length 439;
Best Local Similarity 100.0%; Pred. No. 6.1e-166;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 80 MVDNLQDSSGRGYLLEMLIGTPQKQLIVDTGSSNFAVAGTPSHYIDTYFPTERRSSTYR 139
D 80 MVDNLQDSSGRGYLLEMLIGTPQKQLIVDTGSSNFAVAGTPSHYIDTYFPTERRSSTYR 139
QY 140 SKGFDVTKYTGSGWTGFGVEDLVITIPKGFNTSFLVNIATIFESENFPLPGIKMNGILGL 199
D 140 SKGFDVTKYTGSGWTGFGVEDLVITIPKGFNTSFLVNIATIFESENFPLPGIKMNGILGL 199
QY 200 AVATLAKPSSSLETFPDSLVTOANI PNVSQMCGAGLPVAGSGTNGGSLVUGIEPISLY 259
D 200 AVATLAKPSSSLETFPDSLVTOANI PNVSQMCGAGLPVAGSGTNGGSLVUGIEPISLY 259

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Db 121 AVATLAKPSSSLETFPDSLVTOANI.PNVFSMQMGAGL.PVASSGTNGSLVIGIEPSLY 180
Qy 260 KGDWYTPIKEEWWYQIEILKLEIGGOSLINDCREYNADKAIVDSGTTLLRLPQKVPFAV 319
Db 181 KGDWYTPIKEEWWYQIEILKLEIGGOSLINDCREYNADKAIVDSGTTLLRLPQKVPFAV 240
Qy 320 VEAVARASLIPEFSGFWTGSOLACWTNSETPWSYFPKISITLBDENSSRSFRITILLPOL 379
Db 241 VEAVARASLIPEFSGFWTGSOLACWTNSETPWSYFPKISITLBDENSSRSFRITILLPOL 300
Qy 380 YIOPMAGLNECYRFGISPTNALVIGATWEGFYVIFDRAOKRVGFAASPCAETIGA 439
Db 301 YIOPMAGLNECYRFGISPTNALVIGATWEGFYVIFDRAOKRVGFAASPCAETIGA 360
Qy 440 AVSEISGFSTEDVANSNCVPAQSLEPILMIVSVALMSVCGAILLVLLVLLPFCORR 499
Db 361 AVSEISGFSTEDVANSNCVPAQSLEPILMIVSVALMSVCGAILLVLLVLLPFCORR 420
Qy 500 PRDPEVNDDESLVHRWK 518
Db 421 PRDPEVNDDESLVHRWK 439

```

RESULT 4

```

Q9NZL1 PRELIMINARY; PRT; 396 AA.
ID Q9NZL1;
AC Q9NZL1;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Aspartyl protease.
GN BACE2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX MEDLINE=20422477; PubMed=10965118;
RA Solans A., Estivill X., de la Luna S.;
RT "A new aspartyl protease on 21q22.3, BACE2, is highly similar to
RT Alzheimer's amyloid precursor protein beta-secretase.";
RL Cytochrome Cell Genet. 89:177-184 (2000).
DR EMBL; AF188277; AAF35836.1; -.
DR HSSP; P00797; ZREN.
DR MEROPS; A01.041; -.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_2.
KW Protease.
SQ SEQUENCE 396 AA; 43013 MW; 5023A7AF39ICEAC9 CRC64;

```

Query Match 73.2%; Score 1966; DB 4; Length 396;
 Best Local Similarity 100.0%; Pred. No. 3.7e-141;
 Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 MGALABALLLPLAOMLIRAAPELAPFTLPLRYAATNRYVATPRGPAPRHAAGL 60
Db 1 MGALABALLLPLAOMLIRAAPELAPFTLPLRYAATNRYVATPRGPAPRHAAGL 60
Qy 61 ALALEPALASPAAGANFLAMVDNLQDSDGRGYLEMLIGTFPOKQIIVDTGSSNFAVAG 120
Db 61 ALALEPALASPAAGANFLAMVDNLQDSDGRGYLEMLIGTFPOKQIIVDTGSSNFAVAG 120
Qy 121 TPHSYIDTYFPTERSSTYRSKGFDTVTKYTGSGTWGFGEDLVITIPKGFNTSFLVNIAT 180
Db 121 TPHSYIDTYFPTERSSTYRSKGFDTVTKYTGSGTWGFGEDLVITIPKGFNTSFLVNIAT 180
Qy 181 FESNFPLPGIKMNGIILGLAATLAKPSSSLETFPDSLVTOANI.PNVFSMQMGAGL.PVA 240
Db 181 FESNFPLPGIKMNGIILGLAATLAKPSSSLETFPDSLVTOANI.PNVFSMQMGAGL.PVA 240

```

```

Qy 241 GSGTNGSSLVIGIEPSLYKGDWYTPIKEEWWYQIEILKLEIGGOSLINDCREYNADKA 300
Db 241 GSGTNGSSLVIGIEPSLYKGDWYTPIKEEWWYQIEILKLEIGGOSLINDCREYNADKA 300
Qy 301 IVDGTTLLRLPQKVPFAVAVARASLIPEFSGFWTGSOLACWTNSETPWSYFPKISI 360
Db 301 IVDGTTLLRLPQKVPFAVAVARASLIPEFSGFWTGSOLACWTNSETPWSYFPKISI 360
Qy 361 YLRDENSRSFRITILLPO 378
Db 361 YLRDENSRSFRITILLPO 378

```

RESULT 5

```

Q9RLP7 PRELIMINARY; PRT; 255 AA.
ID Q9RLP7;
AC Q9RLP7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Aspartyl protease (Fragment).
GN BACE2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RX SEQUENCE FROM N.A.
RA Accarino M., Fumagalli P., Taramelli R., Ottolenghi S.;
RT "Cloning of a gene from chromosome 21 Down Region encoding a potential
RT transmembrane protease.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF051150; AAD45964.1; -.
DR MEROPS; A01.041; -.
DR MD; MG1:1860440; Bace2.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
KW Non_Ter.
FT NON_TER 1
SQ SEQUENCE 255 AA; 28685 MW; 53DE317815996D63 CRC64;

```

Query Match 46.4%; Score 1246; DB 11; Length 255;
 Best Local Similarity 91.0%; Pred. No. 9.5e-87;
 Matches 232; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

```

Qy 264 WYTPIKEEWWYQIEILKLEIGGOSLINDCREYNADKAIVDSGTTLLRLPQKVPFAVEAV 323
Db 1 WYTPIKEEWWYQIEILKLEIGGOSLINDCREYNADKAIVDSGTTLLRLPQKVPFAVEAV 60
Qy 324 ARASLIPEFSGFWTGSOLACWTNSETPWSYFPKISITLBDENSSRSFRITILLPOLYIOP 383
Db 324 ARASLIPEFSGFWTGSOLACWTNSETPWSYFPKISITLBDENSSRSFRITILLPOLYIOP 120
Qy 61 ARTSLIPEFSGFWTGSOLACWTNSETPWSYFPKISITLBDENSSRSFRITILLPOLYIOP 120
Db 61 ARTSLIPEFSGFWTGSOLACWTNSETPWSYFPKISITLBDENSSRSFRITILLPOLYIOP 120
Qy 384 MMGAGLNECYRFGISPTNALVIGATWEGFYVIFDRAOKRVGFAASPCAETIGA 443
Db 121 MMGAGLNECYRFGISPTNALVIGATWEGFYVIFDRAOKRVGFAASPCAETIGA 180
Qy 444 ISGFSFTEDEVANSNCVPAQSLEPILMIVSVALMSVCGAILLVLLVLLPFCORRPRDP 503
Db 181 ISGFSFTEDEVANSNCVPAQSLEPILMIVSVALMSVCGAILLVLLVLLPFCORRPRDP 240
Qy 504 EVVNDDESLVHRWK 518
Db 241 EVVNDDESLVHRWK 255

```

RESULT 6

```

Q9ULS1 PRELIMINARY; PRT; 532 AA.
ID Q9ULS1;
AC Q9ULS1;

```

DT 01-MAY-2000 (TRENBLREL. 13, Created)
 DT 01-JUN-2001 (TRENBLREL. 18, Last sequence update)
 DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
 DE KIAA1149 protein (Fragment).
 GN KIAA1149.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 OX [1]
 RN
 RP SEQUENCE FROM N.A.
 RC
 RX MEDLINE=20039618; PubMed=10574461;
 RA Hironaka M., Nagase T., Ishikawa K., Kikuno R., Nomura N., Ohara O.;
 RT "Characterization of cDNA clones selected by the Genemark analysis
 RT from size-fractionated cDNA libraries from human brain."
 RL DNA Res. 6:329-336(1999).
 DR EMBL; AB032975; BAA86463.2; -.
 DR HSSP; P56272; IAMS.
 DR MEROPS; A01.004; -.
 DR InterPro; IPR001461; AspproteaseA1.
 DR InterPro; IPR001969; Aspprotease_site.
 DR Pfam; PF00026; asp.1.
 DR PRINTS; PR00792; PEPsin.
 DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
 DR NON TER
 SQ SEQUENCE 532 AA; 58720 MW; 98B135D0D5FBD2E8 CRC64;
 Query Match 44.0%; Score 1183.5; DB 4; Length 532;
 Best Local Similarity 47.8%; Pred. No. 1.6e-81;
 Matches 231; Conservative 81; Mismatches 154; Indels 17; Gaps 6;
 Oy 44 APTPPGPAERHAGLAL-----EPALSPAGANFLAVNDLQDSCRGYVLE 95
 Db 52 APSTASGCCAAMGAPGLRLPRTDEP--EEPGRRGSFVENVDNLKSGGGYVLE 109
 Oy 96 MLIGTPPKQLIVDTGSSNFAVAGTPHSYIDTYEDTERSSYRSKGFDTVTKYQGSWT 155
 Db 110 MIVGSPPTLNLIVDTGSSNFAVGAHPFLRLRYQROLSSYRDLRKGVVPTYQKME 169
 Oy 156 GFVEDLVITPKGFNTSFLVNIATTPESNFFLPGLIKNGILGLAVATLAKSSSLETFE 215
 Db 170 GELGTDLVSIHPGPVTVANITAITESDKFFINGSMGILGLAVAEIARDDSLPEPF 229
 Oy 216 DSLVQANIPNVFSMOMGAGLPVAGS---GTNGSLVVGIEPSLYKGDWYTPIKEM 272
 Db 230 DSLVQTHVPLFSLOLCAAGFPLNQSSEVLASVSGSMIIGIDHSLYTGSLWYTPIKEM 289
 Oy 273 YVOIEILKLEIGGOSLNDCREYNADKAIVDSGTTLLRLPKVFPDAVAVARASLIPF 332
 Db 290 YVEVLIIVREINQDLKMDCKEYNDKSIYDSGTTNLRPKVFEAAVAKSIKAASTKFE 349
 Oy 333 SDGFMTGSQLACWNTSETPWSYFPKTSIYLKRDENSSRSFRITILLPOLYIQPMAGGLNY 391
 Db 350 PGDFMLGEOLVCMQAGTTPMNIFFPVISLYLMEVTVNQSFRIITLLPOQYLRPEVDATSD 409
 Oy 392 ECFRRGISSTALVIGAVMGEFYIIPDAOKRGVFAASPCAELIGAIVSEISGPFSE 451
 Db 410 DCKYKAISGSTGTWGAIVMEGFVYFRRARRIGFAVSAGCHVDEFTAAVEGPFVL 469
 Oy 452 DVASNCVPAQSLSEPIILVSYALMSVCGAILLVILLVLLPFCOR--RPRDPEVNVDE 509
 Db 470 DMEDCGYNIPTQDESTLMTIAYMAIC-ALFPLPLCLMVCMQRCICRQCHDDPADDI 528
 Oy 510 SSL 512
 Db 529 STL 531

DT 01-JUN-2001 (TRENBLREL. 17, Created)
 DT 01-JUN-2001 (TRENBLREL. 17, Last sequence update)
 DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
 DE Beta-site App cleaving enzyme I-476.
 GN BACE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 OX [1]
 RN
 RP SEQUENCE FROM N.A.
 RC
 RX MEDLINE=21408467; PubMed=11516562;
 RA Tanahashi H., Tabita T.;
 RT "Three novel alternatively spliced isoforms of the human beta-site App
 RT cleaving enzyme (BACE) and their effect on amyloid beta-peptide
 RT production."
 RL Neurosci. Lett. 307:9-12(2001).
 DR EMBL; AB050436; BAB40931.1; -.
 DR HSSP; P33329; IYPS.
 DR InterPro; IPR001461; AspproteaseA1.
 DR InterPro; IPR001969; Aspprotease_site.
 DR Pfam; PF00026; asp.1.
 DR PRINTS; PR00792; PEPsin.
 DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
 DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
 SQ SEQUENCE 476 AA; 52907 MW; 6C8C87F8A953AF66 CRC64;
 Query Match 39.7%; Score 1068; DB 4; Length 476;
 Best Local Similarity 43.2%; Pred. No. 8.2e-74;
 Matches 224; Conservative 78; Mismatches 159; Indels 58; Gaps 10;
 Oy 7 ALLPFLAQMILRAPELAPAFPT----PLRVAAATNRVAVPTPGTPPAERHAGLA 61
 Db 2 AQLPFWLLWM---GAGVLPAGHGTQHGIRLRLRGLG-----GAPL-----GLR 42
 Oy 62 LALE--PALASPAANFLAVNDLQDSCRGYVLEMLIGTPPKQLIVDTGSSNFAV 119
 Db 43 LPRTDEEPPEPGRGSGFVENVDNLKSGGGYVEMTVGSPPTLNLIVDTGSSNFAVG 102
 Oy 120 GTPHSYIDTYEDTERSSYRSKGFDTVTKYQGSMTGFGVEDLVITPKGFNTSFLVNIAT 179
 Db 103 AAPHEFLRRYQROLSSYRDLRKGVVPTYQKMEGLGIDVLSIPHPVTVANITAA 162
 Oy 180 IFENSEFPLPKIKNGILGLAVATLAKSSSLETFPSLVQANIPNVFSMOMGAGLPV 239
 Db 163 ITESDKFFINSNMGILGLAVAEIAR-----LCAGFPL 197
 Oy 240 AGS---GTNGSLVVGIEPSLYKGDWYTPIKEMWYQIEILKLEIGGOSLNDCREYN 296
 Db 198 NQSEVLASVSGSMIIGIDHSLYTGSLWYTPIRREWYEVIIIVEINQDLKMDCKEYN 257
 Oy 297 ADKATVDSGTTLLRLPKVFPDAVAVARASLIPFSDGFMTGSQLACWNTSETPWSYFP 356
 Db 258 YDKSIVDSGTTNLRPKVFEAAVAKSIKAASTKFEFGFGLGEOLVCMQAGTTPMNIFF 317
 Oy 357 KISYILRDENSSRSFRITILLPOLYIQPMAGGLNY--ECYRRGISSTALVIGAVMEGF 415
 Db 318 VISLYLMEVTVNQSFRIITLLPOQYLRPEVDATGDDCKYKAISGSTGTWGAIVMEGF 377
 Oy 416 YVIFDAOKRGVFAASPCAELIGAIVSEISGPFSTEDVYASNCVPAQSLSEPIILVSYAL 475
 Db 378 YVIFDAOKRGVFAASPCAELIGAIVSEISGPFSTEDVYASNCVPAQSLSEPIILVSYAL 437
 Oy 476 MSVCGAILLVILLVLLPFCOR--RPRDPEVNVDESSL 512
 Db 438 AAIC-ALFPLPLCLMVCMQRCICRQCHDDPADDISLL 475

RESULT 7
 Q9BYC1 PRELIMINARY; PRT; 476 AA.
 AC Q9BYC1;
 DT 01-JUN-2001 (TRENBLREL. 17, Created)

RESULT 8
 Q9BYC0 PRELIMINARY; PRT; 457 AA.
 AC Q9BYC0;
 DT 01-JUN-2001 (TRENBLREL. 17, Created)

RESULT 10
 09CUCUS PRELIMINARY; PRT: 266 AA.
 ID 09CUCUS
 AC 09CUCUS;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Beta-site APP cleaving enzyme (Fragment).
 GN BACE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=BRAIN;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai Y., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arikawa T., Hara A., Fukunishi Y., Konno H., Adachi T., Fukuda S.,
 RA Aikawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batzlioglu S., Casavant T.,
 RA Flatschmann W., Gaasterland T., Gissi C., King B., Kochia H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nakado I., Pesole G., Quackenbush J.,
 RA Schirini L.M., Stubbli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baladrelli R., Barsh G.,
 RA Blake Y., Boffelli D., Bojunga N., Cantucci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whiteaker C., Wilming L.,
 RA Wyshak-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL; AK014390; BAB29317.1; -.
 DR MEROPS; A01.004; -.
 DR MCD; MGI:1346542; Bace.
 DR InterPro; IPR001461; Aspproteaseal.
 DR Pfam; PF00026; asp; 1.
 FT NON_TER 1
 SO SEQUENCE 266 AA; 30201 MW; B913FDA8ADBA4238 CRC64;
 Query Match 24.2%; Score 651; DB 11; Length 266;
 Best Local Similarity 45.5%; Pred. No.1.6e-41;
 Matches 121; Conservative 55; Mismatches 86; Indels 4; Gaps 3
 Oy 250 VIGIEPISLYKEDIWTPPIKREYVYIIEILKIEIGGOSLNDGREYNADKAIVDSITLL 309
 Db 1 IIGGIDHSLYTSLWTPPIRREYVEVILVIEINQDQDKMCKEYNYKSIYDSITLL 60
 Oy 310 RLPOKVFDDVVAVARASLIPERFSDGFMTGSOLACWTNSETPSPYKPSIYLRDENSRR 369
 Db 61 RLPKVFVFAVAASIKRASSTKTFPPGFWLGEOLVCMQAGTTPNITFPVSLYMGVTHQ 120
 Oy 370 SFRITTLPOLYIQPMWAGLNT-ECYRFGISPTNALVIGATVMEGFYVIFDRAQRVGF 428
 Db 121 SFRITTLPOQYLRPVEDVATSDODCYKFAVSGSSTGVWGAIVMEGFYVIFDRAQRIGF 180
 Oy 429 AASPCEAIGAVALSEISGPFSTEDVANSNCVPAQSLEPILMIVSYALMSVCGAILLVLLV 488
 Db 181 AASAGCHVHDEFTAAAEVGFVADMDCGYNIPTDSESTLMTIAYVMAIC-ALFMLPLC 239
 Oy 489 LILLPFCOR--RPRDPEVNDSSL 512
 Db 240 LNVQWRCGLRGLRHQHDFFADISLL 265
 RESULT 11

ID	Q9P0D2	PRELIMINARY;	PRT;	213 AA.
AC	Q9P0D2;			
DT	01-OCT-2000 (TReMBLrel. 15, Created)			
DT	01-OCT-2000 (TReMBLrel. 15, Last sequence update)			
DT	01-JUN-2002 (TReMBLrel. 21, Last annotation update)			
DE	HSPC104 (Fragment).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_TaxId=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=CORD BLOOD;			
RA	Zhang Q.H., Ye M., Zhou J., Shen Y., Wu X.Y., Guan Z.Q., Wang L.,			
RA	Fan H.Y., Mao Y.F., Dai M., Huang Q.H., Chen S.J., Chen Z.,			
RT	"Human partial CDS cloned from cd34+ stem cells."			
RL	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF161367; AAF28927.1; -			
DR	InterPro; IPR001461; Aspproteasea1.			
DR	Pfam; PF00026; asp.1.			
FT	NON_TER	1		
SO	SEQUENCE	213 AA;	24338 MW;	EC9D3FA31CFA835C CRC64;
Qy	Query March	17.24;	Score 461;	DB 4;
Qy	Best Local Similarity	51.54;	Pred. No. 3.2e-27;	Length 213;
Db	Matches	84;	Conservative	27;
Db			Mismatches	42;
Db			Indels	10;
Db			Gaps	1;
Qy	252 GGIPESLYKGDWYTPPIKEWYQIETLKELIGGOSLNLDCREYNADKAIVDSGTTLLRL 311			
Db	1 GGIHSLYTGSLWYTPPIRREWYEVIIYVRVINGODLKMCKEYNDKSIYDSGTTNRL 60			
Qy	312 PQKFPDAVVEAVASLIPFESDGFWGSQACWTNSTPMSYPPKISIIYLDENSSRSF 371			
Db	61 PKKFEAAVAKSIKKAASSTKEPDPDFWGEQYVCWQAGTTPNIPFVSLYLMGEVYNOSF 120			
Qy	372 RITLIPOLYIOPMMGAGLNYECVRFGISPTNALYIGATWEG 414			
Db	121 RITLIPQOYLRP-----WKMPRPKTTVTCHLTVIHG 153			
RESULT	12			
Q8MQY9				
AC	Q8MQY9;	PRELIMINARY;	PRT;	244 AA.
DT	01-MAR-2002 (TReMBLrel. 20, Created)			
DT	01-MAR-2002 (TReMBLrel. 20, Last sequence update)			
DT	01-JUN-2002 (TReMBLrel. 21, Last annotation update)			
DE	Asparate protease (Fragment).			
GN	App.			
OS	Apicomplexans vastus.			
OC	Eukaryota; Metazoa; Porifera; Hexactinellida; Hexastrophora;			
OC	Lyssastrosida; Rosellidae; Aphrocalistes.			
OX	NCBI_TaxId=83887;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Mueller W.E.G., Mueller I.M., Grebenjuk V.A.;			
RT	"Umecarzoa: Origin and evolution of the common ancestor of Metazoa."			
RL	Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AJ304963; CAC83293.1; -			
DR	InterPro; IPR001461; Aspproteasea1.			
DR	InterPro; IPR001969; Aspprotease_s1ce.			
DR	Pfam; PF00026; asp.1.			
DR	PROSITE; PS00141; ASP_PROTEASE; UNKNOWN 1.			
DR	PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN 1.			
FT	PROTEASE.			
FT	NON_TER	244		
SO	SEQUENCE	244 AA;	26366 MW;	6536902661E0E4C7 CRC64;
Qy	Query Match	14.44;	Score 386;	DB 5;
Qy	Best Local Similarity	39.34;	Pred. No. 2e-21;	Length 244;
Db	Matches	97;	Conservative	33;
Db			Mismatches	95;
Db			Indels	22;
Db			Gaps	8;